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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 21:15:13 ; Search time 392 Seconds
(Without alignments)
48.553 Million cell updates/sec

Title: US-09-735-363A-8

Perfect score: 3

Sequence: 1 gtc 3

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7173243 seqs, 3172129809 residues

Total number of hits satisfying chosen parameters: 1080

Minimum DB seq length: 0

Maximum DB seq length: 3

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	100.0	3	9	US-09-735-363A-8
2	3	100.0	3	9	US-09-816-763-10
3	3	100.0	3	14	US-10-127-645-1
4	3	100.0	3	15	US-10-264-280-4
5	3	100.0	3	15	US-10-264-280-8
6	3	100.0	3	19	US-10-686-317-13
7	3	100.0	3	19	US-10-686-317-48

3	100.0	3	19	US-10-821-568-10	Sequence 10, Appl
2	66.7	2	9	US-09-735-363A-50	Sequence 50, Appl
2	66.7	2	9	US-09-735-363A-51	Sequence 51, Appl
2	66.7	2	10	US-09-971-894-19	Sequence 19, Appl
2	66.7	2	10	US-09-852-903C-20	Sequence 20, Appl
2	66.7	2	13	US-10-027-632-52280	Sequence 52280, A
2	66.7	2	13	US-10-027-632-175354	Sequence 175354, A
2	66.7	2	13	US-10-027-632-175401	Sequence 175401, A
2	66.7	2	13	US-10-027-632-175403	Sequence 175403, A
2	66.7	2	13	US-10-027-632-175415	Sequence 175415, A
2	66.7	2	13	US-10-027-632-175419	Sequence 175419, A
2	66.7	2	13	US-10-027-632-175426	Sequence 175426, A
2	66.7	2	13	US-10-027-632-175433	Sequence 175433, A
2	66.7	2	13	US-10-027-632-178617	Sequence 178617, A
2	66.7	2	13	US-10-027-632-178640	Sequence 178640, A
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2	66.7	2	17	US-10-027-632-175403	Sequence 175403, A
2	66.7	2	17	US-10-027-632-175415	Sequence 175415, A
2	66.7	2	17	US-10-027-632-175419	Sequence 175419, A
2	66.7	2	17	US-10-027-632-175426	Sequence 175426, A
2	66.7	2	17	US-10-027-632-175433	Sequence 175433, A
2	66.7	2	17	US-10-027-632-178617	Sequence 178617, A
2	66.7	2	17	US-10-027-632-178640	Sequence 178640, A
2	66.7	2	18	US-10-057-783A-33	Sequence 33, Appl
2	66.7	2	3	US-09-735-363A-7	Sequence 7, Appl
2	66.7	2	9	US-09-804-653-11	Sequence 11, Appl
2	66.7	2	10	US-09-971-894-22	Sequence 22, Appl
2	66.7	2	13	US-10-027-632-52136	Sequence 52136, A
2	66.7	2	13	US-10-027-632-52491	Sequence 52491, A
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2	66.7	2	13	US-10-027-632-52508	Sequence 52508, A
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2	66.7	2	13	US-10-027-632-52772	Sequence 52772, A
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2	66.7	2	13	US-10-027-632-178562	Sequence 178562, A
2	66.7	2	15	US-10-043-539-33	Sequence 33, Appl
2	66.7	2	16	US-10-368-442-11	Sequence 11, Appl
2	66.7	2	16	US-10-265-031-17	Sequence 17, Appl
2	66.7	2	16	US-10-265-031-25	Sequence 25, Appl
2	66.7	2	17	US-10-027-632-52136	Sequence 52136, A
2	66.7	2	17	US-10-027-632-52191	Sequence 52191, A
2	66.7	2	17	US-10-027-632-52496	Sequence 52496, A
2	66.7	2	17	US-10-027-632-52508	Sequence 52508, A
2	66.7	2	17	US-10-027-632-52513	Sequence 52513, A
2	66.7	2	17	US-10-027-632-52615	Sequence 52615, A
2	66.7	2	17	US-10-027-632-52633	Sequence 52633, A
2	66.7	2	17	US-10-027-632-52651	Sequence 52651, A
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2	66.7	2	17	US-10-027-632-52772	Sequence 52772, A
2	66.7	2	17	US-10-027-632-176294	Sequence 176294, A
2	66.7	2	17	US-10-027-632-177312	Sequence 177312, A
2	66.7	2	17	US-10-027-632-177323	Sequence 177323, A
2	66.7	2	17	US-10-027-632-177334	Sequence 177334, A
2	66.7	2	17	US-10-027-632-177589	Sequence 177589, A
2	66.7	2	17	US-10-027-632-177959	Sequence 177959, A
2	66.7	2	17	US-10-027-632-178067	Sequence 178067, A

81 Sequence 178091, US-10-027-632-178091 3 17
c 82 Sequence 178562, US-10-027-632-178562 2 66.7
83 Sequence 517, App US-10-317-444-517 3 17
c 84 Sequence 518, App US-10-317-444-518 3 17
85 Sequence 537, App US-10-317-444-537 3 17
c 86 Sequence 538, App US-10-317-444-538 3 17
87 Sequence 45, Appl US-10-452-002A-45 3 17
c 88 Sequence 2, Appli US-10-412-382-2 3 17
c 89 Sequence 3, Appli US-10-412-382-3 3 17
c 90 Sequence 2, Appli US-10-382-754B-2 3 17
c 91 Sequence 42, Appl US-10-057-783A-42 3 18
c 92 Sequence 2, Appli US-10-686-317-2 3 19
c 93 Sequence 19, Appl US-10-686-317-19 3 19
94 Sequence 38, Appl US-10-686-317-38 3 19
95 Sequence 40, Appl US-10-686-317-40 3 19
96 Sequence 53, Appl US-10-686-317-53 3 19
c 97 Sequence 65, Appl US-10-686-317-65 3 19
98 Sequence 118, App US-10-716-029-118 3 19
99 Sequence 119, App US-10-716-029-119 3 19
c 100 Sequence 120, App US-10-716-029-120 3 19

ALIGNMENTS

RESULT 1
US-09-735-363A-8
; Sequence 8, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillips, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735.363A
; PRIOR FILING DATE: 2000-12-12
; PRIOR FILING DATE: 2000-12-12
; PRIOR FILING DATE: 1999-12-13
; PRIOR FILING DATE: 1999-12-13
; PRIOR FILING DATE: 2000-08-29
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-8

Query Match 100.0%; Score 3; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 2e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTG 3
Db |||
1 GTG 3

RESULT 2
US-09-816-763-10
; Sequence 10, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816.763
; CURRENT FILING DATE: 2001-03-23

; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for transcriptional factor ARNT
; NAME/KEY: misc_difference
; LOCATION: (0)...(0)
; OTHER INFORMATION: 3' -half site
US-09-816-763-10

Query Match 100.0%; Score 3; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 2e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTG 3
Db |||
1 GTG 3

RESULT 3
US-10-127-645-1
; Sequence 1, Application US/10127645
; Publication No. US20030045493A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario C.
; APPLICANT: Phillips, Nigel C.
; TITLE OF INVENTION: Oligonucleotide Compositions and Their Use to Induce Differential
; FILE REFERENCE: 02811-0261 (42368-273010)
; CURRENT APPLICATION NUMBER: US/10/127.645
; PRIOR FILING DATE: 2002-10-08
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-127-645-1

Query Match 100.0%; Score 3; DB 14; Length 3;
Best Local Similarity 100.0%; Pred. No. 2e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTG 3
Db |||
1 GTG 3

RESULT 4
US-10-264-280-4
; Sequence 4, Application US/10264280
; Publication No. US20030125290A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario C.
; APPLICANT: Herrera-Gayol, Andrea C.
; TITLE OF INVENTION: Therapeutically Useful Triethyleneglycol Cholesteryl Oligonucleot
; FILE REFERENCE: 02811-0271 42368-277492
; CURRENT APPLICATION NUMBER: US/10/264.280
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 60/326,884
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4

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; LENGTH: 3
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-264-280-4
Query Match      100.0%; Score 3; DB 15; Length 3;
Best Local Similarity 100.0%; Pred. No. 2e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTG 3
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Db 1 GTG 3

RESULT 5
US-10-264-280-8
; Sequence 8, Application US/10264280
; Publication No. US20030125290A1
; GENERAL INFORMATION:
; APPLICANT: Fillon, Mario C.
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Herrera-Gavol, Andrea C.
; TITLE OF INVENTION: Therapeutically Useful Triethyleneglycol Cholesteryl Oligonucleotides
; FILE REFERENCE: 02811-0271 42368-277492
; CURRENT APPLICATION NUMBER: US/10/264,280
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 60/326,884
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
; NAME/KEY: misc feature
; OTHER INFORMATION: 3'-Triethyleneglycol (TEG) Cholesteryl Synthetic Oligonucleotide
US-10-264-280-8
Query Match      100.0%; Score 3; DB 15; Length 3;
Best Local Similarity 100.0%; Pred. No. 2e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTG 3
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Db 1 GTG 3

RESULT 6
US-10-686-317-13/c
; Sequence 13, Application US/10686317
; Publication No. US20040115716A1
; GENERAL INFORMATION:
; APPLICANT: Freier, Susan M.
; APPLICANT: Matveeva, Olga
; APPLICANT: Tsodikov, Alexander
; APPLICANT: Giddings, Michael C.
; APPLICANT: Wyatt, Jacqueline R.
; TITLE OF INVENTION: Methods of Obtaining Active Antisense Compounds
; FILE REFERENCE: ISPH-0457
; CURRENT APPLICATION NUMBER: US/10/686,317
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: US/09/568,165
; PRIOR FILING DATE: 2000-05-09
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: motif
US-10-686-317-48
Query Match      100.0%; Score 3; DB 19; Length 3;
Best Local Similarity 100.0%; Pred. No. 2e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTG 3
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Db 1 GTG 3

RESULT 7
US-10-686-317-48
; Sequence 48, Application US/10686317
; Publication No. US20040115716A1
; GENERAL INFORMATION:
; APPLICANT: Freier, Susan M.
; APPLICANT: Matveeva, Olga
; APPLICANT: Tsodikov, Alexander
; APPLICANT: Giddings, Michael C.
; APPLICANT: Wyatt, Jacqueline R.
; TITLE OF INVENTION: Methods of Obtaining Active Antisense Compounds
; FILE REFERENCE: ISPH-0457
; CURRENT APPLICATION NUMBER: US/10/686,317
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: US/09/568,165
; PRIOR FILING DATE: 2000-05-09
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: motif
US-10-686-317-48
Query Match      100.0%; Score 3; DB 19; Length 3;
Best Local Similarity 100.0%; Pred. No. 2e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTG 3
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Db 1 GTG 3

RESULT 8
US-10-821-568-10
; Sequence 10, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: DETECTION AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: motif
US-10-821-568-10
Query Match      100.0%; Score 3; DB 19; Length 3;
Best Local Similarity 100.0%; Pred. No. 2e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTG 3
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Db 1 GTG 3
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; FEATURE:
; OTHER INFORMATION: Consensus sequence for transcriptional factor ARNT
; FEATURE:
; NAME/KEY: misc_difference
; LOCATION: (0)...(0)
; OTHER INFORMATION: 3'-half site
US-10-821-568-10

Query Match 100.0%; Score 3; DB 19; Length 3;
Best Local Similarity 100.0%; Pred. No. 2e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTG 3
|||
Db 1 GTG 3

RESULT 9
US-09-735-363A-50
; Sequence 50, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 50
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-50

Query Match 66.7%; Score 2; DB 9; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2
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Db 1 GT 2

RESULT 10
US-09-735-363A-51
; Sequence 51, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 51
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-51

Query Match 66.7%; Score 2; DB 9; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TG 3
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Db 1 TG 2

RESULT 11
US-09-971-894-19
; Sequence 19, Application US/09971894
; Publication No. US20030044804A1
; GENERAL INFORMATION:
; APPLICANT: Kaishi, Yechezkel
; APPLICANT: Gur-Arie, Riva
; APPLICANT: Cohen, Cyril
; APPLICANT: Eitan, Yuval
; APPLICANT: Shelef, Leora
; APPLICANT: Hallerman, Eric
; TITLE OF INVENTION: ABUNDANT, WELL DISTRIBUTED AND HYPERPOLYMORPHIC SIMPLE SEQUENCE R
; FILE REFERENCE: 01/22569
; CURRENT APPLICATION NUMBER: US/09/971,894
; CURRENT FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/472,035
; PRIOR FILING DATE: 1999-12-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-971-894-19

Query Match 66.7%; Score 2; DB 10; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2
||
Db 1 GT 2

RESULT 12
US-09-852-903C-20/c
; Sequence 20, Application US/09852903C
; Publication No. US20030104376A1
; GENERAL INFORMATION:
; APPLICANT: Diatech Pty. Ltd.
; TITLE OF INVENTION: An assay
; FILE REFERENCE: 2414918/EJH
; CURRENT APPLICATION NUMBER: US/09/852,903C
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: US 60/202,771
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/202,559
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 2
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ()..(?)
; OTHER INFORMATION: CA-1
US-09-852-903C-20

Query Match 66.7%; Score 2; DB 10; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TG 3
||
Db 2 TG 1

RESULT 13
US-10-027-632-52280/c
; Sequence 52280, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52280
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52280

Query Match 66.7%; Score 2; DB 13; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
||
Db 2 GT 1

RESULT 14
US-10-027-632-175354
; Sequence 175354, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175354
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175354

Query Match 66.7%; Score 2; DB 13; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
||
Db 1 GT 2

RESULT 15
US-10-027-632-175401
; Sequence 175401, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175401
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175401

Query Match 66.7%; Score 2; DB 13; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
||
Db 1 GT 2

RESULT 16
US-10-027-632-175403
; Sequence 175403, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30

;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 175403
;; LENGTH: 2
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-175403

Query Match 66.7%; Score 2; DB 13; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2
||
Db 1 GT 2

RESULT 17

US-10-027-632-175415
;; Sequence 175415, Application US/10027632
;; Publication No. US20020198371A1
;; GENERAL INFORMATION:
;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;; FILE REFERENCE: 108827.129
;; CURRENT APPLICATION NUMBER: US/10/027,632
;; PRIOR FILING DATE: 2002-04-30
;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 175415
;; LENGTH: 2
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-175415

Query Match 66.7%; Score 2; DB 13; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2
||
Db 1 GT 2

RESULT 18

US-10-027-632-175419
;; Sequence 175419, Application US/10027632
;; Publication No. US20020198371A1
;; GENERAL INFORMATION:
;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;; FILE REFERENCE: 108827.129
;; CURRENT APPLICATION NUMBER: US/10/027,632
;; CURRENT FILING DATE: 2002-04-30
;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 175419
;; LENGTH: 2
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-175419

Query Match 66.7%; Score 2; DB 13; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2
||
Db 1 GT 2

RESULT 19

US-10-027-632-175426
;; Sequence 175426, Application US/10027632
;; Publication No. US20020198371A1
;; GENERAL INFORMATION:
;; APPLICANT: Wang, David G.
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;; FILE REFERENCE: 108827.129
;; CURRENT APPLICATION NUMBER: US/10/027,632
;; CURRENT FILING DATE: 2002-04-30
;; PRIOR APPLICATION NUMBER: US 60/218,006
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/198,676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193,483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185,218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167,363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156,358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 175426
;; LENGTH: 2
;; TYPE: DNA
;; ORGANISM: Human

Query Match 66.7%; Score 2; DB 13; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2
||
Db 1 GT 2

US-10-027-632-175426

Query Match 66.7%; Score 2; DB 13; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2
||
Db 1 GT 2

RESULT 20

US-10-027-632-175433
; Sequence 175433, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175433
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human

US-10-027-632-175433

Query Match 66.7%; Score 2; DB 13; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2
||
Db 1 GT 2

RESULT 21

US-10-027-632-178617
; Sequence 178617, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178617
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human

US-10-027-632-178617

Query Match 66.7%; Score 2; DB 13; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TG 3
||
Db 1 TG 2

; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178617
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178617

Query Match 66.7%; Score 2; DB 13; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TG 3
||
Db 1 TG 2

RESULT 22

US-10-027-632-178640
; Sequence 178640, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178640
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human

US-10-027-632-178640

Query Match 66.7%; Score 2; DB 13; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TG 3
||
Db 1 TG 2

RESULT 23

US-10-027-632-52280/c
; Sequence 52280, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178640
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human

US-10-027-632-178640

Query Match 66.7%; Score 2; DB 13; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TG 3
||
Db 1 TG 2

RESULT 23

US-10-027-632-52280/c
; Sequence 52280, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178640
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human

RESULT 24
US-10-027-632-175354
; Sequence 175354, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US 60/167,363
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52280
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52280

Query Match 66.7%; Score 2; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2
||
Db 2 GT 1

RESULT 25
US-10-027-632-175401
; Sequence 175401, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US 60/167,363
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 175401
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175401

Query Match 66.7%; Score 2; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2
||
Db 1 GT 2

RESULT 26
US-10-027-632-175403
; Sequence 175403, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US 60/167,363
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 175403
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175403

Query Match 66.7%; Score 2; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2
||
Db 1 GT 2

```
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175403

Query Match      66.7%; Score 2; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2
Db ||
1 GT 2

RESULT 27
US-10-027-632-175415
; Sequence 175415, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175415
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175415

Query Match      66.7%; Score 2; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2
Db ||
1 GT 2

RESULT 28
US-10-027-632-175419
; Sequence 175419, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
```

```
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175419
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175419

Query Match      66.7%; Score 2; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2
Db ||
1 GT 2

RESULT 29
US-10-027-632-175426
; Sequence 175426, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175426
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175426

Query Match      66.7%; Score 2; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2
Db ||
1 GT 2

RESULT 30
US-10-027-632-175433
; Sequence 175433, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
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; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175433
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175433

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Query Match      66.7%; Score 2; DB 17; Length 2;
Best Local Similarity 100.0%; Pred.No. 3.le+09;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GT 2
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Db      1 GT 2

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Search completed: July 20, 2005, 22:43:05
Job time : 394 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 20:31:28 ; Search time 98 Seconds
(without alignments)
50.090 Million cell updates/sec

Title: US-09-735-363A-8

Perfect score: 3

Sequence: 1 gtc 3

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 112

Minimum DB seq length: 0

Maximum DB seq length: 3

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

- 1: /cgn2_6/prodata/1/ina/5A COMB.seq.*
- 2: /cgn2_6/prodata/1/ina/5B COMB.seq.*
- 3: /cgn2_6/prodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/prodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/prodata/1/ina/PCTUS COMB.seq.*
- 6: /cgn2_6/prodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2	66.7	2	3	US-09-472-035A-19
2	2	66.7	3	1	US-07-791-213D-46
3	2	66.7	3	1	US-07-791-213D-62
4	2	66.7	3	1	US-08-602-036A-2
5	2	66.7	3	1	US-08-293-150A-46
6	2	66.7	3	1	US-08-293-150A-62
7	2	66.7	3	2	US-08-502-374A-2
8	2	66.7	3	2	US-08-642-407A-2
9	2	66.7	3	3	US-08-793-634B-12
10	2	66.7	3	3	US-09-472-035A-22
11	2	66.7	3	4	US-09-307-106-45
12	1.4	46.7	3	3	US-08-873-709-9
13	1.4	46.7	3	3	US-09-032-365A-36
14	1.2	40.0	3	3	US-09-411-862A-10
15	1.2	40.0	3	3	US-09-411-862A-10
16	1.2	40.0	3	3	US-09-411-862A-11
17	1.2	40.0	3	3	US-09-411-862A-11
18	1.2	40.0	3	3	US-09-411-862A-12
19	1.2	40.0	3	3	US-09-411-862A-12
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23	1.2	40.0	3	3	US-09-411-862A-14
24	1.1	33.3	2	1	US-08-268-679B-8
25	1	33.3	2	1	US-08-457-274A-16
26	1	33.3	2	1	US-08-484-192-16
27	1	33.3	2	3	US-09-016-520-35
28	28	33.3	1	33.3	US-09-130-973-35
29	29	33.3	1	33.3	US-09-477-902-35
30	30	33.3	1	33.3	US-08-361-024-3
31	31	33.3	1	33.3	US-08-361-024-3
32	32	33.3	1	33.3	US-09-472-035A-20
33	33	33.3	1	33.3	US-09-472-035A-20
34	34	33.3	1	33.3	US-09-227-782-16
35	35	33.3	1	33.3	US-10-123-597-16
36	36	33.3	1	33.3	PCT-US93-0575B-16
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38	38	33.3	1	33.3	US-07-791-213D-62
39	39	33.3	1	33.3	US-08-268-679B-7
40	40	33.3	1	33.3	US-08-268-679B-7
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46	46	33.3	1	33.3	US-08-642-407A-2
47	47	33.3	1	33.3	US-08-793-634B-12
48	48	33.3	1	33.3	US-08-793-634B-13
49	49	33.3	1	33.3	US-08-793-634B-13
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52	52	33.3	1	33.3	US-09-472-035A-21
53	53	33.3	1	33.3	US-09-472-035A-21
54	54	33.3	1	33.3	US-09-307-106-45
55	55	33.3	1	33.3	US-09-435-806-2
56	56	26.7	2	2	US-08-726-464B-28
57	57	20.0	2	2	US-08-726-464B-28
58	58	20.0	2	2	US-09-129-192C-17
59	59	0.0	1	3	US-09-177-650-79
60	60	0.0	1	3	US-09-177-650-79
61	61	0.0	1	4	US-09-786-569-6
62	62	0.0	1	4	US-09-786-569-6
63	63	0.0	1	4	US-09-786-569-10
64	64	0.0	1	4	US-09-786-569-10
65	65	0.0	1	4	US-09-786-569-11
66	66	0.0	1	4	US-09-786-569-11
67	67	0.0	1	4	US-09-786-569-23
68	68	0.0	1	4	US-09-786-569-23
69	69	0.0	1	4	US-09-786-569-25
70	70	0.0	1	4	US-09-786-569-25
71	71	0.0	1	4	US-09-786-569-27
72	72	0.0	1	4	US-09-786-569-27
73	73	0.0	1	4	US-09-786-569-29
74	74	0.0	1	4	US-09-786-569-29
75	75	0.0	1	4	US-09-786-569-31
76	76	0.0	1	4	US-09-786-569-31
77	77	0.0	1	4	US-09-786-569-33
78	78	0.0	1	4	US-09-786-569-33
79	79	0.0	1	4	US-09-786-569-35
80	80	0.0	1	4	US-09-786-569-35
81	81	0.0	1	4	US-09-786-569-37
82	82	0.0	1	4	US-09-786-569-37
83	83	0.0	1	4	US-09-786-569-39
84	84	0.0	1	4	US-09-786-569-39
85	85	0.0	1	4	US-09-786-569-41
86	86	0.0	1	4	US-09-786-569-41
87	87	0.0	1	4	US-09-786-569-43
88	88	0.0	1	4	US-09-786-569-43
89	89	0.0	1	4	US-09-803-263-19
90	90	0.0	1	4	US-09-803-263-19
91	91	0.0	1	5	PCT-US93-00977-702
92	92	0.0	1	5	PCT-US93-00977-702
93	93	0.0	2	1	US-08-268-679B-8
94	94	0.0	2	1	US-08-457-274A-16
95	95	0.0	2	1	US-08-484-192-16
96	96	0.0	2	3	US-09-016-520-35
97	97	0.0	2	3	US-09-130-973-35
98	98	0.0	2	3	US-09-477-902-35
99	99	0.0	2	3	US-09-472-035A-19
100	100	0.0	2	3	US-09-411-862A-15


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; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-07-791-213D-62

Query Match 66.7%; Score 2; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 5.3e+08;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TG 3
DB 1 TG 2

RESULT 4
US-08-602-036A-2
; Sequence 2, Application US/08602036A
; Patent No. 5789248
; GENERAL INFORMATION:
; APPLICANT: Oeystein, Fodstad
; APPLICANT: Hovig, Eivind
; APPLICANT: Engelbraaten, Olav
; APPLICANT: Maelandsmo, Gunhild H.
; APPLICANT: Agrawal, Sudhir
; TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: METHODS OF INHIBITING METASTATIC CANCER
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE AND DORR LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: United States of America
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,036A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HYZ-039CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA

; FILING DATE: 13-NOV-1991
; ANTI-SENSE: NO
; US-08-602-036A-2

Query Match 66.7%; Score 2; DB 1; Length 3;
Best Local Similarity 50.0%; Pred. No. 5.3e+08;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
DB 1 GU 2

RESULT 5
US-08-293-150A-46
; Sequence 46, Application US/08293150A
; Patent No. 5792629
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,150A
; FILING DATE: 19-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/791,213
; FILING DATE: 13-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-293-150A-46

Query Match 66.7%; Score 2; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 5.3e+08;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TG 3
DB 1 TG 2
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RESULT 6
US-08-293-150A-62
; Sequence 62, Application US/08293150A
; Patent No. 5792629
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSER: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,150A
; FILING DATE: 13-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/791,213
; FILING DATE: 13-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-293-150A-62

Query Match 66.7%; Score 2; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 5.3e+08;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TG 3
Db 1 TG 2

RESULT 7
US-08-502-374A-2
; Sequence 2, Application US/08502374A
; Patent No. 5872007
; GENERAL INFORMATION:
; APPLICANT: Fodstad, Oeystein
; APPLICANT: Hovig, Eivind
; APPLICANT: Engebraaten, Olav
; APPLICANT: Maelandsmo, Gunhild H.
; TITLE OF INVENTION: CAP-1-SPECIFIC OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: METHODS OF INHIBITING METASTATIC CANCER
; NUMBER OF SEQUENCES: 21
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; CORRESPONDENCE ADDRESS:
; ADDRESSER: Hale and Dorr LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/502,374A
; FILING DATE: 14-Jul-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HVZ-039DV2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-526-6000
; TELEFAX: 617-526-5000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-502-374A-2

Query Match 66.7%; Score 2; DB 2; Length 3;
Best Local Similarity 50.0%; Pred. No. 5.3e+08;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2
Db 1 GU 2

RESULT 8
US-08-642-407A-2
; Sequence 2, Application US/08642407A
; Patent No. 5877308
; GENERAL INFORMATION:
; APPLICANT: Oeystein, Fodstad
; APPLICANT: Hovig, Eivind
; APPLICANT: Engebraaten, Olav
; APPLICANT: Maelandsmo, Gunhild H.
; APPLICANT: Agrawal, Sudhir
; TITLE OF INVENTION: CAP1 SPECIFIC OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: METHODS OF INHIBITING METASTATIC CANCER
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSER: HALE AND DORR LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: United States of America
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/642,407A
; FILING DATE: 03-May-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
```

; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HYZ-039CPDV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-642-407A-2

Query Match 66.7%; Score 2; DB 2; Length 3;
Best Local Similarity 50.0%; Pred. No. 5.3e+08;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
Db 1 GU 2

RESULT 9
US-08-793-634B-12
; Sequence 12, Application US/08793634B
; Patent No. 6211431
; GENERAL INFORMATION:
; APPLICANT: Boevink, Petra C.
; APPLICANT: Surin, Brian P.
; APPLICANT: Keese, Paul K.
; APPLICANT: Chu, Paul W.G.
; APPLICANT: Waterhouse, Peter M.
; APPLICANT: Khan, Rafiqul I.
; APPLICANT: Larkin, Philip J.
; APPLICANT: Taylor, William C.
; APPLICANT: Marchall, Jerry S.
; TITLE OF INVENTION: NOVEL PLANT PROMOTERS AND USES
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,634B
; FILING DATE: June 9, 1997
; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:
; NAME: Digilio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-793-634B-12

Query Match 66.7%; Score 2; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 5.3e+08;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TG 3
Db 1 TG 2

RESULT 10
US-09-472-035A-22
; Sequence 22, Application US/09472035A
; Patent No. 6322985
; GENERAL INFORMATION:
; APPLICANT: Yechezkel Kashi et al.
; TITLE OF INVENTION: ABUNDANT, WELL DISTRIBUTED AND
; TITLE OF INVENTION: HYPERPOLYMORPHIC SIMPLE SEQUENCE REPEATS
; TITLE OF INVENTION: IN PROKARYOTE GENOMES AND USE OF SAME FOR
; TITLE OF INVENTION: PROKARYOTE CLASSIFICATION AND TYPING
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
; STREET: 2001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; OPERATING SYSTEM: Windows version 3.11
; SOFTWARE: Word for Windows version 2.0 converted to
; SOFTWARE: an ASCII file
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/472,035A
; FILING DATE:

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedman, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 74/77
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-5625553
; TELEFAX: 972-3-5625554

; TELEX:
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-09-472-035A-22

Query Match 66.7%; Score 2; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 5.3e+08;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
Db 2 GT 3

RESULT 11
US-09-307-106-45
; Sequence 45, Application US/09307106
; Patent No. 6603063
; GENERAL INFORMATION:
; APPLICANT: Feltelson, Jerald S.

```

; APPLICANT: Schnepf, H. Ernest
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stockhoff, Brian A.
; APPLICANT: Schmeits, James
; APPLICANT: Loewer, David
; APPLICANT: Dullum, Charles Joseph
; APPLICANT: Muller-Cohn, Judy
; APPLICANT: Stamp, Lisa
; APPLICANT: Morrill, George
; APPLICANT: Finstad-Lee, Stacey
; TITLE OF INVENTION: No. 6603061el Pesticidal Toxins and Nucleotide
; TITLE OF INVENTION: Sequences Which Encode These Toxins
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606-6669
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/307,106
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/029,848
; FILING DATE: 30-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/960,780
; FILING DATE: 30-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/073,898
; FILING DATE: 05-MAY-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-708C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 352-375-8100
; TELEFAX: 352-372-5800
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-307-106-45

Query Match 66.7%; Score 2; DB 4; Length 3;
Best Local Similarity 100.0%; Pred. No. 5.3e+08;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TG 3
Db 2 TG 3

RESULT 12
US-08-873-709-9
; Sequence 9, Application US/08873709
; Patent No. 6037126
; GENERAL INFORMATION:
; APPLICANT: Grossman, Abraham
; TITLE OF INVENTION: COMPOSITIONS, METHODS, KITS AND
; TITLE OF INVENTION: APPARATUS FOR DETERMINING THE PRESENCE OR ABSENCE OF
; TITLE OF INVENTION: PROTEIN COMPONENT OF TELOMERASE ENZYME
; NUMBER OF SEQUENCES: 25

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```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-411-862A-12
Query Match 40.0%; Score 1.2; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 5.3e+08;
Matches 0; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GT 2
Db ::
2 SW 3

RESULT 19
US-09-411-862A-12/c
; Sequence 12, Application US/09411862A
; Patent No. 6348583
; GENERAL INFORMATION:
; APPLICANT: David Segev
; TITLE OF INVENTION: POLY(ETHER-THIOETHER), POLY(ETHER-SULFONE) NUCLEIC
; ACIDS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sol Sheinbein c/o Anthony Castorina
; STREET: 2001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; Windows version 3.11
; SOFTWARE: Word for Windows version 2.0 converted to
; an ASCII file
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/411.862A
; FILING DATE: 04-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/384,995
; FILING DATE: 20 AUG 1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Sol Sheinbein
; REGISTRATION NUMBER: 25,457
; REFERENCE/DOCKET NUMBER: 00/20719 (previously 513/13)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-6127676
; TELEFAX: 972-3-6127575
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-411-862A-12
Query Match 40.0%; Score 1.2; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 5.3e+08;
Matches 0; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GT 2
Db ::
2 SW 1
```

```
RESULT 20
US-09-411-862A-13
; Sequence 13, Application US/09411862A
; Patent No. 6348583
; GENERAL INFORMATION:
; APPLICANT: David Segev
; TITLE OF INVENTION: POLY(ETHER-THIOETHER), POLY(ETHER-SULFONE) NUCLEIC
; ACIDS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sol Sheinbein c/o Anthony Castorina
; STREET: 2001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; Windows version 3.11
; SOFTWARE: Word for Windows version 2.0 converted to
; an ASCII file
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/411.862A
; FILING DATE: 04-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/384,995
; FILING DATE: 20 AUG 1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Sol Sheinbein
; REGISTRATION NUMBER: 25,457
; REFERENCE/DOCKET NUMBER: 00/20719 (previously 513/13)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-6127676
; TELEFAX: 972-3-6127575
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-411-862A-13
Query Match 40.0%; Score 1.2; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 5.3e+08;
Matches 0; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GT 2
Db ::
2 SW 3

RESULT 21
US-09-411-862A-13/c
; Sequence 13, Application US/09411862A
; Patent No. 6348583
; GENERAL INFORMATION:
; APPLICANT: David Segev
; TITLE OF INVENTION: POLY(ETHER-THIOETHER), POLY(ETHER-SULFONE) NUCLEIC
; ACIDS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sol Sheinbein c/o Anthony Castorina
; STREET: 2001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
```

ATTORNEY/AGENT INFORMATION:
NAME: Sol Sheinbein
REGISTRATION NUMBER: 25,457
REFERENCE/DOCKET NUMBER: 00/20719 (previously 513/13)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-6127676
TELEFAX: 972-3-6127575
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-411-862A-14

Query Match 40.0%; Score 1.2; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 5.3e+08;
Matches 0; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
DB 2 SW 1

RESULT 22
US-09-411-862A-14
Sequence 14, Application US/09411862A
Patent No. 6348583
GENERAL INFORMATION:
APPLICANT: David Segev
TITLE OF INVENTION: POLY(ETHER-THIOETHER), POLY(ETHER-SULFONE) NUCLEIC ACIDS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSER: Sol Sheinbein c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted to
an ASCII file
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/411,862A
FILING DATE: 04-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/384,995
FILING DATE: 20 AUG 1999
ATTORNEY/AGENT INFORMATION:
NAME: Sol Sheinbein
REGISTRATION NUMBER: 25,457
REFERENCE/DOCKET NUMBER: 00/20719 (previously 513/13)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-6127676
TELEFAX: 972-3-6127575
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-411-862A-14

ATTORNEY/AGENT INFORMATION:
NAME: Sol Sheinbein
REGISTRATION NUMBER: 25,457
REFERENCE/DOCKET NUMBER: 00/20719 (previously 513/13)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-6127676
TELEFAX: 972-3-6127575
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-411-862A-14

Query Match 40.0%; Score 1.2; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 5.3e+08;
Matches 0; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
DB 2 SW 3

RESULT 23
US-09-411-862A-14/c
Sequence 14, Application US/09411862A
Patent No. 6348583
GENERAL INFORMATION:
APPLICANT: David Segev
TITLE OF INVENTION: POLY(ETHER-THIOETHER), POLY(ETHER-SULFONE) NUCLEIC ACIDS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSER: Sol Sheinbein c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted to
an ASCII file
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/411,862A
FILING DATE: 04-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/384,995
FILING DATE: 20 AUG 1999
ATTORNEY/AGENT INFORMATION:
NAME: Sol Sheinbein
REGISTRATION NUMBER: 25,457
REFERENCE/DOCKET NUMBER: 00/20719 (previously 513/13)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-6127676
TELEFAX: 972-3-6127575
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-411-862A-14

Query Match 40.0%; Score 1.2; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 5.3e+08;
Matches 0; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
Db 2 SW 1

RESULT 24

US-08-268-679B-8
; Sequence 8, Application US/08268679B
; Patent No. 5674729
; GENERAL INFORMATION:
; APPLICANT: WIMMER, ECKARD; MOLLIA,
; APPLICANT: AKTERUZZAMAN; PAUL, ANIKO V.
; TITLE OF INVENTION: DE NOVO CELL-FREE
; TITLE OF INVENTION: SYNTHESIS PICORNAVIRUS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVE.
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT # 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/268,679B
; FILING DATE: 30-JUN-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/846,914
; FILING DATE: 06-MAR-1992
; CLASSIFICATION: 435
; APPLICATION NUMBER: 07/719,761
; FILING DATE: 24-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MARIA C.H. LIN
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 0887-4095 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
; MOLECULE TYPE:
; DESCRIPTION: OLIGONUCLEOTIDE
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE: N.A.
; POSITION IN GENOME: N.A.

US-08-268-679B-8

Query Match 33.3%; Score 1; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 8e+08;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 G 1
Db 1 G 1

RESULT 25

US-08-457-274A-16/C
; Sequence 16, Application US/08457274A
; Patent No. 5734086
; GENERAL INFORMATION:
; APPLICANT: Scott, Jeffrey G.
; APPLICANT: Tomita, Takashi
; TITLE OF INVENTION: Cytochrome P450lpr Gene and Its Uses
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: P.O. Box 1051, Clinton Square
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,274A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/240 (D-1519)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1304
; TELEFAX: 716-263-1600
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Musca domestica
; STRAIN: Learn-PyR
; DEVELOPMENTAL STAGE: Adult
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: Chromosome 1
; US-08-457-274A-16

Query Match 33.3%; Score 1; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 8e+08;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 T 2
Db 2 T 2

RESULT 26

US-08-484-192-16
; Sequence 16, Application US/08484192
; Patent No. 5756291
; GENERAL INFORMATION:
; APPLICANT: GRIFFIN, LINDA C.
; APPLICANT: ALBRECHT, GLENN
; APPLICANT: LATHAM, JOHN
; APPLICANT: LEUNG, LAWRENCE
; APPLICANT: VERMAAS, ERIC
; APPLICANT: TOOLE, JOHN J.
; TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND
; TITLE OF INVENTION: METHODS OF MAKING
; NUMBER OF SEQUENCES: 181
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER

```

; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,192
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/934,387
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: GRACEY, NANCY J.
; REGISTRATION NUMBER: 28,216
; REFERENCE/DOCKET NUMBER: 246102002221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc difference
; LOCATION: replace(1,"")
; OTHER INFORMATION: /note= "this is a biotin-17
; OTHER INFORMATION: nucleotide stretch of abasic residues."
US-08-484-192-16

Query Match 33.3%; Score 1; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 8e+08; 0; Indels 0; Gaps 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 G 1
Db 2 G 2

RESULT 27
US-09-016-520-35
; Sequence 35, Application US/09016520A
; Patent No. 6127533
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/016,520A
; CURRENT FILING DATE: 1998-01-30
; EARLIER APPLICATION NUMBER: 60/037,143
; PRIOR FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: Sequence
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```

; OTHER INFORMATION: 5-methyl-2'-dimethylaminoxyethoxy
US-09-016-520-35

Query Match 33.3%; Score 1; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 8e+08; 0; Indels 0; Gaps 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 T 2
Db 1 T 1

RESULT 28
US-09-130-973-35
; Sequence 35, Application US/09130973
; Patent No. 6172209
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
; TITLE OF INVENTION: Making Same
; FILE REFERENCE: ISIS2955
; CURRENT APPLICATION NUMBER: US/09/130,973
; CURRENT FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 2'-dimethylaminoxyethyl thymidine (T-2'-DMAOE)
; OTHER INFORMATION: Description of Artificial Sequence: No. 6172209e1
; OTHER INFORMATION: Sequence
US-09-130-973-35

Query Match 33.3%; Score 1; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 8e+08; 0; Indels 0; Gaps 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 T 2
Db 1 T 1

RESULT 29
US-09-477-902-35
; Sequence 35, Application US/09477902
; Patent No. 6194598
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/477,902
; CURRENT FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 09/016,520
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/037,143
; PRIOR FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: Sequence
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Search completed: July 20, 2005, 21:47:41
Job time : 100 secs

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; OTHER INFORMATION: Sequence
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 5-methyl-2'-dimethylaminooxyethoxy
US-09-477-902-35

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Best Local Similarity 100.0%; Pred. No. 8e+08;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 T 2
Db      1 T 1

RESULT 30
US-08-361-024-3
; Sequence 3, Application US/08361024
; Patent No. 6207368
; GENERAL INFORMATION:
; APPLICANT: Adams, Craig W.
; TITLE OF INVENTION: Method, Reagent and Kit
; TITLE OF INVENTION: for Detection and
; TITLE OF INVENTION: Amplification of
; TITLE OF INVENTION: Nucleic Acid Sequence
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beckman Instruments, Inc.
; STREET: 2500 Harbor Boulevard
; CITY: Fullerton
; STATE: California
; COUNTRY: USA
; ZIP: 92634
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 1.44 Mb
; COMPUTER: IBM
; OPERATING SYSTEM: MS.DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,024
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/925,059
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Burgoon, Richard P.
; REGISTRATION NUMBER: 34,787
; REFERENCE/DOCKET NUMBER: 128D-126
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 773-7610
; TELEFAX: (714) 773-7936
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: yes
; ANTI-SENSE: no
US-08-361-024-3
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Query Match          33.3%; Score 1; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 8e+08;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 G 1
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 20:09:32 ; Search time 1842 Seconds
(without alignments)
61.994 Million cell updates/sec

Title: US-09-735-363A-8

Perfect score: 3

Sequence: 1 gtc 3

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 882

Minimum DB seq length: 0

Maximum DB seq length: 3

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

- EST:*
- 1: gb_est1:*
 - 2: gb_est2:*
 - 3: gb_hic:*
 - 4: gb_est3:*
 - 5: gb_est4:*
 - 6: gb_est5:*
 - 7: gb_est6:*
 - 8: gb_gssi:*
 - 9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	3	100.0	3	9	CL423861 01S0750-0
C 2	2	66.7	2	7	CF301411 7LEAF--06
C 3	2	66.7	2	7	CF306288 HDAL--03
C 4	2	66.7	2	7	CF331310 NACL--07
C 5	2	66.7	2	7	CF333014 JMT--01-L
C 6	2	66.7	2	7	CO792627 NT015C-D1
C 7	2	66.7	2	9	CL661289 PRI0139b
C 8	2	66.7	2	9	CL670560 PRI0162b
C 9	2	66.7	2	9	CL682684 PRI0134c
C 10	2	66.7	2	9	CL688205 PRI0148d
C 11	2	66.7	2	9	CL872635 abe83g10-
C 12	2	66.7	2	9	CL874640 abe96h02.
C 13	2	66.7	2	9	CL876415 abf13c11.
C 14	2	66.7	2	9	CL883717 abf63c08.
C 15	2	66.7	2	3	CA850938 D08D06_H1
C 16	2	66.7	3	6	CA851961 DI9E06_I1
C 17	2	66.7	3	7	CF305942 HDAL--02
C 18	2	66.7	3	7	CF308858 ABF--02-N
C 19	2	66.7	3	7	CF310006 ABF--04-H
C 20	2	66.7	3	7	CF311628 ABF--06-O
C 21	2	66.7	3	7	CF313258 HD--01-FO
C 22	2	66.7	3	7	CF315632 HD--04-KO
C 23	2	66.7	3	7	CF317717 HD--07-I0
C 24	2	66.7	3	7	CF338538 RCL1--01-

CF339357	RCL1--04-	25	2	66.7	3	7	CF339357
CF339421	RCL1--04-	26	2	66.7	3	7	CF339421
CF339646	RCL1--05-	27	2	66.7	3	7	CF339646
CF340077	RCL1--06-	C 28	2	66.7	3	7	CF340077
CF372478	CSECS052H	C 29	2	66.7	3	7	CF372478
CK575874	IST_WT5_9	C 30	2	66.7	3	7	CK575874
CK632435	AM1-AP000	C 31	2	66.7	3	7	CK632435
CO793948	NT019B_A0	C 32	2	66.7	3	7	CO793948
CO819398	CSECS153H	C 33	2	66.7	3	7	CO819398
CV179297	CSECS016C	C 34	2	66.7	3	7	CV179297
CL656746	PRI0127b	C 35	2	66.7	3	9	CL656746
CL664603	PRI0147c	C 36	2	66.7	3	9	CL664603
CL68376	PRI0157c	C 37	2	66.7	3	9	CL68376
CL689749	PRI0160b	C 38	2	66.7	3	9	CL689749
CL679295	PRI0125C	C 39	2	66.7	3	9	CL679295
CL884066	abf65h10.	C 40	2	66.7	3	9	CL884066
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CF339761	RCL1--05-	42	1.4	46.7	3	7	CF339761
CK449137	nsgepl1E4	C 43	1.4	46.7	3	7	CK449137
AL039341	DKFZp434F	C 44	1	33.3	2	1	AL039341
AL039341	DKFZp434F	C 45	1	33.3	2	1	AL039341
AL039455	DKFZp434N	C 46	1	33.3	2	1	AL039455
AL039455	DKFZp434N	C 47	1	33.3	2	1	AL039455
AL042337	DKFZp434O	C 48	1	33.3	2	1	AL042337
AL042337	DKFZp434O	C 49	1	33.3	2	1	AL042337
AL043859	DKFZp434B	C 50	1	33.3	2	1	AL043859
AL043859	DKFZp434B	C 51	1	33.3	2	1	AL043859
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BX266185	BX266185	C 54	1	33.3	2	5	BX266185
BX266563	BX266563	C 55	1	33.3	2	5	BX266563
BX267110	BX267110	C 56	1	33.3	2	5	BX267110
BX267110	BX267110	C 57	1	33.3	2	5	BX267110
BX267118	BX267118	C 58	1	33.3	2	5	BX267118
CA850819	D06H04_H0	C 59	1	33.3	2	6	CA850819
CA850842	D07B06_C1	C 60	1	33.3	2	6	CA850842
CA850864	D07D08_G2	C 61	1	33.3	2	6	CA850864
CA850952	D08B09_J2	C 62	1	33.3	2	6	CA850952
CA851273	D12A01_B1	C 63	1	33.3	2	6	CA851273
CF280384	14ETL--07	C 64	1	33.3	2	7	CF280384
CF280384	14ETL--07	C 65	1	33.3	2	7	CF280384
CF280511	14ETL--07	C 66	1	33.3	2	7	CF280511
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CF281609	14ETL--08	C 69	1	33.3	2	7	CF281609
CF282353	14ETL--09	C 70	1	33.3	2	7	CF282353
CF291112	14ROOT--0	C 71	1	33.3	2	7	CF291112
CF292081	14ROOT--0	C 72	1	33.3	2	7	CF292081
CF295832	30DGS--05	C 73	1	33.3	2	7	CF295832
CF296698	30DGS--07	C 74	1	33.3	2	7	CF296698
CF299103	7LEAF--02	C 75	1	33.3	2	7	CF299103
CF299550	7LEAF--03	C 76	1	33.3	2	7	CF299550
CF299550	7LEAF--03	C 77	1	33.3	2	7	CF299550
CF299571	7LEAF--03	C 78	1	33.3	2	7	CF299571
CF299728	7LEAF--03	C 79	1	33.3	2	7	CF299728
CF299728	7LEAF--03	C 80	1	33.3	2	7	CF299728
CF299820	7LEAF--05	C 81	1	33.3	2	7	CF299820
CF300639	7LEAF--05	C 82	1	33.3	2	7	CF300639
CF301112	7LEAF--07	C 83	1	33.3	2	7	CF301112
CF302235	7LEAF--07	C 84	1	33.3	2	7	CF302235
CF302259	7LEAF--07	C 85	1	33.3	2	7	CF302259
CF307078	HDAL--05-	C 86	1	33.3	2	7	CF307078
CF307078	HDAL--05-	C 87	1	33.3	2	7	CF307078
CF307123	HDAL--05-	C 88	1	33.3	2	7	CF307123
CF307878	ABF--01-H	C 89	1	33.3	2	7	CF307878
CF307878	ABF--01-H	C 90	1	33.3	2	7	CF307878
CF311389	ABF--06-J	C 91	1	33.3	2	7	CF311389
CF311389	ABF--06-J	C 92	1	33.3	2	7	CF311389
CF311851	ABF--07-E	C 93	1	33.3	2	7	CF311851
CF312294	ABF--07-O	C 94	1	33.3	2	7	CF312294
CF312294	ABF--07-O	C 95	1	33.3	2	7	CF312294
CF315237	HD--04-B0	C 96	1	33.3	2	7	CF315237
CF348132	NACL--02-	C 97	1	33.3	2	7	CF348132

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c 99      1 33.3      2 7 CF329006      CF329006 NACL--04-
c 100     1 33.3      2 7 CF329006      CF329006 NACL--04-

ALIGNMENTS

RESULT 1
CL423861/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
1 (bases 1 to 2)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
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/tissue_type="leaf"
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/dev_stages="7 days after germination"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 1.9e+10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
Db |||
2 GT 1

RESULT 3
CF306288/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
CF306288 2 bp mRNA linear EST 15-AUG-2003
HDAL--03-E23.g1 OshDACL-overexpressing transgenic rice lambda phage
cDNA library I (HDAL) Oryza sativa (japonica cultivar-group) cDNA
clone HDAL--03-E23, mRNA sequence.
CF306288
CF306288.1 GI:33678049
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
1 (bases 1 to 2)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HDAL--03-E23"

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CF301411
7LEAF--06-E07.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--06-E07, mRNA
sequence.
CF301411
CF301411.1 GI:33673172
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)

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/tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli SOLR"
 /clone_lib="OSHDA1-overexpressing transgenic rice lambda
 phage cDNA library I (HDA1)"
 /notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
 was inserted into lambda Uni-ZAP XR vector at 5' end with
 EcoRI and 3' end with XhoI site. mRNA was derived from
 rice Histone Deacetylase overexpression line."

ORIGIN

Query Match 66.7%; Score 2; DB 7; Length 2;
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 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TG 3
 ||
 Db 2 TG 1

RESULT 4

CF331310/c

LOCUS
 DEFINITION
 NACL--07-G04.g1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa (japonica cultivar-group) cDNA clone NACL--07-G04, mRNA
 sequence.

CF331310

CF331310.1 GI:33810838

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 2)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

Of Bioscience and Bioinformatics, Myongji University

Yongin, Gyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

Location/Qualifiers

1. . 2

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="NACL--07-G04"

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/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli DH10B"

/clone_lib="Rice callus plasmid cDNA library (NACL)"

/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

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RT-PCR."

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 Db 2 GT 1

RESULT 5

CF333014/c

LOCUS

DEFINITION

JMT--01-L21.b1 AtJMT-overexpressing transgenic rice plasmid cDNA

library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone

JMT--01-L21, mRNA sequence.

CF333014/c

LOCUS

DEFINITION

JMT--01-L21.b1 AtJMT-overexpressing transgenic rice plasmid cDNA

library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone

JMT--01-L21, mRNA sequence.

CF333014

CF333014.1 GI:33814278

EST.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 2)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

Of Bioscience and Bioinformatics, Myongji University

Yongin, Gyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

Location/Qualifiers

1. . 2

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="JMT--01-L21"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="AtJMT-overexpressing transgenic rice plasmid

cDNA library (JMT)"

/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA

was reverse transcribed and then used for PCR. mRNA was

prepared from Arabidopsis Jasmonate Carboxyl

methyltransferase overexpression line."

Query Match 66.7%; Score 2; DB 7; Length 2;
 Best Local Similarity 100.0%; Pred. No. 1.9e+10;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GT 2
 ||
 Db 2 GT 1

RESULT 6

CF792627

LOCUS

DEFINITION

NT015C_D12 St18-22 Neural tube (NT) Ambystoma mexicanum cDNA 5'

similar to hypothetical protein, mRNA sequence.

CF792627

CF792627.1 GI:51008598

EST.

Ambystoma mexicanum (axolotl)

Ambystoma mexicanum

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;

Ambystoma.

1 (bases 1 to 2)

Habermann,B., Bebin,A.G., Herklotz,S., Volkmer,M., Eckelt,K.,

Fehlke,K., Sperlein,H.H., Schackert,H.K., Wiebe,G. and Tanaka,E.M.

An Ambystoma mexicanum EST sequencing project: Analysis of 17,352

expressed sequence tags from embryonic and regenerating blastema

cDNA libraries

Genome Biol. (2004) In press

Contact: Eilly M. Tanaka

Tanaka Lab
Max Planck Institute of Molecular Cell Biology and Genetics,
Dresden
Pfortenhauerstrasse 108, 01307 Dresden, Germany
Tel: 0049 351 210 2620
Fax: 0049 351 210 1489
Email: tanaka@mpi-cbg.de
Plate: NT015C row: 12 column: D
Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.

FEATURES
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Unnormalized cDNA plasmid library prepared by Invitrogen.
Size fractionated mRNA was polydT primed and cloned into
NotI-SalI site of pCMVSPORT6. Bacterial host is
EMDH10B-TONA. Average insert size is 1.5 KB.
TAG_LIB=NT"

ORIGIN
Query Match 66.7%; Score 2; DB 7; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+10; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
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Db 1 GT 2

RESULT 7
CL661289
LOCUS
DEFINITION
CL661289.1 GI:50147615
VERSION
KEYWORDS
SOURCE
ORGANISM
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
AppADB: an AcedB database for the nematode satellite organism
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
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/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"

FEATURES
source
1. . 2
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
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/db_xref="taxon:54126"
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ORIGIN
Query Match 66.7%; Score 2; DB 9; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+10; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
||
Db 1 GT 2

RESULT 8
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LOCUS
DEFINITION
CL670560.1 GI:50168602
VERSION
KEYWORDS
SOURCE
ORGANISM
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
AppADB: an AcedB database for the nematode satellite organism
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1. . 2
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Query Match 66.7%; Score 2; DB 9; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.9e+10; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TG 3
||
Db 2 TG 1

RESULT 9
CL682684/c
LOCUS
DEFINITION
CL682684.1 GI:50190105
VERSION
KEYWORDS
SOURCE
ORGANISM
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
AppADB: an AcedB database for the nematode satellite organism
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
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Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1. . 2
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE

1 (bases 1 to 2)
Numberg,A., Bedell,J.A., Citek,R.W., Robbins,D., McMenamy,J., Peterson,S., Jones,J., Fries,J., Budiman,M.A., Nguyen,H. and Stacey,G.

Methylation filtered genomic sequences from Glycine max
Unpublished (2004)

JOURNAL

CONTACT: Gary Stacey
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108 Waters Hall, Columbia, MO 65211, USA
Tel: 573-884-1267
Fax: 573-882-0588
Email: stacey@missouri.edu
LibID: 227
Class: shotgun.

FEATURES

source

1..2

Location/Qualifiers
/organism="Glycine max"
/mol_type="genomic DNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
/tissue_type="Young leaves"
/clone_lib="Soybean methylation filtered genomic library"
/note="Vector: pOT2; Site 1: BstXI; Randomly sheared genomic DNA ranging from 0.7-1.5 kb were end repaired and ligated to BstXI linkers prior to cloning in BstXI-cut pOT2. LibID: 227"

ORIGIN

Query Match 66.7%; Score 2; DB 9; Length 2;
Best Local Similarity 100.0%; Pred.No. 1.9e+10; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 2 TG 3

Db 1 TG 2

RESULT 13

CL876415/c

LOCUS
DEFINITION
abf13c11.y1 Soybean methylation filtered genomic library Glycine max genomic, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Glycine max (soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE

1 (bases 1 to 2)
Numberg,A., Bedell,J.A., Citek,R.W., Robbins,D., McMenamy,J., Peterson,S., Jones,J., Fries,J., Budiman,M.A., Nguyen,H. and Stacey,G.

Methylation filtered genomic sequences from Glycine max
Unpublished (2004)

JOURNAL

CONTACT: Gary Stacey
University of Missouri
108 Waters Hall, Columbia, MO 65211, USA
Tel: 573-884-1267
Fax: 573-882-0588
Email: stacey@missouri.edu
LibID: 227
Class: shotgun.

FEATURES

source

1..2

Location/Qualifiers
/organism="Glycine max"
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/cultivar="Williams 82"
/db_xref="taxon:3847"
/tissue_type="Young leaves"
/clone_lib="Soybean methylation filtered genomic library"
/note="Vector: pOT2; Site 1: BstXI; Randomly sheared genomic DNA ranging from 0.7-1.5 kb were end repaired and ligated to BstXI linkers prior to cloning in BstXI-cut pOT2. LibID: 227"

ORIGIN

Query Match 66.7%; Score 2; DB 9; Length 2;
Best Local Similarity 100.0%; Pred.No. 1.9e+10; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 1 GT 2

Db 2 GT 1

RESULT 14

CL883717

LOCUS

DEFINITION
abf63c08.y1 Soybean random, unfiltered genomic library Glycine max genomic, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Glycine max (soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE

1 (bases 1 to 2)
Numberg,A., Bedell,J.A., Citek,R.W., Robbins,D., McMenamy,J., Peterson,S., Jones,J., Fries,J., Budiman,M.A., Nguyen,H. and Stacey,G.

Methylation filtered genomic sequences from Glycine max
Unpublished (2004)

JOURNAL

CONTACT: Gary Stacey
University of Missouri
108 Waters Hall, Columbia, MO 65211, USA
Tel: 573-884-1267
Fax: 573-882-0588
Email: stacey@missouri.edu
LibID: 230
Class: shotgun.

FEATURES

source

1..2

Location/Qualifiers
/organism="Glycine max"
/mol_type="genomic DNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
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/clone_lib="Soybean random, unfiltered genomic library"
/note="Vector: pOT2; Site 1: BstXI; Randomly sheared genomic DNA ranging from 0.7-1.5 kb were end repaired and ligated to BstXI linkers prior to cloning in BstXI-cut pOT2. LibID: 230"

ORIGIN

Query Match 66.7%; Score 2; DB 9; Length 2;
Best Local Similarity 100.0%; Pred.No. 1.9e+10; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 2 TG 3

Db 1 TG 2

RESULT 15

CA850938

LOCUS

3 bp mRNA linear EST 01-AUG-2003

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DEFINITION D08D06 H18.07.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
cDNA clone D08D06 5', mRNA sequence.
ACCESSION CA850938
VERSION CA850938.1 GI:33387731
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 3)
REFERENCE Alkharouf, N.W., Khan, R. and Matthews, B.F.
AUTHORS Analysis of expressed sequence tags from roots of resistant soybean
TITLE infected by the soybean cyst nematode
JOURNAL Unpublished (2002)
COMMENT Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.

FEATURES
source
1..3
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D08D06"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/notes="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."

ORIGIN
Query Match 66.7%; Score 2; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TG 3
Db 1 TG 2

RESULT 16
LOCUS CA851961
DEFINITION D19E06 H18.09.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
cDNA clone D19E06 5', mRNA sequence.
ACCESSION CA851961
VERSION CA851961.1 GI:33388754
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 3)
REFERENCE Alkharouf, N.W., Khan, R. and Matthews, B.F.
AUTHORS Analysis of expressed sequence tags from roots of resistant soybean
TITLE infected by the soybean cyst nematode
JOURNAL Unpublished (2002)
COMMENT Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.

FEATURES
source
1..3
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D08D06"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/notes="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."

ORIGIN
Query Match 66.7%; Score 2; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TG 3
Db 1 TG 2

RESULT 17
LOCUS CF305942
DEFINITION HDAL--02-D03.g1 OsHDAC1-overexpressing transgenic rice lambda phage
cDNA library I (HDAL) Oryza sativa (japonica cultivar-group) cDNA
clone HDAL--02-D03, mRNA sequence.
ACCESSION CF305942
VERSION CF305942.1 GI:33677703
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 3)
REFERENCE Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
AUTHORS Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..3
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HDAL--02-D03"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OsHDAC1-overexpressing transgenic rice lambda
phage cDNA library I (HDAL)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
was inserted into lambda Uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."

ORIGIN
Query Match 66.7%; Score 2; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2 TG 3
      ||
Db      2 TG 3

RESULT 18
CF308858/c
LOCUS
DEFINITION
ABF--02-N09.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--02-N09, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 3)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..3
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--04-H03"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
FEATURES
source
ORIGIN
Query Match 66.7%; Score 2; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TG 3
      ||
Db      2 TG 3

RESULT 20
CF311628/c
LOCUS
DEFINITION
ABF--06-O16.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--06-O16, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 3)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..3
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--02-N09"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
FEATURES
source
ORIGIN
Query Match 66.7%; Score 2; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GT 2
      ||
      3 GT 2

RESULT 19
CF310006
LOCUS
DEFINITION
ABF--04-H03.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--04-H03, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

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/tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid
 cDNA library (ABF)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and
 then used for PCR. mRNA was prepared from ABA-responsive
 element binding transcription factor 3 overexpression
 line."

ORIGIN

Query Match 66.7%; Score 2; DB 7; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.3e+10;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TG 3
 ||
 Db 2 TG 1

RESULT 21

CF313258/c

LOCUS

DEFINITION HD--01-F06.b1 OshDACL1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION

CF313258

VERSION

CF313258.1

GI:33685019

KEYWORDS

EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

TITLE

JOURNAL

COMMENT

Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 321 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1..3
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
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 /clone_lib="OshDACL1-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

ORIGIN

Query Match 66.7%; Score 2; DB 7; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.3e+10;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
 ||
 Db 2 GT 1

RESULT 22

CF315632/c

LOCUS

DEFINITION

HD--04-K01.b1 OshDACL1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION

CF315632

VERSION

CF315632.1

GI:33687393

KEYWORDS

EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

TITLE

JOURNAL

COMMENT

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 321 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

Location/Qualifiers

1..3

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="HD--04-K01"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli DH10B"

/clone_lib="OshDACL1-overexpressing transgenic rice plasmid

cDNA library (HD)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was

treated with ABA(20um) for 1hr. Oligo-capped mRNA was

reverse transcribed and then used for PCR. mRNA was

derived from rice Histone Deacetylase overexpression

line."

Query Match 66.7%; Score 2; DB 7; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.3e+10;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 GT 2
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 Db 3 GT 2

RESULT 23

CF317717/c

LOCUS

DEFINITION

HD--07-I05.b1 OshDACL1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION

CF317717

VERSION

CF317717.1

GI:33689478

KEYWORDS

EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

```

TITLE
JOURNAL
COMMENT
Large-scale Sequencing Analysis of Rice ESTs
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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1..3
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--07-105"
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

ORIGIN
Query Match 66.7%; Score 2; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
||
2 GT 1

Db

RESULT 24
CF338538
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone RCL1--01-P24,
mRNA sequence.
ACCESSION
CF338538
VERSION
CF338538.1 GI:33825464
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 3)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..3
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="RCL1--04-K02"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library
(RCL1)"
/notes="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with SstI and 3' end with XhoI site. Callus was
induced on 2N6 media for 30 days and cultured for 36hrs on
regenerated media"

ORIGIN
Query Match 66.7%; Score 2; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TG 3
||
1 TG 2

Db

RESULT 26
CF339357
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone RCL1--04-K02,
mRNA sequence.
ACCESSION
CF339357
VERSION
CF339357.1 GI:33827102
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 3)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Location/Qualifiers
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/clone="RCL1--04-K02"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library
(RCL1)"
/notes="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with SstI and 3' end with XhoI site. Callus was
induced on 2N6 media for 30 days and cultured for 36hrs on
regenerated media"

ORIGIN
Query Match 66.7%; Score 2; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TG 3
||
1 TG 2

Db

RESULT 26
CF339357
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone RCL1--04-K02,
mRNA sequence.
ACCESSION
CF339357
VERSION
CF339357.1 GI:33827102
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 3)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="RCL1--01-P24"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"

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CF339421
LOCUS       CF339421               3 bp     mRNA       linear       EST 18-AUG-2003
DEFINITION   RCL1--04-N02.g1 Regenerated callus lambda phage cDNA library (RCL1)
             Oryza sativa (japonica cultivar-group) cDNA clone RCL1--04-N02,
             mRNA sequence.
ACCESSION   CF339421
VERSION     CF339421.1   GI:33827229
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
            Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 3)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongui University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
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            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
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            /clone="RCL1--04-N02"
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            /lab_host="E.coli SOLR"
            /clone_lib="Regenerated callus lambda phage cDNA library
            (RCL1)"
            /note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
            XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
            end with SstI and 3' end with XhoI site. Callus was
            induced on 2N6 media for 30 days and cultured for 36hrs on
            regenerated media"

ORIGIN
Query Match      66.7%; Score 2; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 TG 3
        |||
Db      1 TG 2

RESULT 28
CF340077/c
LOCUS       CF340077               3 bp     mRNA       linear       EST 18-AUG-2003
DEFINITION   RCL1--06-001.g1 Regenerated callus lambda phage cDNA library (RCL1)
             Oryza sativa (japonica cultivar-group) cDNA clone RCL1--06-001,
             mRNA sequence.
ACCESSION   CF340077
VERSION     CF340077.1   GI:33828517
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
            Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 3)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongui University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
            1. .3
            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
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            /lab_host="E.coli SOLR"
            /clone_lib="Regenerated callus lambda phage cDNA library
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            /note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
            XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
            end with SstI and 3' end with XhoI site. Callus was
            induced on 2N6 media for 30 days and cultured for 36hrs on
            regenerated media"

ORIGIN
Query Match      66.7%; Score 2; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 TG 3
        |||
Db      1 TG 2

RESULT 27
CF339646
LOCUS       CF339646               3 bp     mRNA       linear       EST 18-AUG-2003
DEFINITION   RCL1--05-I07.g1 Regenerated callus lambda phage cDNA library (RCL1)
             Oryza sativa (japonica cultivar-group) cDNA clone RCL1--05-I07,
             mRNA sequence.
ACCESSION   CF339646
VERSION     CF339646.1   GI:33827664
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
            Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 3)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.

```

```

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
            1. .3
            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
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            /lab_host="E.coli SOLR"
            /clone_lib="Regenerated callus lambda phage cDNA library
            (RCL1)"
            /note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
            XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
            end with SstI and 3' end with XhoI site. Callus was
            induced on 2N6 media for 30 days and cultured for 36hrs on
            regenerated media"

ORIGIN
Query Match      66.7%; Score 2; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 TG 3
        |||
Db      1 TG 2

RESULT 28
CF340077/c
LOCUS       CF340077               3 bp     mRNA       linear       EST 18-AUG-2003
DEFINITION   RCL1--06-001.g1 Regenerated callus lambda phage cDNA library (RCL1)
             Oryza sativa (japonica cultivar-group) cDNA clone RCL1--06-001,
             mRNA sequence.
ACCESSION   CF340077
VERSION     CF340077.1   GI:33828517
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
            Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 3)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongui University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
            1. .3
            /organism="Oryza sativa (japonica cultivar-group)"
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            /lab_host="E.coli SOLR"
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            /note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:

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XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

ORIGIN

Query Match 66.7%; Score 2; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
||
3 GT 2

RESULT 29

CF372478/C

LOCUS

DEFINITION CSECS052H02 FLON0012 CabSau Normalised Flower Stage 12 (FLON0012)
Vitis vinifera cDNA clone CSECS052H02 3', mRNA sequence.

ACCESSION

CF372478

VERSION

CF372478.1

KEYWORDS

EST.

SOURCE

Vitis vinifera

ORGANISM

Vitis vinifera

REFERENCE

Iocco, P., Hua, C., Davies, C. and Thomas, M.R.

AUTHORS

TITLE

Expressed sequence tags from the grapevine cultivar Cabernet Sauvignon

JOURNAL

Unpublished (2003)

COMMENT

Contact: Mark R. Thomas

CSIRO Plant Industry

CSIRO

PO Box 350, Glen Osmond, SA, 5064, Australia

Tel: 61 8 83038600

Fax: 61 8 83038601

Email: Mark.R.Thomas@csiro.au

Seq primer: CCCAGTCACGACGTGTGTAACG (M13 Forward)

POLYA=Yes.

FEATURES

source

1. .3

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/mol_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="CSECS052H02"

/sex="Hermaphrodite"

/dev_stage="12 - modified E-L system"

/clone_lib="CabSau Normalised Flower Stage 12 (FLON0012)"

/note="Organ: Inflorescence including flowers; Vector: pZL; Normalised cDNA library from immature inflorescences at stage 12 of the modified E-L system. Tissue collected from field grown plants. A description of the modified E-L system can be found in the paper by B. G. Coombe 'Adoption of a system for identifying grapevine growth stages' (1995) Aust. J. Grape and Wine Res. 1: 104-110."

ORIGIN

Query Match 66.7%; Score 2; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
||
2 GT 1

RESULT 30

CK575874

LOCUS

DEFINITION CSECS052H02 FLON0012 CabSau Normalised Flower Stage 12 (FLON0012)
Vitis vinifera cDNA clone CSECS052H02 3', mRNA sequence.

ACCESSION

CK575874

VERSION

CK575874.1

KEYWORDS

EST

DEFINITION

IST_W15_9516 AD-wrmcDNA library Caenorhabditis elegans cDNA 5', similar to ZK858.4, mRNA sequence.

ACCESSION

CK575874

VERSION

CK575874.1

KEYWORDS

EST.

SOURCE

Caenorhabditis elegans

ORGANISM

Caenorhabditis elegans

REFERENCE

Li, S., Armstrong, C.M., Bertin, N., Ge, H., Milstein, S., Boxem, M., Vidalain, P.O., Han, J.D., Chesneau, A., Hao, T., Goldberg, D.S., Li, N., Martinez, M., Rual, J.F., Lamesch, P., Xu, L., Tewari, M., Wong, S.L., Zhang, L.V., Berriz, G.F., Jacotot, L., Vaglio, P., Reboul, J., Hirozane-Kishikawa, T., Li, O., Gabel, H.W., Elewa, A., Baumgartner, B., Rose, D.J., Yu, H., Bosak, S., Sequerra, R., Fraser, A., Mango, S.E., Saxton, W.M., Strome, S., Van Den Heuvel, S., Piano, F., Vandenhaute, J., Sardet, C., Gerstein, M., Doucette-Stamm, L., Gunsalus, K.C., Harper, J.W., Cusick, M.E., Roth, F.P., Hill, D.E. and Vidal, M.

AUTHORS

A Map of the Interactome Network of the Metazoan C. elegans

JOURNAL

Science (2004) In press

COMMENT

Contact: Vidal M

Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc.Vidal@dfci.harvard.edu

For the purpose of protein interaction mapping, we generated a C. elegans cDNA library (AD-wrmcDNA) in which poly(dT)-primed reverse transcribed cDNA are fused to the AD-encoding sequence of the yeast transcription factor GAL4. cDNAs were generated and cloned into the two hybrid vector pPC86. This interacting sequence Tag IST_W15_9516 (ZK858.4) interacts as a prey with the bait F10C5.1

PCR Primers

FORWARD: CGCGTTTGGAAATCACTACAGG

BACKWARD: GGAGACTTGACCAACCTCTGGCG

Insert Length: 3 Std Error: 2.00

Plate: 115 row: 10 column: B

Seq primer: CGCGTTTGGAAATCACTACAGG

High quality sequence stop: 2

POLYA=No.

FEATURES

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/strain="N2"

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/dev_stage="embryos, L1, L2, L3, L4, adult, dauer"

/clone_lib="AD-wrmcDNA library"

/note="Vector: pPC86; For the purpose of protein interaction mapping, we generated a C. elegans cDNA library (AD-wrmcDNA) in which poly(dT)-primed reverse transcribed cDNA are fused to the AD-encoding sequence of the yeast transcription factor GAL4. This library was made with poly(A)+ RNA isolated from mated populations of wild-type (N2 strain) animals of all stages of development including embryonic, larval (L1 to L4 stages), adults and dauer. Approximately equal quantities of RNA from different populations were acquired. cDNAs were generated and cloned into the two hybrid vector pPC86. The library contains ~3*10e7 clones. Reference - GATEWAY recombinational cloning: application to the cloning of large numbers of open reading frames or ORFomes - Walhout AJ, Temple GF, Bräsch MA, Hartley JL, Iorson MA, van den Heuvel S, Vidal M - Methods Enzymol. 2000;328:575-92"

ORIGIN

Query Match 66.7%; Score 2; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TG 3
Db 2 TG 3

Search completed: July 20, 2005, 21:46:02
Job time : 1851 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 18:56:37 ; Search time 277 Seconds
(without alignments)
64.113 Million cell updates/sec

Title: US-09-735-363A-8

Perfect score: 3

Sequence: 1 gtc 3

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 34

Minimum DB seq length: 0

Maximum DB seq length: 3

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : N Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	2	66.7	2	6	ABK24295 Human mic
C 2	2	66.7	3	2	AAT33326 CAPL trin
C 3	2	66.7	3	4	AAL20244 Human bre
4	1.4	46.7	3	3	AAA94655 Human TUB
5	1	33.3	2	6	ABK94446 Human BRC
C 6	1	33.3	2	6	ABK94446 Human BRC
C 7	1	33.3	3	2	AAT33326 CAPL trin
8	1	33.3	3	4	AAL20244 Human bre
C 9	1	33.3	3	6	ABN73392 Bovine em
10	1	33.3	3	6	ABN73392 Bovine em
C 11	1	33.3	3	6	ABN73302 Bovine em
C 12	1	33.3	3	6	ABN73302 Bovine em
C 13	1	33.3	3	10	ADBS8066 Human gen
C 14	1	33.3	3	10	ADBS8066 Human gen
C 15	1	33.3	3	12	ADG28481 Modified
C 16	1	33.3	3	12	ADG28481 Modified
C 17	1	33.3	3	12	ADG28481 Part of r
C 18	0.2	6.7	3	1	ADG28481 Part of r
C 19	0.2	6.7	3	1	ADG28481 Sequence
C 20	0	0.0	1	2	ADG28481 Sequence
					Aax57131 Human mut

C	21	0	0.0	1	2	AAX57131	Aax57131 Human mut
C	22	0	0.0	1	6	ABK94535	Abk94535 Human BRC
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C	25	0	0.0	1	12	ACH82100	Ach82100 Human gen
C	26	0	0.0	1	12	ACH81204	Ach81204 Human gen
C	27	0	0.0	1	12	ACH81204	Ach81204 Human gen
C	28	0	0.0	2	6	ABK24295	Abk24295 Human mic
C	29	0	0.0	3	2	AAQ85491	Aaq85491 Plasmid p
C	30	0	0.0	3	2	AAQ85491	Aaq85491 Plasmid p
C	31	0	0.0	3	3	AAA94655	Aaa94655 Human TUB
C	32	0	0.0	3	10	ADD25606	Add25606 Binding d
C	33	0	0.0	3	10	ADD25606	Add25606 Binding d
C	34	0	0.0	3	12	ADG28481	Adg28481 Modified

ALIGNMENTS

RESULT 1
ID ABK24295/c
XX ABK24295 standard; DNA; 2 BP.
AC ABK24295;
XX
DT 09-APR-2002 (first entry)
XX
DE Human microsatellite DIS191 detection PCR primer #3.
XX
KW Microsatellite; ligase-assisted spacer addition assay; LASA; cancer;
KW nucleotide length polymorphism detection; neurodegenerative disease;
KW fragile X syndrome; Huntington's disease; muscular dystrophy; forensic;
KW gene mapping; population study; human; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200185987-A1.
XX
PD 15-NOV-2001.
XX
XX
PF 09-MAY-2001; 2001WO-AU000526.
XX
PR 09-MAY-2000; 2000US-0202771P.
PR 10-MAY-2000; 2000US-0202559P.
XX
PA (DIAT-) DIATECH PTY LTD.
XX
PI Brockhurst V, Timms P, Wolter L, Barnard R, Giffard PM;
XX
DR WPI; 2002-121948/16.
XX

PT Detecting a nucleotide repeat region in a nucleic acid having a
PT particular length, useful for identifying nucleotide length polymorphism
PT associated with a neurodegenerative disease, comprises using a ligase-
PT assisted spacer addition assay.
XX
XX Example 10; Page 55; 89pp; English.
XX
XX The invention relates to a method of identifying or detecting a
XX nucleotide repeat region in a nucleic acid molecule characterised by a
XX particular length, comprising employing ligase-assisted spacer addition
XX (LASA) assay. The method is useful in the identifying or detecting a
XX nucleotide repeat region in a nucleic acid molecule characterised by a
XX particular length. In particular, the method is useful for identification
XX of a nucleotide length polymorphism in animals or humans, which is
XX associated with a neurodegenerative disease including fragile X syndrome,
XX Huntington's disease, or muscular dystrophy. Furthermore, the method may
XX be used for identifying and/or typing microorganisms including yeasts and
XX lower uni- and multi-cellular organisms, as well as prokaryotic
XX microorganisms; and for genotyping subjects including humans. The method
XX is also useful for detecting certain cancers and other malignancies.
XX Moreover, the method can be used to provide markers for use in
XX identification of human and non-human individuals, plants and

PR 06-NOV-2000; 2000WO-IB001607.
 XX (SCSC-) ACAD APPLIED SCI.
 XX Viig J;
 XX WPI; 2002-471507/50.
 XX Detecting mutations in the BRCA1 and hMLH1 gene comprises subjecting
 PT amplification products to 2-dimensional gel electrophoresis to produce a
 PT characteristic spot pattern for a specific mutation in either the BRCA1
 PT or the hMLH1 gene.
 XX Claim 1; Page 27; 57pp; English.
 XX The invention relates to detecting mutations in the BRCA1 and hMLH1 gene
 CC comprising subjecting a set of amplification products to two-dimensional
 CC DNA electrophoresis (TGDS) to produce a characteristic spot pattern for a
 CC specific mutation in either the BRCA1 or the hMLH1 gene. Also included
 CC are test kits for enabling BRCA1 or hMLH1 gene testing comprising short
 CC PCR primers given in the specification, mixed in 20 mM of Tris-HCl, 50 mM
 CC KCl, 25 micro M of dNTP, and 5 % formamide. The method is useful for
 CC detecting mutations in the BRCA1 (breast and ovarian cancer
 CC susceptibility gene, a tumour suppressor gene) and hMLH1 gene (a DNA
 CC mismatch repair gene). The present sequence is a PCR clamp sequence used
 CC in the method of the invention
 XX Sequence 2 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 0 Other;
 SQ Query Match 33.3%; Score 1; DB 6; Length 2;
 Best Local Similarity 100.0%; Pred. No. 2.9e+09;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 G 1
 Db 1 G 1
 RESULT 7
 ART33326/c
 ID AAT33326 standard; RNA; 3 BP.
 XX AC AAT33326;
 XX 12-NOV-1996 (first entry)
 DT CAPL trinucleotide.
 DE CAPL; antisense oligonucleotide; ribozyme; cancer; metastasis;
 KW osteosarcoma; therapy; ss.
 XX Synthetic.
 OS WO9625499-A1.
 PN 22-AUG-1996.
 PD 16-FEB-1996; 96WO-US002108.
 PF 17-FEB-1995; 95US-00391375.
 XX (HYBR-) HYBRIDON INC.
 PA (NORA-) NORWEGIAN RADIUM HOSPITAL RES FOUND.
 XX Fodstad O, Hovig E, Engebraaten O, Maelandsmo GJ, Agrawal S;
 PI Von Hofe E;
 XX WPI; 1996-393400/39.
 XX Synthetic oligo:nucleotide(s) inhibiting CAPL gene expression - useful to
 PT inhibit metastatic cancer, partic. osteo:sarcoma.
 XX Claim 2; Page 56; 70pp; English.

XX Novel antisense oligonucleotides capable of inhibiting CAPL gene
 CC expression may include the trinucleotide GUC (AAT33326, given in 5' to 3'
 CC direction) found in codon 14 of CAPL mRNA. These and other antisense
 CC oligonucleotides (AAT33327-36) complementary to specific regions of the
 CC CAPL gene (see also AAT33345), as well as CAPL-specific ribozymes
 CC (AAT33337-40) can be administered to a patient as a means of inhibiting
 CC metastatic cancer
 XX Sequence 3 BP; 0 A; 1 C; 1 G; 0 T; 1 U; 0 Other;
 SQ Query Match 33.3%; Score 1; DB 2; Length 3;
 Best Local Similarity 100.0%; Pred. No. 2e+09;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 G 1
 Db 1 G 1
 RESULT 8
 AAL20244
 ID AAL20244 standard; cDNA; 3 BP.
 XX AC AAL20244;
 XX 07-DEC-2001 (first entry)
 DT Human breast cancer expressed polynucleotide 12701.
 DE Human; breast cancer; cell marker; cytostatic; ss.
 XX Homo sapiens.
 OS WO200151628-A2.
 PN 19-JUL-2001.
 PD 10-JAN-2001; 2001WO-US000798.
 PF 14-JAN-2000; 2000US-0176077P.
 PR 14-MAR-2000; 2000US-0189167P.
 PR 24-MAR-2000; 2000US-0192099P.
 PR 29-MAR-2000; 2000US-0193480P.
 PR 15-MAY-2000; 2000US-0205230P.
 PR 09-JUN-2000; 2000US-0211315P.
 PR 25-JUL-2000; 2000US-0220534P.
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PA Lillie J, Xu Y, Wang Y, Steinmann K;
 XX WPI; 2001-451856/48.
 DR New peptide useful as a marker for the diagnosis of breast cancer.
 PT Claim 1; Page 2245; 3695pp; English.
 PS The invention relates to human breast cancer expressed polynucleotides
 CC (AAL07544-AAL26789) and methods of assessing whether a patient is
 CC afflicted with breast cancer by examining the correlation between the
 CC expression of certain markers and the cancerous state of breast cells.
 CC The polynucleotides and encoded polypeptides are potential markers for
 CC detecting, diagnosing, monitoring, characterising treating and
 CC potentially preventing breast cancer. The polynucleotides and encoded
 CC polypeptides are also useful for isolating compounds with cytostatic
 CC activity
 XX Sequence 3 BP; 1 A; 1 C; 0 G; 1 T; 0 U; 0 Other;
 SQ Query Match 33.3%; Score 1; DB 4; Length 3;
 Best Local Similarity 100.0%; Pred. No. 2e+09;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 T 2
Db 3 T 3

RESULT 9
ABN73392
ID ABN73392 standard; cDNA; 3 BP.

AC ABN73392;

DT 03-JUL-2002 (first entry)

DE Bovine embryonic germ (EG) cell cDNA EST 000203a CONTIG 76.

XX Bovine; Bos taurus; EST; expressed sequence tag; totipotence;
KW development; gene; ss.

XX Bos taurus.

XX WO200194550-A2.

XX 13-DEC-2001.

XX 07-JUN-2001; 2001WO-US018576.

XX 07-JUN-2000; 2000US-0209874P.

XX 06-JUN-2001; 2001US-00876143.

XX (INFI-) INFIGEN INC.

XX Eilertsen KJ, Pfister-Genskow M, Childs L;

XX WPI; 2002-351289/38.

XX An expressed sequence tag (EST), the expression of which, or its
PT complementary sequence, in a cell identifies the cell as a
PT developmentally competent or incompetent cell.

XX Example 16; Page 163; 584pp; English.

XX The present invention describes an expressed sequence tag (EST), where
CC the EST is an isolated, enriched, or purified nucleic acid sequence
CC representing all or part of a gene, the expression of which, or its
CC complementary sequence, in a cell identifies the cell as a
CC developmentally competent or incompetent cell. Molecules which induce
CC developmental competence in a cell line are useful for inducing
CC totipotence in one or more cells. Molecules which induce developmental
CC incompetence in a cell line are useful for preventing a full term
CC pregnancy in an animal and inhibiting totipotence. The molecules are also
CC useful for treating a disease in an animal by inducing development of one
CC or more cells of the animal into a specific cell type. The present
CC sequence represents a bovine EST which is given in the exemplification of
CC the present invention

XX Sequence 3 BP; 1 A; 0 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 33.3%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 2e+09;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 T 2
Db 1 T 1

RESULT 10
ABN73392/c
ID ABN73392 standard; cDNA; 3 BP.

XX AC ABN73392;

XX

DT 03-JUL-2002 (first entry)

DE Bovine embryonic germ (EG) cell cDNA EST 000203a CONTIG 76.

XX Bovine; Bos taurus; EST; expressed sequence tag; totipotence;
KW development; gene; ss.

XX Bos taurus.

XX WO200194550-A2.

XX 13-DEC-2001.

XX 07-JUN-2001; 2001WO-US018576.

XX 07-JUN-2000; 2000US-0209874P.

XX 06-JUN-2001; 2001US-00876143.

XX (INFI-) INFIGEN INC.

XX Eilertsen KJ, Pfister-Genskow M, Childs L;

XX WPI; 2002-351289/38.

XX An expressed sequence tag (EST), the expression of which, or its
PT complementary sequence, in a cell identifies the cell as a
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XX Example 16; Page 163; 584pp; English.

XX The present invention describes an expressed sequence tag (EST), where
CC the EST is an isolated, enriched, or purified nucleic acid sequence
CC representing all or part of a gene, the expression of which, or its
CC complementary sequence, in a cell identifies the cell as a
CC developmentally competent or incompetent cell. Molecules which induce
CC developmental competence in a cell line are useful for inducing
CC totipotence in one or more cells. Molecules which induce developmental
CC incompetence in a cell line are useful for preventing a full term
CC pregnancy in an animal and inhibiting totipotence. The molecules are also
CC useful for treating a disease in an animal by inducing development of one
CC or more cells of the animal into a specific cell type. The present
CC sequence represents a bovine EST which is given in the exemplification of
CC the present invention

XX Sequence 3 BP; 1 A; 0 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 33.3%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 2e+09;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 T 2
Db 2 T 2

RESULT 11
ABN73302
ID ABN73302 standard; cDNA; 3 BP.

XX AC ABN73302;

DT 03-JUL-2002 (first entry)

DE Bovine embryonic germ (EG) cell cDNA EST 000203a CONTIG 76.

XX Bovine; Bos taurus; EST; expressed sequence tag; totipotence;
KW development; gene; ss.

XX Bos taurus.

XX WO200194550-A2.

XX 13-DEC-2001.

```
XX 07-JUN-2001; 2001WO-US018576.
PF
XX
XX 07-JUN-2000; 2000US-0209874P.
PR
XX 06-JUN-2001; 2001US-00876143.
PR
XX (INFI-) INFIGEN INC.
PA
XX Bilertsen KJ, Pfister-Genskow M, Childs L;
XX
XX WPI; 2002-351289/38.
DR
XX
XX An expressed sequence tag (EST), the expression of which, or its
PT complementary sequence, in a cell identifies the cell as a
PT developmentally competent or incompetent cell.
XX
XX Example 16; Page 146; 584pp; English.
PS
XX The present invention describes an expressed sequence tag (EST), where
CC the EST is an isolated, enriched, or purified nucleic acid sequence
CC representing all or part of a gene, the expression of which, or its
CC complementary sequence, in a cell identifies the cell as a
CC developmentally competent or incompetent cell. Molecules which induce
CC developmental competence in a cell line are useful for inducing
CC totipotency in one or more cells. Molecules which induce developmental
CC incompetence in a cell line are useful for preventing a full term
CC pregnancy in an animal and inhibiting totipotency. The molecules are also
CC useful for treating a disease in an animal by inducing development of one
CC or more cells of the animal into a specific cell type. The present
CC sequence represents a bovine EST which is given in the exemplification of
CC the present invention
XX
XX Sequence 3 BP; 1 A; 0 C; 0 G; 2 T; 0 U; 0 Other;
SQ
Query Match 33.3%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 2e+09;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 T 2
Db 1 T 1
RESULT 12
ABN73302/C
ID ABN73302 standard; cDNA; 3 BP.
XX
XX AC ABN73302;
XX
XX DT 03-JUL-2002 (first entry)
XX
XX DE Bovine embryonic germ (EG) cell cDNA EST 000203a CONTIG 76.
XX
XX KW Bovine; Bos taurus; EST; expressed sequence tag; totipotency;
XX KW development; gene; ss.
XX
XX OS Bos taurus.
XX
XX PN WO200194550-A2.
XX
XX PD 13-DEC-2001.
XX
XX PF 07-JUN-2001; 2001WO-US018576.
XX
XX PR 07-JUN-2000; 2000US-0209874P.
XX PR 06-JUN-2001; 2001US-00876143.
XX
XX PA (INFI-) INFIGEN INC.
XX
XX PI Bilertsen KJ, Pfister-Genskow M, Childs L;
XX
XX WPI; 2002-351289/38.
XX
XX An expressed sequence tag (EST), the expression of which, or its
PT complementary sequence, in a cell identifies the cell as a
PT developmentally competent or incompetent cell.
XX
XX Example 16; Page 146; 584pp; English.
PS
XX The present invention describes an expressed sequence tag (EST), where
CC the EST is an isolated, enriched, or purified nucleic acid sequence
CC representing all or part of a gene, the expression of which, or its
CC complementary sequence, in a cell identifies the cell as a
CC developmentally competent or incompetent cell. Molecules which induce
CC developmental competence in a cell line are useful for inducing
CC totipotency in one or more cells. Molecules which induce developmental
CC incompetence in a cell line are useful for preventing a full term
CC pregnancy in an animal and inhibiting totipotency. The molecules are also
CC useful for treating a disease in an animal by inducing development of one
CC or more cells of the animal into a specific cell type. The present
CC sequence represents a bovine EST which is given in the exemplification of
CC the present invention
XX
XX Sequence 3 BP; 1 A; 0 C; 0 G; 2 T; 0 U; 0 Other;
SQ
Query Match 33.3%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 2e+09;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 T 2
Db 1 T 1
RESULT 13
ADE58066
ID ADE58066 standard; DNA; 3 BP.
XX
XX AC ADE58066;
XX
XX DT 29-JAN-2004 (first entry)
XX
XX DE Human gene L11696, SEQ ID NO 3935.
XX
XX KW Human; ds; gene; pain; neuronal tissue; gene therapy;
XX KW spinal segmental nerve injury; chronic constriction injury; CCI;
XX KW spared nerve injury; SNI; Chung.
XX
XX OS Homo sapiens.
XX
XX PN WO2003016475-A2.
XX
XX PD 27-FEB-2003.
XX
XX PF 14-AUG-2002; 2002WO-US025765.
XX
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-033347P.
XX
XX PA (GEHO) GEN HOSPITAL CORP.
XX PA (FARB) BAYER AG.
XX
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX
XX DR WPI; 2003-268312/26.
XX DR GENBANK; L11696.
XX
XX PT New composition comprising two or more isolated polypeptides, useful for
XX PT preparing a medicament for treating pain in an animal.
XX
XX PS Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
```

CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human DNA (shown in Table 2 of the
 CC specification) which encodes one of the polypeptides of the invention
 CC which is differentially expressed during pain. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 3 BP; 0 A; 2 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 33.3%; Score 1; DB 10; Length 3;
 Best Local Similarity 100.0%; Pred. No. 2e+09;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 T 2
 DB 3 T 3

RESULT 14
 ADE58066/c
 ID ADE58066 standard; DNA; 3 BP.

AC ADE58066;

XX 29-JAN-2004 (first entry)

DE Human gene L11696, SEQ ID NO 3935.

XX Human; ds; gene; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.

XX Homo sapiens.

OS WO2003016475-A2.

PN 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

DR GENBANK; L11696.

XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human DNA (shown in Table 2 of the
 CC specification) which encodes one of the polypeptides of the invention
 CC which is differentially expressed during pain. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 3 BP; 0 A; 2 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 33.3%; Score 1; DB 10; Length 3;
 Best Local Similarity 100.0%; Pred. No. 2e+09;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 G 1
 DB 2 G 2

RESULT 15
 ADG28481/c
 ID ADG28481 standard; DNA; 3 BP.

XX AC ADG28481;

XX 26-FEB-2004 (first entry)

XX Modified oligonucleotide seq id 2.

DE antibacterial; protozoacide; antialgal; fungicide;

KW internucleotide linkage; 2',5'-internucleotide linkage; 3'-substituent;

KW antisense; pharmaceutical; RNA-DNA transcription;

KW RNA-protein translation; infection; diagnostic; therapeutic;

XX nuclelease resistance; ss.

OS Synthetic.

XX US6653458-B1.

XX 25-NOV-2003.

XX 08-NOV-1999; 99US-00435806.

XX 03-SEP-1993; 93US-00117363.

PR 02-SEP-1994; 94WO-US010131.

PR 28-FEB-1996; 96US-00602862.

PR 14-JUL-1998; 98US-00115043.

XX (ISIS-) ISIS PHARM INC.

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XX
PI Manoharan M, Cook PD, Guinosso CU;
DR WPI; 2004-079586/08.
XX
PT New oligonucleotide comprising at least one 2',5'-internucleotide linkage
PT useful for treating organisms having disease caused by undesired
PT production of protein e.g. bacteria, yeast, protozoa and algae.
XX
XX Example 49; SEQ ID NO 2; 30pp; English.
XX
XX The invention describes an oligonucleotide comprising several nucleotides
CC covalently linked together by internucleotide linkages. At least one of
CC the nucleotides is linked to an adjacent nucleotide by 2',5'-
CC internucleotide linkage and bears a 3'-substituent. The oligonucleotides
CC are useful: as antisense oligonucleotides; in pharmaceutical compositions
CC ; for treating organisms having disease caused by undesired production of
CC protein e.g. organism that utilises RNA-DNA transcription or RNA-protein
CC translation, bacteria, yeast, protozoa, algae and warm-blooded animals;
CC for developing diagnostic and therapeutic agents. The modified
CC oligonucleotide exhibits improved properties of nuclease resistance and
CC binding affinity. The oligonucleotides are easy to synthesise and exhibit
CC good properties of nuclease resistance and hybridisation to target
CC nucleic acids. The oligonucleotide is potent antisense agent with longer
CC duration of action. This sequence represents an oligonucleotide of the
CC invention.
XX
XX Sequence 3 BP; 3 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Match 33.3%; Score 1; DB 12; Length 3;
Best Local Similarity 100.0%; Pred. No. 2e+09;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 T 2
Db 3 T 3
RESULT 16
AD014091
ID AD014091 standard; DNA; 3 BP.
XX
AC AD014091;
XX
DT 29-JUL-2004 (first entry)
XX
DE Part of rolling circle padlock probe used to detect p53 SNP3.
XX
KW ss; probe; single nucleotide polymorphism; SNP; p53; p53 SNP3.
XX
OS Synthetic.
XX
PN US2004086892-A1.
XX
PD 06-MAY-2004.
XX
PF 24-APR-2003; 2003US-00424542.
XX
PR 06-NOV-2002; 2002US-0424656P.
XX
PA (CROT/) CROTHERS D M.
PA (HOLM/) HOLMLIN R E.
XX
PI Crothers DM, Holmlin RE;
XX
DR WPI; 2004-418412/39.
XX
PT Detecting target nucleotide sequence in sample involves incubating tagged
PT molecules having identifier tags corresponding to targets, with detection
PT probes, and hybridization of tag to complementary probe indicates
PT presence of target.
XX
XX Example 1; SEQ ID NO 6; 35pp; English.
PS

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```

XX
CC The invention relates to methods of detecting a target nucleotide
CC sequence (T) in a sample. The methods involve generating at least one
CC tagged molecule (G) comprising at least one identifier tag (I) selected
CC as an identifier for (T), where (I) is generated only when (T) with a
CC corresponding to (I) is present in sample; incubating (G) with a
CC universal detector having at least one detection probe (P) complementary
CC to (I); and measuring hybridisation of (I) to (P) complementary to (I);
CC where hybridisation of (I) to (P) complementary to (I) indicates (T)
CC corresponding to (I) is present in sample. The methods are useful for
CC detecting several target nucleotide sequences in a sample, where each (T)
CC in several (T) has a distinct (I), such that hybridisation of each
CC distinct (I) to a complementary (P) indicates the presence of the
CC corresponding (T). The methods are useful for detecting at least one
CC variant sequence of (T), where the variant sequence is a single
CC nucleotide polymorphism (SNP), an allelic variant, or a splice variant,
CC preferably SNP. The methods are useful for identifying an organism or
CC individual by detecting one or more target nucleotide sequences chosen to
CC serve as distinguishing features for the organisms or individuals. The
CC universal tag assay utilises target-dependent procedures to generate
CC tagged molecules, advantageously increasing accuracy and minimising
CC spurious signals without the need to employ special conditions or special
CC reagents. The universal tag assay can easily be used to assay a wide
CC variety of samples. The universal tag assay can be performed in a single
CC vessel and easily be automated. The present sequence represents the a 3
CC nucleotide gap used to help transcription from T7 promoter of a rolling
CC circle padlock probe used to detect a SNP in the p53 gene known as p53
CC SNP3.
XX
SQ Sequence 3 BP; 1 A; 0 C; 1 G; 1 T; 0 U; 0 Other;
Query Match 33.3%; Score 1; DB 12; Length 3;
Best Local Similarity 100.0%; Pred. No. 2e+09;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 G 1
Db 1 G 1
RESULT 17
AD014091/c
ID AD014091 standard; DNA; 3 BP.
XX
AC AD014091;
XX
DT 29-JUL-2004 (first entry)
XX
DE Part of rolling circle padlock probe used to detect p53 SNP3.
XX
KW ss; probe; single nucleotide polymorphism; SNP; p53; p53 SNP3.
XX
OS Synthetic.
XX
PN US2004086892-A1.
XX
PD 06-MAY-2004.
XX
PF 24-APR-2003; 2003US-00424542.
XX
PR 06-NOV-2002; 2002US-0424656P.
XX
PA (CROT/) CROTHERS D M.
PA (HOLM/) HOLMLIN R E.
XX
PI Crothers DM, Holmlin RE;
XX
DR WPI; 2004-418412/39.
XX
PT Detecting target nucleotide sequence in sample involves incubating tagged
PT molecules having identifier tags corresponding to targets, with detection
PT probes, and hybridization of tag to complementary probe indicates
PT presence of target.
XX
XX Example 1; SEQ ID NO 6; 35pp; English.
PS

```

XX Example 1; SEQ ID NO 6; 35pp; English.

XX The invention relates to methods of detecting a target nucleotide

CC sequence (T) in a sample. The methods involve generating at least one

CC tagged molecule (G) comprising at least one identifier tag (I) selected

CC as an identifier for (T), where (I) is generated only when (T)

CC corresponding to (I) is present in sample; incubating (G) with a

CC universal detector having at least one detection probe (P) complementary

CC to (I); and measuring hybridisation of (I) to (P) complementary to (I);

CC where hybridisation of (I) to (P) complementary to (I) indicates (T)

CC corresponding to (I) is present in sample. The methods are useful for

CC detecting several target nucleotide sequences in a sample, where each (T)

CC in several (T) has a distinct (I), such that hybridisation of each

CC distinct (I) to a complementary (P) indicates the presence of the

CC corresponding (T). The methods are useful for detecting at least one

CC variant sequence of (T), where the variant sequence is a single

CC nucleotide polymorphism (SNP), an allelic variant, or a splice variant,

CC preferably SNP. The methods are useful for identifying an organism or

CC individual by detecting one or more target nucleotide sequences chosen to

CC serve as distinguishing features for the organisms or individuals. The

CC universal tag assay utilises target-dependent procedures to generate

CC tagged molecules, advantageously increasing accuracy and minimising

CC spurious signals without the need to employ special conditions or special

CC reagents. The universal tag assay can easily be used to assay a wide

CC variety of samples. The universal tag assay can be performed in a single

CC vessel and easily be automated. The present sequence represents the a 3

CC nucleotide gap used to help transcription from T7 promoter of a rolling

CC circle padlock probe used to detect a SNP in the p53 gene known as p53

CC SNP3.

XX SQ Sequence 3 BP; 1 A; 0 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 33.3%; Score 1; DB 12; Length 3;

Best Local Similarity 100.0%; Pred. No. 2e+09;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 T 2

Db 2 T 2

RESULT 18

AAN80743

ID AAN80743 standard; DNA; 3 BP.

XX AC AAN80743;

XX AC AAN80743;

XX DT 25-MAR-2003 (revised)

DT 10-SEP-1990 (first entry)

XX Sequence encoding complete mature and precursor forms of human tissue

DE factor heavy chain proteins (huTfH & pre-huTfH, respectively).

XX Human tissue factor heavy chain (huTfH); immunoassays;

KW precursor human tissue factor heavy chain (pre-huTfH);

KW human tissue factor detection.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 34..921

FT /*tag= a

FT /product= "pre-huTfH"

FT mat_peptide 130..921

FT /*tag= b

FT /product= "huTfH"

XX WO8807543-A.

XX 06-OCT-1988.

XX 31-MAR-1987; 87US-00033047.

XX 31-MAR-1987; 87US-00033047.

XX 25-JUN-1987; 87US-00067103.

XX 09-MAR-1988; 88US-00165939.

XX 31-MAR-1987; 87US-00033047.

PR 25-JUN-1987; 87US-00067103.

PR 09-MAR-1988; 88US-00165939.

XX (SCRI) SCRIPPS CLINIC & RES FOUND.

XX Edgington TS, Morrissey JH;

PI WPI; 1988-292837/41.

XX P-PSDB; AAP80713.

DR New DNA segment - has gene encoding human tissue factor heavy chain

XX protein and is useful for inhibiting coagulation.

PS Disclosure; Page ?; 148pp; English.

XX A DNA segment with a nucleotide sequence from about 130 to about 918 of

CC the sequence given here is claimed. Also claimed are antibodies which

CC immunoreact with huTfH and the claimed peptides (given in AAP80713). The

CC antibodies may be used in immunoassays for detection of huTfH. The

CC claimed peptides may be used to inhibit the binding of huTfH to

CC coagulation factor VII/VIII in vivo. (Updated on 25-MAR-2003 to correct

CC PR field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-

CC MAR-2003 to correct PI field.)

XX SQ Sequence 3 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 3 Other;

Query Match 6.7%; Score 0.2; DB 1; Length 3;

Best Local Similarity 0.0%; Pred. No. 2e+09;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 G 1

Db 2 D 2

RESULT 19

AAN80743/c

ID AAN80743 standard; DNA; 3 BP.

XX AC AAN80743;

XX AC AAN80743;

XX DT 25-MAR-2003 (revised)

DT 10-SEP-1990 (first entry)

XX Sequence encoding complete mature and precursor forms of human tissue

DE factor heavy chain proteins (huTfH & pre-huTfH, respectively).

XX Human tissue factor heavy chain (huTfH); immunoassays;

KW precursor human tissue factor heavy chain (pre-huTfH);

KW human tissue factor detection.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 34..921

FT /*tag= a

FT /product= "pre-huTfH"

FT mat_peptide 130..921

FT /*tag= b

FT /product= "huTfH"

XX WO8807543-A.

XX 06-OCT-1988.

XX 31-MAR-1987; 87US-00033047.

XX 31-MAR-1987; 87US-00033047.

XX 25-JUN-1987; 87US-00067103.

XX 09-MAR-1988; 88US-00165939.

(SCRI) SCRIPPS CLINIC & RES FOUND.
 PA Edgington TS, Morrissey JH;
 PI WPI; 1988-292837/41.
 XX P-PSDB; AAP80713.
 DR New DNA segment - has gene encoding human tissue factor heavy chain
 XX protein and is useful for inhibiting coagulation.
 PT Disclosure; Page ?; 148pp; English.
 XX A DNA segment with a nucleotide sequence from about 130 to about 918 of
 CC the sequence given here is claimed. Also claimed are antibodies which
 CC immunoreact with hTGF and the claimed peptides (given in AAP80713). The
 CC antibodies may be used in immunoassays for detection of hTGF. The
 CC claimed peptides may be used to inhibit the binding of hTGF to
 CC coagulation factor VII/VIII in vivo. (Updated on 25-MAR-2003 to correct
 CC PR field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-
 CC MAR-2003 to correct PI field.)
 XX
 SQ Sequence 3 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 3 Other;
 Query Match 6.7%; Score 0.2; DB 1; Length 3;
 Best Local Similarity 0.0%; Pred. No. 2e+09;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 T 2
 Db 2 H 2
 RESULT 20
 AAX57131
 ID AAX57131 standard; DNA; 1 BP.
 AC AAX57131;
 DT 22-JUL-1999 (first entry)
 XX Human mutant KCNQ3 primer 26.
 DE KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;
 KW benign familial neonatal epilepsy; BFNE; juvenile myotonic epilepsy; JME;
 KW rolandic epilepsy; mutant; treatment; screening; epilepsy; detection;
 KW gene therapy; drug screening; primer; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX WO9921875-A1.
 PN 06-MAY-1999.
 XX 23-OCT-1998; 98WO-US022375.
 PF 24-OCT-1997; 97US-0063147P.
 PR (UTAH) UNIV UTAH RES FOUND.
 PA Singh NA, Leppert MF, Charlier C;
 PI WPI; 1999-312938/26.
 XX Nucleic acid encoding potassium channels KCNQ2 and 3.
 PT Claim 65; Page 151; 195pp; English.
 XX This invention describes novel human and mouse potassium channel proteins
 CC KCNQ2 and KCNQ3. Detecting mutations in sequences that encode KCNQ2 or
 CC KCNQ3, or the loss of one copy of these genes, is used for diagnosis and
 CC prognosis of benign familial neonatal epilepsy (BFNE), juvenile myotonic
 CC epilepsy (JME) or rolandic epilepsy (RE). Cells (or transgenic animals)
 CC that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves
 CC in cell-free form) are used to screen for agents that can be used to
 CC treat or prevent these forms of epilepsy. Fragments of the encoding
 CC nucleic acids are used as probes or primers, either for detecting
 CC mutations or for isolation of related sequences, while the complete
 CC sequences may be used in gene therapy to provide wild-type protein.
 CC Antibodies specific for mutant or wild-type proteins are used as

CC that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves
 CC in cell-free form) are used to screen for agents that can be used to
 CC treat or prevent these forms of epilepsy. Fragments of the encoding
 CC nucleic acids are used as probes or primers, either for detecting
 CC mutations or for isolation of related sequences, while the complete
 CC sequences may be used in gene therapy to provide wild-type protein.
 CC Antibodies specific for mutant or wild-type proteins are used as

Query Match 0.0%; Score 0; DB 2; Length 1;
 Best Local Similarity 0.0%; Pred. No. 5.9e+09;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 G 1
 Db 1 A 1
 RESULT 21
 AAX57131/c
 ID AAX57131 standard; DNA; 1 BP.
 AC AAX57131;
 DT 22-JUL-1999 (first entry)
 XX Human mutant KCNQ3 primer 26.
 DE KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;
 KW benign familial neonatal epilepsy; BFNE; juvenile myotonic epilepsy; JME;
 KW rolandic epilepsy; mutant; treatment; screening; epilepsy; detection;
 KW gene therapy; drug screening; primer; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX WO9921875-A1.
 PN 06-MAY-1999.
 XX 23-OCT-1998; 98WO-US022375.
 PF 24-OCT-1997; 97US-0063147P.
 PR (UTAH) UNIV UTAH RES FOUND.
 PA Singh NA, Leppert MF, Charlier C;
 PI WPI; 1999-312938/26.
 XX Nucleic acid encoding potassium channels KCNQ2 and 3.
 PT Claim 65; Page 151; 195pp; English.
 XX This invention describes novel human and mouse potassium channel proteins
 CC KCNQ2 and KCNQ3. Detecting mutations in sequences that encode KCNQ2 or
 CC KCNQ3, or the loss of one copy of these genes, is used for diagnosis and
 CC prognosis of benign familial neonatal epilepsy (BFNE), juvenile myotonic
 CC epilepsy (JME) or rolandic epilepsy (RE). Cells (or transgenic animals)
 CC that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves
 CC in cell-free form) are used to screen for agents that can be used to
 CC treat or prevent these forms of epilepsy. Fragments of the encoding
 CC nucleic acids are used as probes or primers, either for detecting
 CC mutations or for isolation of related sequences, while the complete
 CC sequences may be used in gene therapy to provide wild-type protein.
 CC Antibodies specific for mutant or wild-type proteins are used as

CC diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins are
CC useful in rational design of drugs and therapeutically (in replacement
CC therapies). The forms of epilepsy associated with mutations in KCNQ2 and
CC 3 sequences can now be diagnosed early (before symptoms are manifest),
CC and better treatment options will be available. AAX57074-X57139 are
CC primers used in the method of the invention

SQ Sequence 1 BP; 1 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.0%; Score 0; DB 2; Length 1;
Best Local Similarity 100.0%; Pred. No. 5.9e+09;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 T 2
DB 1 T 1

RESULT 22

ABK94535
ID ABK94535 standard; DNA; 1 BP.

XX
AC ABK94535;

XX
DT 27-AUG-2002 (first entry)

XX
DE Human BRCA1 gene, PCR clamping sequence #3.

XX hMLH1; DNA mismatch repair; BRCA1; ss; clamp sequence; BRCA1;
KW breast and ovarian cancer susceptibility gene; TGDS; PCR;
KW two-dimensional DNA electrophoresis; tumour suppressor gene;
KW breast cancer; ovarian cancer; tumour.

XX
OS Homo sapiens.

XX
PN WO200236819-A1.

XX
PD 10-MAY-2002.

XX
PF 06-NOV-2000; 2000WO-IB001607.

XX
PR 06-NOV-2000; 2000WO-IB001607.

XX
PA (SCSC-) ACAD APPLIED SCI.

XX
PI Vijg J;

XX
DR WPI; 2002-471507/50.

XX
PT Detecting mutations in the BRCA1 and hMLH1 gene comprises subjecting
PT amplification products to 2-dimensional gel electrophoresis to produce a
PT characteristic spot pattern for a specific mutation in either the BRCA1
PT or the hMLH1 gene.

XX
PS Claim 1; Page 54; 57pp; English.

XX
CC The invention relates to detecting mutations in the BRCA1 and hMLH1 gene
CC comprising subjecting a set of amplification products to two-dimensional
CC DNA electrophoresis (TGDS) to produce a characteristic spot pattern for a
CC specific mutation in either the BRCA1 or the hMLH1 gene. Also included
CC are test kits for enabling BRCA1 or hMLH1 gene testing comprising short
CC PCR primers given in the specification, mixed in 20 mM of Tris-HCl, 50 mM
CC KCl, 25 micro M of dNTP, and 5 % formamide. The method is useful for
CC detecting mutations in the BRCA1 (breast and ovarian cancer
CC susceptibility gene, a tumour suppressor gene) and hMLH1 gene (a DNA
CC mismatch repair gene). The present sequence is a PCR clamp sequence used
CC in the method of the invention

XX
SQ Sequence 1 BP; 0 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 0.0%; Score 0; DB 6; Length 1;
Best Local Similarity 100.0%; Pred. No. 5.9e+09;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 G 1
DB 1 G 1

RESULT 23

ABK94535/c
ID ABK94535 standard; DNA; 1 BP.

XX
AC ABK94535;

XX
DT 27-AUG-2002 (first entry)

XX
DE Human BRCA1 gene, PCR clamping sequence #3.

XX hMLH1; DNA mismatch repair; BRCA1; ss; clamp sequence; BRCA1;
KW breast and ovarian cancer susceptibility gene; TGDS; PCR;
KW two-dimensional DNA electrophoresis; tumour suppressor gene;
KW breast cancer; ovarian cancer; tumour.

XX
OS Homo sapiens.

XX
PN WO200236819-A1.

XX
PD 10-MAY-2002.

XX
PF 06-NOV-2000; 2000WO-IB001607.

XX
PR 06-NOV-2000; 2000WO-IB001607.

XX
PA (SCSC-) ACAD APPLIED SCI.

XX
PI Vijg J;

XX
DR WPI; 2002-471507/50.

XX
PT Detecting mutations in the BRCA1 and hMLH1 gene comprises subjecting
PT amplification products to 2-dimensional gel electrophoresis to produce a
PT characteristic spot pattern for a specific mutation in either the BRCA1
PT or the hMLH1 gene.

XX
PS Claim 1; Page 54; 57pp; English.

XX
CC The invention relates to detecting mutations in the BRCA1 and hMLH1 gene
CC comprising subjecting a set of amplification products to two-dimensional
CC DNA electrophoresis (TGDS) to produce a characteristic spot pattern for a
CC specific mutation in either the BRCA1 or the hMLH1 gene. Also included
CC are test kits for enabling BRCA1 or hMLH1 gene testing comprising short
CC PCR primers given in the specification, mixed in 20 mM of Tris-HCl, 50 mM
CC KCl, 25 micro M of dNTP, and 5 % formamide. The method is useful for
CC detecting mutations in the BRCA1 (breast and ovarian cancer
CC susceptibility gene, a tumour suppressor gene) and hMLH1 gene (a DNA
CC mismatch repair gene). The present sequence is a PCR clamp sequence used
CC in the method of the invention

XX
SQ Sequence 1 BP; 0 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 0.0%; Score 0; DB 6; Length 1;
Best Local Similarity 0.0%; Pred. No. 5.9e+09;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 G 1
DB 1 C 1

RESULT 24

ACH82100
ID ACH82100 standard; DNA; 1 BP.

XX
AC ACH82100;

XX

DT 29-JUL-2004 (first entry)
XX Human genome derived single exon probe #15295.
DE Human; probe; ss; gene expression; single exon probe; microarray;
XX alternative splicing event; genomic alteration.
KW Homo sapiens.
OS US2003194704-A1.
XX 16-OCT-2003.
PD 03-APR-2002; 2002US-00029386.
XX 03-APR-2002; 2002US-00029386.
PF (PENN/) PENN S G.
XX (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
XX Penn SG, Rank DR, Hanzel DK;
PI WPI; 2004-119264/12.
DR New human genome-derived single exon nucleic acid probes useful for human
XX gene expression analysis, for identifying or characterizing alternative
XX splicing events, for assessing genomic alterations or as tools for
XX surveying tissues.
PS Claim 1; SEQ ID NO 15295; 80pp; English.
XX The invention relates to a nucleic acid probe for measuring human gene
XX expression, comprising any of the 27,400 fully defined nucleotide
XX sequences in the specification, or their complements or fragments, and
XX encoding at least 8 amino acids of any of the 6888 amino acid sequences
XX fully defined in the specification. The probe is a single exon probe that
XX hybridizes under high stringency conditions to a nucleic acid molecule
XX expressed in human cells or tissues. Also included are a spatially-
XX addressable set of single exon nucleic acid probes for measuring human
XX gene expression (comprising a plurality of single exon nucleic acid
XX probes cited above, where each of the plurality of probes is separately
XX and addressably isolatable or amplifiable from the plurality), a single
XX exon microarray for measuring human gene expression, a method of
XX measuring human gene expression, a vector comprising the single exon
XX probe cited above, an ORF-encoded peptide comprising at least 8
XX contiguous amino acids of any of the above-mentioned amino acid
XX sequences (optionally with conservative amino acid substitutions), an
XX isolated antibody that binds specifically to a peptide cited above,
XX methods of selling and/or licensing single exon probes or microarrays to
XX a customer desiring to measure gene expression, a method of providing
XX human gene expression data by subscription, and a computer-readable
XX storage medium which contains a database having a plurality of records
XX (each record including data on the expression of a single exon probe
XX cited above. The probe, methods and apparatus are useful in gene
XX expression analysis. The probes may be used as tools for surveying
XX tissues to detect the presence of expressed messages that contain their
XX specific exon, or in constructing genome-derived single exon microarrays.
XX In addition, the probes are used in identifying and characterizing
XX alternative splicing events, in detecting and characterizing gross
XX alterations in the genomic locus that includes their exon, in assessing
XX smaller genomic alterations, in priming the synthesis of nucleic acids
XX or in expressing the ORF-encoded peptide. The present sequence is a human
XX single exon probe of the invention. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html?DocID=20030194704
XX Sequence 1 BP; 0 A; 1 C; 0 G; 0 T; 0 U; 0 Other;
XX Query Watch 0.0%; Score 0; DB 12; Length 1;
XX Best Local Similarity 0.0%; Pred. No. 5.9e+09;
XX Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 G 1
Db 1 C 1
RESULT 25
ACH82100/c
ID ACH82100 standard; DNA; 1 BP.
XX ACH82100;
AC ACH82100;
XX 29-JUL-2004 (first entry)
DT Human genome derived single exon probe #15295.
XX Human; probe; ss; gene expression; single exon probe; microarray;
KW alternative splicing event; genomic alteration.
XX Homo sapiens.
OS US2003194704-A1.
XX 16-OCT-2003.
PD 03-APR-2002; 2002US-00029386.
XX 03-APR-2002; 2002US-00029386.
PF (PENN/) PENN S G.
XX (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
XX Penn SG, Rank DR, Hanzel DK;
PI WPI; 2004-119264/12.
DR New human genome-derived single exon nucleic acid probes useful for human
XX gene expression analysis, for identifying or characterizing alternative
XX splicing events, for assessing genomic alterations or as tools for
XX surveying tissues.
PS Claim 1; SEQ ID NO 15295; 80pp; English.
XX The invention relates to a nucleic acid probe for measuring human gene
XX expression, comprising any of the 27,400 fully defined nucleotide
XX sequences in the specification, or their complements or fragments, and
XX encoding at least 8 amino acids of any of the 6888 amino acid sequences
XX fully defined in the specification. The probe is a single exon probe that
XX hybridizes under high stringency conditions to a nucleic acid molecule
XX expressed in human cells or tissues. Also included are a spatially-
XX addressable set of single exon nucleic acid probes for measuring human
XX gene expression (comprising a plurality of single exon nucleic acid
XX probes cited above, where each of the plurality of probes is separately
XX and addressably isolatable or amplifiable from the plurality), a single
XX exon microarray for measuring human gene expression, a method of
XX measuring human gene expression, a vector comprising the single exon
XX probe cited above, an ORF-encoded peptide comprising at least 8
XX contiguous amino acids of any of the above-mentioned amino acid
XX sequences (optionally with conservative amino acid substitutions), an
XX isolated antibody that binds specifically to a peptide cited above,
XX methods of selling and/or licensing single exon probes or microarrays to
XX a customer desiring to measure gene expression, a method of providing
XX human gene expression data by subscription, and a computer-readable
XX storage medium which contains a database having a plurality of records
XX (each record including data on the expression of a single exon probe
XX cited above. The probe, methods and apparatus are useful in gene
XX expression analysis. The probes may be used as tools for surveying
XX tissues to detect the presence of expressed messages that contain their
XX specific exon, or in constructing genome-derived single exon microarrays.
XX In addition, the probes are used in identifying and characterizing
XX alternative splicing events, in detecting and characterizing gross
XX alterations in the genomic locus that includes their exon, in assessing
XX smaller genomic alterations, in priming the synthesis of nucleic acids
XX or in expressing the ORF-encoded peptide. The present sequence is a human
XX single exon probe of the invention. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html?DocID=20030194704

CC smaller genomic alterations, in priming the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030194704
 XX
 SQ Sequence 1 BP; 0 A; 1 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.0%; Score 0; DB 12; Length 1;
 Best Local Similarity 100.0%; Pred. No. 5.9e+09;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 G 1
 Db 1 G 1

RESULT 26

ACH81204
 ID ACH81204 standard; DNA; 1 BP.

XX
 AC ACH81204;

XX
 DT 29-JUL-2004 (first entry)

XX
 DE Human genome derived single exon probe #14399.

XX
 KW Human; probe; ss; gene expression; single exon probe; microarray;
 KW alternative splicing event; genomic alteration.

OS Homo sapiens.

XX
 PN US2003194704-A1.

XX
 PD 16-OCT-2003.

XX
 PF 03-APR-2002; 2002US-00029386.

XX
 PR 03-APR-2002; 2002US-00029386.

XX
 PA (PENN/) PENN S G.

XX
 PA (RANK/) RANK D R.

XX
 PA (HANKZ/) HANZEL D K.

XX
 PI Penn SG, Rank DR, Hanzel DK;

XX
 DR WPI; 2004-119264/12.

XX
 PT New human genome-derived single exon nucleic acid probes useful for human
 PT gene expression analysis, for identifying or characterizing alternative
 PT splicing events, for assessing genomic alterations or as tools for
 PT surveying tissues.

XX
 PS Claim 1; SEQ ID NO 14399; 80pp; English.

XX
 CC The invention relates to a nucleic acid probe for measuring human gene
 CC expression, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that
 CC hybridises under high stringency conditions to a nucleic acid molecule
 CC expressed in human cells or tissues. Also included are a spatially-
 CC addressable set of single exon nucleic acid probes for measuring human
 CC gene expression (comprising a plurality of single exon nucleic acid
 CC probes cited above, where each of the plurality of probes is separately
 CC and addressably isolatable or amplifiable from the plurality), a single
 CC exon microarray for measuring human gene expression, a method of
 CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,

CC methods of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing
 CC human gene expression data by subscription, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above). The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterising
 CC alternative splicing events, in detecting and characterising gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030194704
 XX

SQ Sequence 1 BP; 0 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 0.0%; Score 0; DB 12; Length 1;
 Best Local Similarity 100.0%; Pred. No. 5.9e+09;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 G 1
 Db 1 G 1

RESULT 27

ACH81204/c

ID ACH81204 standard; DNA; 1 BP.

XX
 AC ACH81204;

XX
 DT 29-JUL-2004 (first entry)

XX
 DE Human genome derived single exon probe #14399.

XX
 KW Human; probe; ss; gene expression; single exon probe; microarray;
 KW alternative splicing event; genomic alteration.

XX
 OS Homo sapiens.

XX
 PN US2003194704-A1.

XX
 PD 16-OCT-2003.

XX
 PF 03-APR-2002; 2002US-00029386.

XX
 PR 03-APR-2002; 2002US-00029386.

XX
 PA (PENN/) PENN S G.

XX
 PA (RANK/) RANK D R.

XX
 PA (HANKZ/) HANZEL D K.

XX
 PI Penn SG, Rank DR, Hanzel DK;

XX
 DR WPI; 2004-119264/12.

XX
 PT New human genome-derived single exon nucleic acid probes useful for human
 PT gene expression analysis, for identifying or characterizing alternative
 PT splicing events, for assessing genomic alterations or as tools for
 PT surveying tissues.

XX
 PS Claim 1; SEQ ID NO 14399; 80pp; English.

XX
 CC The invention relates to a nucleic acid probe for measuring human gene
 CC expression, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that

PR 09-JUL-1993; 93US-00089248.
XX (LASK/) LASKOWSKI M.
PA (ANDE/) ANDERSON S.
XX Laskowski M, Anderson S;
XX WPI; 1995-066900/09.
DR
XX Protein inhibitors of serine proteinase(s), e.g. furin, deriv. from
XX turkey ovomucoid third domain - used as laboratory reagents to study the
PT proteinase(s), or as chemotherapeutic agents to treat diseases associated
PT with them.
XX
PS Disclosure; Page 42-45; 66pp; English.
XX
XX In synthetic analogs of turkey ovomucoid domain protein (6-56) (OMTKY3),
CC given in AAR69818-24, the region immediately adjacent to the reactive
CC site peptide bond is mutated to include the consensus sequence of furin
CC or other serine protease. Polynucleotides encoding such analogs are
CC incorporated into pEZ2318.thy2 and expressed in Escherichia coli RV308
CC (ATCC 31608). (Updated on 25-MAR-2003 to correct PN field.)
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SQ Sequence 3 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 3 Other;
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Best Local Similarity 0.0%; Pred. No. 2e+09;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 G 1
Db 1 N 1
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ID AAQ85491 standard; cDNA; 3 BP.
XX AC AAQ85491;
XX
XX 25-MAR-2003 (revised)
DT 18-AUG-1995 (first entry)
XX
XX Plasmid pEZ2318.thy2.
XX
XX OMTKY3; turkey ovomucoid third domain peptide inhibitor; furin inhibitor;
KW protease inhibitor; pEZ2318.thy2; probe; Escherichia coli; ss.
XX Synthetic.
XX
XX WO9502055-A1.
XX
XX 19-JAN-1995.
XX
XX 08-JUL-1994; 94WO-US007779.
XX
XX 09-JUL-1993; 93US-00089248.
XX
XX (LASK/) LASKOWSKI M.
PA (ANDE/) ANDERSON S.
XX Laskowski M, Anderson S;
XX WPI; 1995-066900/09.
DR
XX Protein inhibitors of serine proteinase(s), e.g. furin, deriv. from
XX turkey ovomucoid third domain - used as laboratory reagents to study the
PT proteinase(s), or as chemotherapeutic agents to treat diseases associated
PT with them.
XX
PS Disclosure; Page 42-45; 66pp; English.
XX
XX In synthetic analogs of turkey ovomucoid domain protein (6-56) (OMTKY3),
CC given in AAR69818-24, the region immediately adjacent to the reactive
CC site peptide bond is mutated to include the consensus sequence of furin
CC or other serine protease. Polynucleotides encoding such analogs are
CC incorporated into pEZ2318.thy2 and expressed in Escherichia coli RV308
CC (ATCC 31608). (Updated on 25-MAR-2003 to correct PN field.)
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Best Local Similarity 0.0%; Pred. No. 2e+09;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 G 1
Db 3 N 3
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Job time : 280 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 18:59:06 ; Search time 1696 Seconds
(without alignments)
85.711 Million cell updates/sec

Title: US-09-735-363A-8
Perfect score: 3
Sequence: 1 stg 3

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 550

Minimum DB seq length: 0
Maximum DB seq length: 3

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

- 1: gb_ba.*
- 2: gb_hcg.*
- 3: gb_in.*
- 4: gb_on.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	3	100.0	3	6	CQ787755 Sequence
C 2	3	100.0	3	6	CQ787827 Sequence
C 3	3	100.0	3	6	AX092473 Sequence
C 4	3	100.0	3	6	AX092502 Sequence
C 5	3	100.0	3	6	AX175244 Sequence
C 6	3	100.0	3	6	AX743312 Sequence
C 7	3	100.0	3	6	AX743316 Sequence
C 8	3	100.0	3	6	AX816713 Sequence
C 9	2	66.7	2	6	CQ787746 Sequence
C 10	2	66.7	2	6	CQ787759 Sequence
C 11	2	66.7	2	6	CQ787816 Sequence
C 12	2	66.7	2	6	CQ787830 Sequence
C 13	2	66.7	2	6	CQ787891 Sequence
C 14	2	66.7	2	6	CQ787892 Sequence
C 15	2	66.7	2	6	CQ787893 Sequence
C 16	2	66.7	2	6	CQ787923 Sequence
C 17	2	66.7	2	6	CQ787936 Sequence
C 18	2	66.7	2	6	CQ787937 Sequence
C 19	2	66.7	2	6	CQ787938 Sequence

C 20	2	66.7	2	6	CQ787939 Sequence
C 21	2	66.7	2	6	CQ787940 Sequence
C 22	2	66.7	2	6	CQ787941 Sequence
C 23	2	66.7	2	6	CQ787964 Sequence
C 24	2	66.7	2	6	CQ787967 Sequence
C 25	2	66.7	2	6	CQ787969 Sequence
C 26	2	66.7	2	6	CQ787976 Sequence
C 27	2	66.7	2	6	CQ788021 Sequence
C 28	2	66.7	2	6	CQ788022 Sequence
C 29	2	66.7	2	6	CQ788023 Sequence
C 30	2	66.7	2	6	CQ788025 Sequence
C 31	2	66.7	2	6	CQ788052 Sequence
C 32	2	66.7	2	6	CQ788053 Sequence
C 33	2	66.7	2	6	CQ788067 Sequence
C 34	2	66.7	2	6	AX092441 Sequence
C 35	2	66.7	2	6	AX092444 Sequence
C 36	2	66.7	2	6	AX092451 Sequence
C 37	2	66.7	2	6	AX092454 Sequence
C 38	2	66.7	2	6	AX092528 Sequence
C 39	2	66.7	2	6	AX092538 Sequence
C 40	2	66.7	2	6	AX175286 Sequence
C 41	2	66.7	2	6	AX175287 Sequence
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C 52	2	66.7	3	6	CQ787823 Sequence
C 53	2	66.7	3	6	CQ787828 Sequence
C 54	2	66.7	3	6	CQ787829 Sequence
C 55	2	66.7	3	6	CQ787911 Sequence
C 56	2	66.7	3	6	CQ787955 Sequence
C 57	2	66.7	3	6	CQ787960 Sequence
C 58	2	66.7	3	6	CQ787961 Sequence
C 59	2	66.7	3	6	CQ787962 Sequence
C 60	2	66.7	3	6	CQ787963 Sequence
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C 63	2	66.7	3	6	CQ788065 Sequence
C 64	2	66.7	3	6	CQ788066 Sequence
C 65	2	66.7	3	6	E09178 Synthetic O
C 66	2	66.7	3	6	E09494 Phosphoroth
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C 68	2	66.7	3	6	AX092460 Sequence
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C 75	2	66.7	3	6	AX092474 Sequence
C 76	2	66.7	3	6	AX092475 Sequence
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C 82	2	66.7	3	6	AX092499 Sequence
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C 86	2	66.7	3	6	AX092505 Sequence
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C 90	2	66.7	3	6	AX092514 Sequence
C 91	2	66.7	3	6	AX092515 Sequence
C 92	2	66.7	3	6	AX092518 Sequence

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ALIGNMENTS

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 LOCUS CQ787755 3 bp DNA linear PAT 24-MAR-2004
 DEFINITION Sequence 61 from Patent WO2004020664.
 ACCESSION CQ787755
 VERSION CQ787755.1 GI:45722713
 KEYWORDS Bos taurus (cow)
 SOURCE Bos taurus
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
 REFERENCE 1
 AUTHORS Geldermann,H., Preuss,S. and Han,Y.
 TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
 purposes
 JOURNAL Patent: WO 2004020664-A 61 11-MAR-2004;
 Universitaet Hohenheim (DE)
 FEATURES Location/Qualifiers
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QY 1 GTG 3
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 Db 3 GTG 1

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 LOCUS CQ787827 3 bp DNA linear PAT 24-MAR-2004
 DEFINITION Sequence 133 from Patent WO2004020664.
 ACCESSION CQ787827
 VERSION CQ787827.1 GI:45722785
 KEYWORDS Ovis aries (sheep)
 SOURCE Ovis aries
 ORGANISM Ovis aries
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Caprinae; Ovis.

REFERENCE 1
 AUTHORS Geldermann,H., Preuss,S. and Han,Y.
 TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
 purposes
 JOURNAL Patent: WO 2004020664-A 133 11-MAR-2004;
 Universitaet Hohenheim (DE)
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 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTG 3
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 Db 3 GTG 1

RESULT 3
 AX092473/c
 LOCUS AX092473 3 bp DNA linear PAT 21-MAR-2001
 DEFINITION Sequence 34 from Patent WO0116366.
 ACCESSION AX092473
 VERSION AX092473.1 GI:13444568
 KEYWORDS .
 SOURCE unidentified
 ORGANISM unidentified

REFERENCE 1 (bases 1 to 3)
 AUTHORS Kless,H.
 TITLE Template-dependent nucleic acid polymerization using
 oligonucleotide triphosphates building blocks
 Patent: WO 0116366-A 34 08-MAR-2001;
 YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
 (IL)
 JOURNAL Location/Qualifiers
 FEATURES source 1..3
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 /note="synthetic oligonucleotide"

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Query Match 100.0%; Score 3; DB 6; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTG 3
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 Db 3 GTG 1

RESULT 4
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 LOCUS AX092502 3 bp DNA linear PAT 21-MAR-2001
 DEFINITION Sequence 63 from Patent WO0116366.
 ACCESSION AX092502
 VERSION AX092502.1 GI:13444597
 KEYWORDS .
 SOURCE unidentified
 ORGANISM unidentified

REFERENCE 1 (bases 1 to 3)
 AUTHORS Kless,H.
 TITLE Template-dependent nucleic acid polymerization using
 oligonucleotide triphosphates building blocks
 Patent: WO 0116366-A 63 08-MAR-2001;
 YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
 (IL)
 JOURNAL Location/Qualifiers
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QY 1 GTG 3
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Db 1 GTG 3

RESULT 5

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LOCUS AX175244 3 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 8 from Patent WO0144465.
ACCESSION AX175244
VERSION AX175244.1 GI:14598612

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 3)
AUTHORS Phillips,N.C. and Filion,M.C.

TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 8 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)

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QY 1 GTG 3
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Db 1 GTG 3

RESULT 6

AX743312
LOCUS AX743312 3 bp DNA linear PAT 12-MAY-2003
DEFINITION Sequence 4 from Patent WO03028764.
ACCESSION AX743312
VERSION AX743312.1 GI:30577238

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Phillips,N.C., Filion,M.C. and Herrera-Gayol,A.C.

TITLE Therapeutically useful triethyleneglycol cholesteryl oligonucleotides
JOURNAL Patent: WO 03028764-A 4 10-APR-2003;
Bioniche Life Sciences Inc. (CA) ; Phillips, Nigel C. (CA)

FEATURES
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Db 1 GTG 3

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LOCUS AX743316 3 bp DNA linear PAT 12-MAY-2003
DEFINITION Sequence 8 from Patent WO03028764.
ACCESSION AX743316
VERSION AX743316.1 GI:30577242

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1

AUTHORS Phillips,N.C., Filion,M.C. and Herrera-Gayol,A.C.
TITLE Therapeutically useful triethyleneglycol cholesteryl oligonucleotides

JOURNAL Patent: WO 03028764-A 8 10-APR-2003;
Bioniche Life Sciences Inc. (CA) ; Phillips, Nigel C. (CA)

FEATURES
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Location/Qualifiers

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Db 1 GTG 3

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AX816713
LOCUS AX816713 3 bp DNA linear PAT 09-DEC-2003
DEFINITION Sequence 1 from Patent WO02085340.
ACCESSION AX816713
VERSION AX816713.1 GI:39647042

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1

AUTHORS Filion,M.C. and Phillips,N.C.
TITLE Oligonucleotide compositions and their use to induce differentiation of cells

JOURNAL Patent: WO 02085340-A 1 31-OCT-2002;
Bioniche Life Sciences Inc. (CA)

FEATURES
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Location/Qualifiers

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/mol_type="unassigned DNA"
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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Sequence 52 from Patent WO2004020664.

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VERSION     CQ787746.1  GI:45722704
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SOURCE      Bos taurus
ORGANISM    Bos taurus
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            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1
AUTHORS    Geldermann,H., Preuss,S. and Han,Y.
TITLE      Polymorphous microsatellite loci in genes for pre-diagnostic
            purposes
JOURNAL    Patent: WO 2004020664-A 52 11-MAR-2004;
            Universitaet Hohenheim (DE)
FEATURES    Location/Qualifiers
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Db      2 TG 1

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LOCUS       CQ787759
DEFINITION Sequence 65 from Patent WO2004020664.
ACCESSION   CQ787759
VERSION     CQ787759.1  GI:45722717
KEYWORDS    Bos taurus (cow)
SOURCE      Bos taurus
ORGANISM    Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1
AUTHORS    Geldermann,H., Preuss,S. and Han,Y.
TITLE      Polymorphous microsatellite loci in genes for pre-diagnostic
            purposes
JOURNAL    Patent: WO 2004020664-A 65 11-MAR-2004;
            Universitaet Hohenheim (DE)
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Db      2 GT 1

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DEFINITION Sequence 122 from Patent WO2004020664.
ACCESSION   CQ787816
VERSION     CQ787816.1  GI:45722774
KEYWORDS    Ovis aries (sheep)
SOURCE      Ovis aries
ORGANISM    Ovis aries
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Caprinae; Ovis.
REFERENCE   1
AUTHORS    Geldermann,H., Preuss,S. and Han,Y.
TITLE      Polymorphous microsatellite loci in genes for pre-diagnostic
            purposes
JOURNAL    Patent: WO 2004020664-A 122 11-MAR-2004;
            Universitaet Hohenheim (DE)
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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TG 3
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Db      2 TG 1

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DEFINITION Sequence 136 from Patent WO2004020664.
ACCESSION   CQ787830
VERSION     CQ787830.1  GI:45722788
KEYWORDS    Ovis aries (sheep)
SOURCE      Ovis aries
ORGANISM    Ovis aries
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Caprinae; Ovis.
REFERENCE   1
AUTHORS    Geldermann,H., Preuss,S. and Han,Y.
TITLE      Polymorphous microsatellite loci in genes for pre-diagnostic
            purposes
JOURNAL    Patent: WO 2004020664-A 136 11-MAR-2004;
            Universitaet Hohenheim (DE)
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QY      1 GT 2
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Db      2 GT 1

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RESULT 13
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ACCESSION CQ787891
VERSION CQ787891.1 GI:45722849
KEYWORDS
SOURCE Bos taurus (cow)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1
REFERENCE Geldermann,H., Preuss,S. and Han,Y.
AUTHORS Polymorphous microsatellite loci in genes for pre-diagnostic
TITLE purposes
JOURNAL Patent: WO 2004020664-A 197 11-MAR-2004;
UNIVERSITAET HOHENHEIM (DE)
FEATURES
source 1..2
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/db_xref="taxon:9913"
repeat_unit 1..2
/note="Anzahl der Wiederholungen: 12"
satellite 1..2
/note="R11, Allel R"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TG 3
Db 2 TG 1
RESULT 14
CQ787892/c
LOCUS
DEFINITION Sequence 198 from Patent WO2004020664.
ACCESSION CQ787892
VERSION CQ787892.1 GI:45722850
KEYWORDS
SOURCE Bos taurus (cow)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1
REFERENCE Geldermann,H., Preuss,S. and Han,Y.
AUTHORS Polymorphous microsatellite loci in genes for pre-diagnostic
TITLE purposes
JOURNAL Patent: WO 2004020664-A 198 11-MAR-2004;
UNIVERSITAET HOHENHEIM (DE)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:9913"
repeat_unit 1..2
/note="Anzahl der Wiederholungen: 10"
satellite 1..2
/note="R11, Allel A"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TG 3
Db 2 TG 1
RESULT 15
CQ787893/c
LOCUS
DEFINITION Sequence 199 from Patent WO2004020664.
ACCESSION CQ787893
VERSION CQ787893.1 GI:45722851
KEYWORDS
SOURCE Bos taurus (cow)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1
REFERENCE Geldermann,H., Preuss,S. and Han,Y.
AUTHORS Polymorphous microsatellite loci in genes for pre-diagnostic
TITLE purposes
JOURNAL Patent: WO 2004020664-A 199 11-MAR-2004;
UNIVERSITAET HOHENHEIM (DE)
FEATURES
source 1..2
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/db_xref="taxon:9913"
repeat_unit 1..2
/note="Anzahl der Wiederholungen: 13"
satellite 1..2
/note="R11, Allel C"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TG 3
Db 2 TG 1
RESULT 16
CQ787923/c
LOCUS
DEFINITION Sequence 229 from Patent WO2004020664.
ACCESSION CQ787923
VERSION CQ787923.1 GI:45722881
KEYWORDS
SOURCE Bos taurus (cow)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1
REFERENCE Geldermann,H., Preuss,S. and Han,Y.
AUTHORS Polymorphous microsatellite loci in genes for pre-diagnostic
TITLE purposes
JOURNAL Patent: WO 2004020664-A 229 11-MAR-2004;
UNIVERSITAET HOHENHEIM (DE)
FEATURES
source 1..2
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satellite 1..2
/note="R27, Allel R"
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QY 1 GT 2
Db 2 GT 1

RESULT 17
CQ787936/c
LOCUS CQ787936 2 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 242 from Patent WO2004020664.
ACCESSION CQ787936
VERSION CQ787936.1 GI:45722894
KEYWORDS Ovis aries (sheep)
SOURCE Ovis aries
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
REFERENCE 1
AUTHORS Geldermann,H., Preuss,S. and Han,Y.
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
purposes
JOURNAL Patent: WO 2004020664-A 242 11-MAR-2004;
Universitaet Hohenheim (DE)
FEATURES
source 1..2
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/db_xref="taxon:9940"
repeat_unit 1..2
satellite 1..2
/notes="Anzahl der Wiederholungen: 12"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TG 3
Db 2 TG 1

RESULT 18
CQ787937/c
LOCUS CQ787937 2 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 243 from Patent WO2004020664.
ACCESSION CQ787937
VERSION CQ787937.1 GI:45722895
KEYWORDS Ovis aries (sheep)
SOURCE Ovis aries
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
REFERENCE 1
AUTHORS Geldermann,H., Preuss,S. and Han,Y.
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
purposes
JOURNAL Patent: WO 2004020664-A 243 11-MAR-2004;
Universitaet Hohenheim (DE)
FEATURES
source 1..2
/organism="Ovis aries"
/mol_type="unassigned DNA"
/db_xref="taxon:9940"
repeat_unit 1..2
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/notes="Anzahl der Wiederholungen: 8"

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TG 3
Db 2 TG 1

RESULT 19
CQ787938/c
LOCUS CQ787938 2 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 244 from Patent WO2004020664.
ACCESSION CQ787938
VERSION CQ787938.1 GI:45722896
KEYWORDS Ovis aries (sheep)
SOURCE Ovis aries
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
REFERENCE 1
AUTHORS Geldermann,H., Preuss,S. and Han,Y.
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
purposes
JOURNAL Patent: WO 2004020664-A 244 11-MAR-2004;
Universitaet Hohenheim (DE)
FEATURES
source 1..2
/organism="Ovis aries"
/mol_type="unassigned DNA"
/db_xref="taxon:9940"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TG 3
Db 2 TG 1

RESULT 20
CQ787939/c
LOCUS CQ787939 2 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 245 from Patent WO2004020664.
ACCESSION CQ787939
VERSION CQ787939.1 GI:45722897
KEYWORDS Ovis aries (sheep)
SOURCE Ovis aries
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
REFERENCE 1
AUTHORS Geldermann,H., Preuss,S. and Han,Y.
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
purposes
JOURNAL Patent: WO 2004020664-A 245 11-MAR-2004;
Universitaet Hohenheim (DE)
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source 1..2
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satellite
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 TG 3
||
2 TG 1
Db

RESULT 21
CQ787940/c
LOCUS CQ787940 2 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 246 from Patent WO2004020664.
ACCESSION CQ787940
VERSION CQ787940.1 GI:45722898
KEYWORDS Ovis aries (sheep)
SOURCE Ovis aries
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
REFERENCE 1
AUTHORS Geldermann,H., Preuss,S. and Han,Y.
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
purposes
JOURNAL Patent: WO 2004020664-A 246 11-MAR-2004;
Universitaet Hohenheim (DE)
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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 TG 3
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2 TG 1
Db

RESULT 22
CQ787941/c
LOCUS CQ787941 2 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 247 from Patent WO2004020664.
ACCESSION CQ787941
VERSION CQ787941.1 GI:45722899
KEYWORDS Ovis aries (sheep)
SOURCE Ovis aries
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
REFERENCE 1
AUTHORS Geldermann,H., Preuss,S. and Han,Y.
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
purposes
JOURNAL Patent: WO 2004020664-A 247 11-MAR-2004;
Universitaet Hohenheim (DE)
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/note="S11, Allel E"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 TG 3
||
2 TG 1
Db

RESULT 23
CQ787964/c
LOCUS CQ787964 2 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 270 from Patent WO2004020664.
ACCESSION CQ787964
VERSION CQ787964.1 GI:45722922
KEYWORDS Ovis aries (sheep)
SOURCE Ovis aries
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
REFERENCE 1
AUTHORS Geldermann,H., Preuss,S. and Han,Y.
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
purposes
JOURNAL Patent: WO 2004020664-A 270 11-MAR-2004;
Universitaet Hohenheim (DE)
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/db_xref="taxon:9940"
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satellite
1..2
/note="S27, Allel R"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GT 2
||
2 GT 1
Db

RESULT 24
CQ787967
LOCUS CQ787967 2 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 273 from Patent WO2004020664.
ACCESSION CQ787967
VERSION CQ787967.1 GI:45722925
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Geldermann,H., Preuss,S. and Han,Y.
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
purposes
JOURNAL Patent: WO 2004020664-A 273 11-MAR-2004;
Universitaet Hohenheim (DE)
FEATURES
Location/Qualifiers
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repeat_unit
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/notes="Anzahl der Wiederholungen: 21"

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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
Db 1 GT 2

RESULT 25
CQ787969/c
LOCUS
DEFINITION
Sequence 275 from Patent WO2004020664.
ACCESSION
CQ787969
VERSION
CQ787969.1 GI:45722927
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Geldermann,H., Preuss,S. and Han,Y.
TITLE
Polymorphous microsatellite loci in genes for pre-diagnostic
purposes
JOURNAL
Patent: WO 2004020664-A 275 11-MAR-2004;
Universitaet Hohenheim (DE)
FEATURES
Location/Qualifiers
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repeat_unit
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ORIGIN
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Best Local Similarity 66.7%; Score 2; DB 6; Length 2;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
Db 2 GT 1

RESULT 26
CQ787976/c
LOCUS
DEFINITION
Sequence 282 from Patent WO2004020664.
ACCESSION
CQ787976
VERSION
CQ787976.1 GI:45722934
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Geldermann,H., Preuss,S. and Han,Y.
TITLE
Polymorphous microsatellite loci in genes for pre-diagnostic
purposes
JOURNAL
Patent: WO 2004020664-A 282 11-MAR-2004;
Universitaet Hohenheim (DE)

source
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QY 1 GT 2
Db 1 GT 2

RESULT 27
CQ788021
LOCUS
DEFINITION
Sequence 327 from Patent WO2004020664.
ACCESSION
CQ788021
VERSION
CQ788021.1 GI:45722978
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Geldermann,H., Preuss,S. and Han,Y.
TITLE
Polymorphous microsatellite loci in genes for pre-diagnostic
purposes
JOURNAL
Patent: WO 2004020664-A 327 11-MAR-2004;
Universitaet Hohenheim (DE)
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satellite
1..2
/notes="M03, Allel R (PrP-Gen)"

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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GT 2
Db 1 GT 2

RESULT 28
CQ788022
LOCUS
DEFINITION
Sequence 328 from Patent WO2004020664.
ACCESSION
CQ788022
VERSION
CQ788022.1 GI:45722979
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Geldermann,H., Preuss,S. and Han,Y.
TITLE
Polymorphous microsatellite loci in genes for pre-diagnostic
purposes
JOURNAL
Patent: WO 2004020664-A 328 11-MAR-2004;
Universitaet Hohenheim (DE)

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/organism="Homo sapiens"
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/notes="Anzahl der Wiederholungen: 18"

ORIGIN
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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TG 3
Db 2 TG 1

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JOURNAL Patent: WO 2004020664-A 331 11-MAR-2004;
Universitaet Hohenheim (DE)
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GT 2
Db 1 GT 2

RESULT 29
LOCUS CQ788023 2 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 329 from Patent WO2004020664.
ACCESSION CQ788023
VERSION CQ788023.1 GI:45722980
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Geldermann,H., Preuss,S. and Han,Y.
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
JOURNAL Patent: WO 2004020664-A 329 11-MAR-2004;
Universitaet Hohenheim (DE)
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Query Match 66.7%; Score 2; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GT 2
Db 1 GT 2

RESULT 30
LOCUS CQ788025 2 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 331 from Patent WO2004020664.
ACCESSION CQ788025
VERSION CQ788025.1 GI:45722981
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Geldermann,H., Preuss,S. and Han,Y.
TITLE Polymorphous microsatellite loci in genes for pre-diagnostic

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JOURNAL Patent: WO 2004020664-A 331 11-MAR-2004;
Universitaet Hohenheim (DE)
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GT 2
Db 1 GT 2

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Search completed: July 20, 2005, 21:15:06
Job time : 1699 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 21:47:48 ; Search time 738.2 Seconds
(without alignments)

393.838 Million cell updates/sec

Title: US-09-735-363A-10

Perfect score: 6

Sequence: 1 ggtgtg 6

Scoring table: IDENTITY NUC

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Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 4754

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	6	100.0	6	6	AX175246 Sequence
2	6	100.0	6	6	AX175307 Sequence
3	5	83.3	6	6	E06868 Substrate O
4	5	83.3	6	6	AX175245 Sequence
5	5	83.3	6	6	AX175306 Sequence
6	5	83.3	6	6	AX239662 Sequence
7	4.4	73.3	6	6	CQ755831 Sequence
8	4.4	73.3	6	6	CQ755836 Sequence
9	4.4	73.3	6	6	CQ758069 Sequence
10	4.4	73.3	6	6	CQ758074 Sequence
11	4.4	73.3	6	6	CQ788027 Sequence
12	4.4	73.3	6	6	AX764869 Sequence
13	4.4	73.3	6	6	AX764874 Sequence
14	4.4	66.7	4	6	AX805867 Sequence
15	4	66.7	4	6	AX175290 Sequence
16	4	66.7	4	6	AX175295 Sequence
17	4	66.7	5	6	CQ868954 Sequence
18	4	66.7	5	6	CQ868982 Sequence
19	4	66.7	5	6	CQ869103 Sequence

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C	22	4	66.7	5	6	AX449528 Sequence
C	23	4	66.7	5	6	AX805861 Sequence
C	24	4	66.7	5	6	CQ755803 Sequence
C	25	4	66.7	6	6	CQ758041 Sequence
C	26	4	66.7	6	6	AX104453 Sequence
C	27	4	66.7	6	6	AX107946 Sequence
C	28	4	66.7	6	6	AX107947 Sequence
C	29	4	66.7	6	6	AX107950 Sequence
C	30	4	66.7	6	6	AX175275 Sequence
C	31	4	66.7	6	6	AX355021 Sequence
C	32	4	66.7	6	6	AX359851 Sequence
C	33	4	66.7	6	6	AX547506 Sequence
C	34	4	66.7	6	6	AX764841 Sequence
C	35	3.4	56.7	5	6	A97990 Sequence 20
C	36	3.4	56.7	5	6	CQ787740 Sequence
C	37	3.4	56.7	5	6	CQ787812 Sequence
C	38	3.4	56.7	5	6	CQ787970 Sequence
C	39	3.4	56.7	5	6	CQ868947 Sequence
C	40	3.4	56.7	5	6	CQ868949 Sequence
C	41	3.4	56.7	5	6	CQ869003 Sequence
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C	43	3.4	56.7	5	6	CQ869035 Sequence
C	44	3.4	56.7	5	6	CQ869096 Sequence
C	45	3.4	56.7	5	6	CQ869098 Sequence
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C	48	3.4	56.7	5	6	CQ869184 Sequence
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C	50	3.4	56.7	5	6	AX046167 Sequence
C	51	3.4	56.7	5	6	AX175297 Sequence
C	52	3.4	56.7	5	6	AX186622 Sequence
C	53	3.4	56.7	5	6	AX268756 Sequence
C	54	3.4	56.7	5	6	AX268758 Sequence
C	55	3.4	56.7	5	6	AX805865 Sequence
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C	58	3.4	56.7	6	6	A91411 Sequence 1
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C	60	3.4	56.7	6	6	CQ755676 Sequence
C	61	3.4	56.7	6	6	CQ755702 Sequence
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C	63	3.4	56.7	6	6	CQ755726 Sequence
C	64	3.4	56.7	6	6	CQ755734 Sequence
C	65	3.4	56.7	6	6	CQ755744 Sequence
C	66	3.4	56.7	6	6	CQ755763 Sequence
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C	69	3.4	56.7	6	6	CQ755849 Sequence
C	70	3.4	56.7	6	6	CQ756048 Sequence
C	71	3.4	56.7	6	6	CQ756230 Sequence
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C	76	3.4	56.7	6	6	CQ757964 Sequence
C	77	3.4	56.7	6	6	CQ757972 Sequence
C	78	3.4	56.7	6	6	CQ757982 Sequence
C	79	3.4	56.7	6	6	CQ758001 Sequence
C	80	3.4	56.7	6	6	CQ758009 Sequence
C	81	3.4	56.7	6	6	CQ758010 Sequence
C	82	3.4	56.7	6	6	CQ758087 Sequence
C	83	3.4	56.7	6	6	CQ758286 Sequence
C	84	3.4	56.7	6	6	CQ758468 Sequence
C	85	3.4	56.7	6	6	CQ758739 Sequence
C	86	3.4	56.7	6	6	CQ787756 Sequence
C	87	3.4	56.7	6	6	CQ787918 Sequence
C	88	3.4	56.7	6	6	CQ787945 Sequence
C	89	3.4	56.7	6	6	CQ787946 Sequence
C	90	3.4	56.7	6	6	CQ787947 Sequence
C	91	3.4	56.7	6	6	CQ787948 Sequence
C	92	3.4	56.7	6	6	CQ788051 Sequence

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 94 3.4 56.7 6 6 AX069170 Sequence
 c 95 3.4 56.7 6 6 AX166334 Sequence
 96 3.4 56.7 6 6 AX175239 Sequence
 97 3.4 56.7 6 6 AX175260 Sequence
 98 3.4 56.7 6 6 AX175261 Sequence
 99 3.4 56.7 6 6 AX175262 Sequence
 100 3.4 56.7 6 6 AX175266 Sequence

ALIGNMENTS

RESULT 1
 AX175246
 LOCUS AX175246 6 bp DNA linear PAT 03-JUL-2001
 DEFINITION Sequence 10 from Patent WO0144465.
 ACCESSION AX175246
 VERSION AX175246.1 GI:14598614
 KEYWORDS
 SOURCE
 ORGANISM
 synthetic construct
 other sequences; artificial sequences.
 REFERENCE 1 (bases 1 to 6)
 AUTHORS Phillips,N.C. and Filion,M.C.
 TITLE Therapeutically useful synthetic oligonucleotides
 JOURNAL Patent: WO 0144465-A 10 21-JUN-2001;
 Bioniche Life Sciences Inc. (CA)
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 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

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 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGTGT 6

Db 1 GTGTGT 6

RESULT 2

AX175307
 LOCUS AX175307 6 bp DNA linear PAT 03-JUL-2001
 DEFINITION Sequence 71 from Patent WO0144465.
 ACCESSION AX175307
 VERSION AX175307.1 GI:14598675
 KEYWORDS
 SOURCE
 ORGANISM
 synthetic construct
 other sequences; artificial sequences.
 REFERENCE 1 (bases 1 to 6)
 AUTHORS Phillips,N.C. and Filion,M.C.
 TITLE Therapeutically useful synthetic oligonucleotides
 JOURNAL Patent: WO 0144465-A 71 21-JUN-2001;
 Bioniche Life Sciences Inc. (CA)
 FEATURES
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 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

ORIGIN

Query Match 100.0%; Score 6; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 8.1e+09;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGTGT 6

Db 1 GTGTGT 6

RESULT 3

E06868
 LOCUS E06868 6 bp RNA linear PAT 29-SEP-1997
 DEFINITION Substrate of ribozyme.
 ACCESSION E06868
 VERSION E06868.1 GI:5708533
 KEYWORDS
 SOURCE
 ORGANISM
 synthetic construct
 other sequences; artificial sequences.
 REFERENCE 1 (bases 1 to 6)
 AUTHORS Otsuka,E. and Koizumi,M.
 TITLE RIBOZYME HAVING THERMODYNAMICALLY STABLE LOOP STRUCTURE
 JOURNAL Patent: JP 1994070774-A 16 15-MAR-1994;
 SANKYO CO LTD
 COMMENT
 OS Artificial gene
 OC Artificial sequence; Genes.
 PN JP 1994070774-A/16
 PD 15-MAR-1994
 PF 01-JUL-1993 JP 1993163530
 PR 02-JUL-1992 JP 92P 175706
 PI OTSUKA EIKO, KOIZUMI MAKOTO
 PC C12N15/11,C12N1/21,C12N9/00,C12N15/10,(C12N1/21,C12R1:19); CC
 strandedness: Single;
 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: No;
 FH Key
 FH Location/Qualifiers
 FT misc_feature 1. .6
 /note='Substrate of ribozyme'.

FEATURES

source

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Query Match 83.3%; Score 5; DB 6; Length 6;
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 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGTG 5

Db 1 GTGTG 5

RESULT 4

AX175245
 LOCUS AX175245 6 bp DNA linear PAT 03-JUL-2001
 DEFINITION Sequence 9 from Patent WO0144465.
 ACCESSION AX175245
 VERSION AX175245.1 GI:14598613
 KEYWORDS
 SOURCE
 ORGANISM
 synthetic construct
 other sequences; artificial sequences.
 REFERENCE 1 (bases 1 to 6)
 AUTHORS Phillips,N.C. and Filion,M.C.
 TITLE Therapeutically useful synthetic oligonucleotides
 JOURNAL Patent: WO 0144465-A 9 21-JUN-2001;
 Bioniche Life Sciences Inc. (CA)
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 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

ORIGIN

Query Match 83.3%; Score 5; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 8.1e+09;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTG 5
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Db 2 GTGTG 6

RESULT 5
LOCUS AX175306
DEFINITION Sequence 70 from Patent WO0144465.
ACCESSION AX175306
VERSION AX175306.1 GI:14598674
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 6)
AUTHORS Phillips, N.C. and Filion, M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 70 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
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source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTG 5
|||||

Db 2 GTGTG 6

RESULT 6
LOCUS AX239662/c
DEFINITION Sequence 2 from Patent WO0164948.
ACCESSION AX239662
VERSION AX239662.1 GI:15797327
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 6)
AUTHORS van Haeringen, W.A. and van Haeringen, H.
TITLE Universal variable fragments
JOURNAL Patent: WO 0164948-A 2 07-SEP-2001;
Dr. van Haeringen Laboratorium B.V. (NL)
FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="primer"

ORIGIN
Query Match 83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTG 5
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Db 5 GTGTG 1

RESULT 7
LOCUS CQ755831/c
DEFINITION Sequence 332 from Patent WO2003106674.
ACCESSION CQ755831
VERSION CQ755831.1 GI:44846636
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Otte, A.P., Kruckeberg, A.L. and Satijn, D.P.
TITLE Means and methods for regulating gene expression
JOURNAL Patent: WO 2003106674-A 332 24-DEC-2003;
Chromagenics B.V. (NL)
FEATURES
source Location/Qualifiers
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Query Match 73.3%; Score 4.4; DB 6; Length 6;
Best Local Similarity 83.3%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGTGT 6
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Db 6 GTGGGT 1

RESULT 8
LOCUS CQ755836/c
DEFINITION Sequence 337 from Patent WO2003106674.
ACCESSION CQ755836
VERSION CQ755836.1 GI:44846641
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Otte, A.P., Kruckeberg, A.L. and Satijn, D.P.
TITLE Means and methods for regulating gene expression
JOURNAL Patent: WO 2003106674-A 337 24-DEC-2003;
Chromagenics B.V. (NL)
FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
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Query Match 73.3%; Score 4.4; DB 6; Length 6;
Best Local Similarity 83.3%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGTGT 6
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Db 6 GGGTGT 1

RESULT 9
LOCUS CQ758069/c
DEFINITION Sequence 373 from Patent WO2003106684.
ACCESSION CQ758069
VERSION CQ758069.1 GI:44848090
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

ORIGIN
Query Match 73.3%; Score 4.4; DB 6; Length 6;
Best Local Similarity 83.3%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGTGT 6
|||||

Db 6 GGGTGT 1

REFERENCE 1
 AUTHORS Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
 TITLE A method for the simultaneous production of multiple proteins;
 vectors and cells for use therein
 JOURNAL Patent: WO 2003106684-A 373 24-DEC-2003;
 Chromagenics B.V. (NL)
 FEATURES Location/Qualifiers
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 /db_xref="taxon:32630"
 /note="oligonucleotide patterns over-represented in STAR
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 Best Local Similarity 83.3%; Pred. No. 8.1e+09;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GTGTGT 6
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 Db 6 GTGGGT 1
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 LOCUS CQ758074/c 6 bp DNA linear PAT 01-MAR-2004
 DEFINITION Sequence 378 from Patent WO2003106684.
 ACCESSION CQ758074
 VERSION CQ758074.1 GI:44848095
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
 TITLE A method for the simultaneous production of multiple proteins;
 vectors and cells for use therein
 JOURNAL Patent: WO 2003106684-A 378 24-DEC-2003;
 Chromagenics B.V. (NL)
 FEATURES Location/Qualifiers
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 Best Local Similarity 83.3%; Pred. No. 8.1e+09;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GTGTGT 6
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 Db 6 GGGTGT 1
 RESULT 11
 LOCUS CQ788027/c 6 bp DNA linear PAT 24-MAR-2004
 DEFINITION Sequence 333 from Patent WO2004020664.
 ACCESSION CQ788027
 VERSION CQ788027.1 GI:45722983
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Geldermann,H., Preuss,S. and Han,Y.
 TITLE Polymorphous microsatellite loci in genes for pre-diagnostic
 purposes

JOURNAL Patent: WO 2004020664-A 333 11-MAR-2004;
 Universitaet Hohenheim (DE)
 FEATURES Location/Qualifiers
 source 1..6
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 satellite 1..6
 /note="M05, Allel R (PrP-Gen)"
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 /note="Anzahl der Wiederholungen: 2"
 repeat_unit 5..6
 /note="Anzahl der Wiederholungen: 2"
 ORIGIN
 Query Match 73.3%; Score 4.4; DB 6; Length 6;
 Best Local Similarity 83.3%; Pred. No. 8.1e+09;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GTGTGT 6
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 Db 6 GTTGT 1
 RESULT 12
 LOCUS AX764869/c 6 bp DNA linear PAT 25-JUN-2003
 DEFINITION Sequence 339 from Patent WO03004704.
 ACCESSION AX764869
 VERSION AX764869.1 GI:32259077
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Otte,A.P. and Kruckeberg,A.L.
 TITLE Dna sequences comprising gene transcription regulatory qualities
 and methods for detecting and using such dna sequences
 JOURNAL Patent: WO 03004704-A 339 16-JAN-2003;
 Chromagenics B.V. (NL)
 FEATURES Location/Qualifiers
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 /organism="synthetic construct"
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 /db_xref="taxon:32630"
 /note="oligonucleotide patterns over-represented in STAR
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 Query Match 73.3%; Score 4.4; DB 6; Length 6;
 Best Local Similarity 83.3%; Pred. No. 8.1e+09;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 Db 6 GTGGGT 1
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 LOCUS AX764874/c 6 bp DNA linear PAT 25-JUN-2003
 DEFINITION Sequence 344 from Patent WO03004704.
 ACCESSION AX764874
 VERSION AX764874.1 GI:32259082
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Otte,A.P. and Kruckeberg,A.L.
 TITLE Dna sequences comprising gene transcription regulatory qualities
 and methods for detecting and using such dna sequences
 JOURNAL Patent: WO 03004704-A 344 16-JAN-2003;

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  Db 6 GGGTGT 1
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  DEFINITION Sequence 13 from Patent WO03060163.
  ACCESSION AX805867
  VERSION AX805867.1 GI:38522778
  KEYWORDS
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  SOURCE
    synthetic construct
    other sequences; artificial sequences.
  ORGANISM
    van Bijl, M.J. and van Schaik, C.
  REFERENCE
    1
  AUTHORS
    van Bijl, M.J. and van Schaik, C.
  TITLE
    Discrimination and detection of target nucleotide sequences using
    mass spectrometry
  JOURNAL
    Patent: WO 03060163-A 13 24-JUL-2003;
    Keygene N.V. (NL)
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  Db 6 GTGGGT 1
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  LOCUS AX175290
  DEFINITION Sequence 54 from Patent WO0144465.
  ACCESSION AX175290
  VERSION AX175290.1 GI:14598658
  KEYWORDS
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  SOURCE
    synthetic construct
    other sequences; artificial sequences.
  ORGANISM
    Phillips, N.C. and Fillion, M.C.
  REFERENCE
    1 (bases 1 to 4)
  AUTHORS
    Phillips, N.C. and Fillion, M.C.
  TITLE
    Therapeutically useful synthetic oligonucleotides
  JOURNAL
    Patent: WO 0144465-A 54 21-JUN-2001;
    Bioniche Life Sciences Inc. (CA)
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        /db_xref="taxon:32630"
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    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 1 GTGT 4
  Db 1 GTGT 4
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  LOCUS AX175295
  DEFINITION Sequence 59 from Patent WO0144465.
  ACCESSION AX175295
  VERSION AX175295.1 GI:14598663
  KEYWORDS
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  SOURCE
    synthetic construct
    other sequences; artificial sequences.
  ORGANISM
    Phillips, N.C. and Fillion, M.C.
  REFERENCE
    1 (bases 1 to 4)
  AUTHORS
    Phillips, N.C. and Fillion, M.C.
  TITLE
    Therapeutically useful synthetic oligonucleotides
  JOURNAL
    Patent: WO 0144465-A 59 21-JUN-2001;
    Bioniche Life Sciences Inc. (CA)
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  QY 2 TGTG 5
  Db 1 TGTG 4
  RESULT 17
  LOCUS CQ868954
  DEFINITION Sequence 108 from Patent WO2004074429.
  ACCESSION CQ868954
  VERSION CQ868954.1 GI:51998881
  KEYWORDS
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  SOURCE
    synthetic construct
    other sequences; artificial sequences.
  ORGANISM
    freskg Rd, P.O., Goulliaev, A.H., Thisted, T. and Olsen, E.K.
  REFERENCE
    1
  AUTHORS
    freskg Rd, P.O., Goulliaev, A.H., Thisted, T. and Olsen, E.K.
  TITLE
    Method for producing second-generation library
  JOURNAL
    Patent: WO 2004074429-A 108 02-SEP-2004;
    Nuevolution A/S (DK)
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        /note="synthetic construct"
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    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 1 GTGT 4
  Db 1 GTGT 4
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RESULT 18
CQ868982/c
LOCUS          CQ868982          5 bp      DNA          linear          PAT 13-SEP-2004
DEFINITION     Sequence 136 from Patent WO2004074429.
ACCESSION      CQ868982
VERSION        CQ868982.1 GI:51998909
KEYWORDS       .
SOURCE          synthetic construct
ORGANISM        other sequences; artificial sequences.
REFERENCE      1
AUTHORS         freskg Rd.P.O., Gouliaev,A.H., Thisted,T. and Olsen,E.K.
TITLE           Method for producing second-generation library
JOURNAL         Patent: WO 2004074429-A 136 02-SEP-2004;
                Nuevolution A/S (DK)
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Query Match          66.7%; Score 4; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.7e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGT 4
    ||||
Db 4 GTGT 1

RESULT 19
CQ869103
LOCUS          CQ869103          5 bp      DNA          linear          PAT 13-SEP-2004
DEFINITION     Sequence 257 from Patent WO2004074429.
ACCESSION      CQ869103
VERSION        CQ869103.1 GI:51999030
KEYWORDS       .
SOURCE          synthetic construct
ORGANISM        other sequences; artificial sequences.
REFERENCE      1
AUTHORS         freskg Rd.P.O., Gouliaev,A.H., Thisted,T. and Olsen,E.K.
TITLE           Method for producing second-generation library
JOURNAL         Patent: WO 2004074429-A 257 02-SEP-2004;
                Nuevolution A/S (DK)
FEATURES       .
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                source
                1..5
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Query Match          66.7%; Score 4; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.7e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGT 4
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Db 4 GTGT 1

RESULT 20
CQ869131/c
LOCUS          CQ869131          5 bp      DNA          linear          PAT 13-SEP-2004
DEFINITION     Sequence 285 from Patent WO2004074429.
ACCESSION      CQ869131
VERSION        CQ869131.1 GI:51999058
KEYWORDS       .
SOURCE          synthetic construct
ORGANISM        other sequences; artificial sequences.
REFERENCE      1
AUTHORS         Inze,D., Boudolf,V., de Veylder,L., Acosta,J.A. and Magyar,Z.
TITLE           Nucleic acid molecules encoding plant cell cycle proteins and uses
                thereof
                Patent: WO 0185946-A 247 15-NOV-2001;
                Nuevolution A/S (DK)
FEATURES       .
                Location/Qualifiers
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Query Match          66.7%; Score 4; DB 6; Length 5;
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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGT 4
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Db 1 GTGT 4

RESULT 21
AX163835/c
LOCUS          AX163835          5 bp      DNA          linear          PAT 22-JUN-2001
DEFINITION     Sequence 4 from Patent WO0140804.
ACCESSION      AX163835
VERSION        AX163835.1 GI:14544907
KEYWORDS       .
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 5)
AUTHORS         Hol,E.M. and van Leeuwen,F.W.
TITLE           Clearance of aberrant protein in correlation with disease
                Patent: WO 0140804-A 4 07-JUN-2001;
                Koninklijke Nederlandse Akademie van Wetenschappen (NL)
FEATURES       .
                Location/Qualifiers
                source
                1..5
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
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                1..5 Repeat sequence, wherein N represents any
                nucleotide"
ORIGIN
Query Match          66.7%; Score 4; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.7e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTG 5
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Db 4 TGTG 1

RESULT 22
AX449528/c
LOCUS          AX449528          5 bp      DNA          linear          PAT 03-JUL-2002
DEFINITION     Sequence 247 from Patent WO0185946.
ACCESSION      AX449528
VERSION        AX449528.1 GI:21698177
KEYWORDS       .
SOURCE          synthetic construct
ORGANISM        synthetic construct
                other sequences; artificial sequences.
REFERENCE      1
AUTHORS         Inze,D., Boudolf,V., de Veylder,L., Acosta,J.A. and Magyar,Z.
TITLE           Nucleic acid molecules encoding plant cell cycle proteins and uses
                thereof
                Patent: WO 0185946-A 247 15-NOV-2001;
                Nuevolution A/S (DK)
FEATURES       .
                Location/Qualifiers
                source
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                /note="synthetic construct"
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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 TGTG 5
Db 5 TGTG 2

RESULT 23
AX805861/c
LOCUS
DEFINITION
Sequence 7 from Patent WO03060163.
ACCESSION
AX805861
VERSION
AX805861.1 GI:38522772
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
van Eijk,M.J. and van Schaik,C.
TITLE
Discrimination and detection of target nucleotide sequences using
mass spectrometry
JOURNAL
Patent: WO 03060163-A 7 24-JUL-2003;
Keygene N.V. (NL)
FEATURES
Location/Qualifiers
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QY 2 TGTG 5
Db 5 TGTG 2

RESULT 24
CQ755803/c
LOCUS
DEFINITION
Sequence 304 from Patent WO2003106674.
ACCESSION
CQ755803
VERSION
CQ755803.1 GI:44846608
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
TITLE
Means and methods for regulating gene expression
JOURNAL
Patent: WO 2003106674-A 304 24-DEC-2003;
Chromagenics B.V. (NL)
FEATURES
Location/Qualifiers
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QY 1 GTGT 4
Db 5 GTGT 2

RESULT 25
CQ758041/c
LOCUS
DEFINITION
Sequence 345 from Patent WO2003106684.
ACCESSION
CQ758041
VERSION
CQ758041.1 GI:44848062
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
TITLE
A method for the simultaneous production of multiple proteins;
vectors and cells for use therein
JOURNAL
Patent: WO 2003106684-A 345 24-DEC-2003;
Chromagenics B.V. (NL)
FEATURES
Location/Qualifiers
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elements"
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Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGT 4
Db 5 GTGT 2

RESULT 26
AX104453
LOCUS
DEFINITION
Sequence 645 from Patent WO0122972.
ACCESSION
AX104453
VERSION
AX104453.1 GI:13920650
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 6)
AUTHORS
Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE
Immunostimulatory nucleic acids
JOURNAL
Patent: WO 0122972-A 645 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
source

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Best Local Similarity 100.0%; Pred. No. 8.1e+09;
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QY 1 GTGT 4

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RESULT 27
LOCUS      AX107946/c
DEFINITION Sequence 3 from Patent WO0123559.
ACCESSION  AX107946
VERSION     AX107946.1  GI:13923327
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 6)
AUTHORS   Chandrasekhar,S., Halladay,D.L. and Martin,T.J.
TITLE     Osteoclast differentiation factor regulatory region
JOURNAL   Patent: WO 0123559-A 3 05-APR-2001;
            ELI LILLY AND COMPANY (US) ; Miles, Rebecca, Ruth (US) ; Onyia,
            Jude, Emeke (US) ; Thirunavukkarasu, Kannan (US)
FEATURES   source
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ORIGIN
Query Match      66.7%; Score 4; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TGTG 5
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Db      6 TGTG 3

RESULT 28
LOCUS      AX107947
DEFINITION Sequence 4 from Patent WO0123559.
ACCESSION  AX107947
VERSION     AX107947.1  GI:13923328
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 6)
AUTHORS   Chandrasekhar,S., Halladay,D.L. and Martin,T.J.
TITLE     Osteoclast differentiation factor regulatory region
JOURNAL   Patent: WO 0123559-A 4 05-APR-2001;
            ELI LILLY AND COMPANY (US) ; Miles, Rebecca, Ruth (US) ; Onyia,
            Jude, Emeke (US) ; Thirunavukkarasu, Kannan (US)
FEATURES   source
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Query Match      66.7%; Score 4; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TGTG 5
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Db      6 TGTG 3

RESULT 29
LOCUS      AX107950/c
DEFINITION Sequence 7 from Patent WO0123559.
ACCESSION  AX107950
VERSION     AX107950.1  GI:13923331
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 6)
AUTHORS   Chandrasekhar,S., Halladay,D.L. and Martin,T.J.
TITLE     Osteoclast differentiation factor regulatory region
JOURNAL   Patent: WO 0123559-A 7 05-APR-2001;
            ELI LILLY AND COMPANY (US) ; Miles, Rebecca, Ruth (US) ; Onyia,
            Jude, Emeke (US) ; Thirunavukkarasu, Kannan (US)
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Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TGTG 5
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Db      2 TGTG 5

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 21:46:09 ; Search time 187.4 Seconds
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Title: US-09-735-363A-10

Perfect score: 6

Sequence: 1 ggtgtg 6

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Searched: 4390206 seqs, 2959870667 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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C 4	5	83.3	6	13	ADR33262
C 5	4.4	73.3	6	2	AAQ78699
C 6	4.4	73.3	6	6	ABN73213
C 7	4	66.7	5	5	AAQ96420
C 8	4	66.7	6	2	AAQ58436
C 9	4	66.7	6	6	ABK72534
C 10	4	66.7	6	6	ABK78161
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C 29	4	66.7	6	13	ADR35669
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C 33	3.4	56.7	5	4	AAZ14908
C 34	3.4	56.7	5	4	AAZ14903
C 35	3.4	56.7	5	8	ABZ75664
C 36	3.4	56.7	5	9	ACD25823
C 37	3.4	56.7	5	9	ACD25825
C 38	3.4	56.7	6	1	AAZ10696
C 39	3.4	56.7	6	1	AAZ10696
C 40	3.4	56.7	6	2	AAZ10696
C 41	3.4	56.7	6	3	AAZ10696
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C 95 3 50.0 6 2 AAV11643
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C 97 3 50.0 6 3 AA289327 Human UCP
Aa289327 Human UCP
Aa28793 Tethered
Aaf91831 Breast-Ga
Aaf91845 Breast-Ga
100 3 50.0 6 4 AAF91845

ALIGNMENTS

RESULT 1
AD081155/c
ID AD081155 standard; DNA; 6 BP.
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AC AD081155;
XX
DT 29-JUL-2004 (first entry)
XX
DE Prion protein polymorphic microsatellite marker consensus sequence #33.
XX
KW gene typing; polymorphic microsatellite loci; PML;
KW disease predisposition; microsatellite marker; prion disease;
KW cystic fibrosis; malignant hyperthermia syndrome; metabolic disease;
KW milk protein; hormone; transcription factor; pT7-blue-vector; sheep;
KW microsatellite; ds.
XX
OS Synthetic.
XX
PN DE10236711-A1.
XX
PD 26-FEB-2004.
XX
PF 09-AUG-2002; 2002DE-01036711.
XX
PR 09-AUG-2002; 2002DE-01036711.
XX
PA (UYHO-) UNIV HOHENHEIM.
XX
PI Geldermann H, Preuss S, Han Y;
XX
PS WPI; 2004-215730/21.
XX
DR Typing genes that contain polymorphic microsatellite loci, useful for
XX identifying predisposition to disease, by amplification and determining
XX length of amplicons.
XX
PS Claim 9; Page 50; 64pp; German.
XX
CC The invention describes a method of typing (M1) a gene (I) that has one
CC or more polymorphic microsatellite loci (PML). The method comprises: PCR
CC amplification of at least one DNA region of (I) that includes PML, using
CC as template a DNA sample containing at least one segment of (I); and
CC determining the length of the resulting amplicon(s). Also described are:
CC a method of determining (M2) microsatellite markers (MW) for
CC predisposition to a disease, associated with a gene that includes one or
CC more PML; and prediagnosis (M3) of diseases associated with gene that
CC include PML. The method is used to identify microsatellite markers, in a
CC disease-related gene, that are associated with a predisposition to
CC diseases and for prediagnosis of such diseases, especially prion diseases
CC but also cystic fibrosis, malignant hyperthermia syndrome in pigs and
CC metabolic diseases; also to type genes that encode milk proteins
CC hormones or transcription factors. The method is simpler, quicker and
CC particularly less expensive than known methods based on sequencing. This
CC sequence represents a prion protein polymorphic microsatellite marker
CC consensus sequence.
XX
SQ Sequence 6 BP; 3 A; 3 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 6; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTGT 6
Db 6 GTGTGT 1
RESULT 2
AAD17580/c
ID AAD17580 standard; DNA; 6 BP.
XX
AC AAD17580;
XX
DT 10-DEC-2001 (first entry)
XX
DE AC repeat sequence #2 of 5' variation generator.
XX
KW Genomic DNA analysis; 5' variation generator; 3' fragment generator;
KW endangered animal identification; ss.
XX
OS Unidentified.
XX
PN EP130114-A1.
XX
PD 05-SEP-2001.
XX
PF 03-MAR-2000; 2000EP-00200757.
XX
PR 03-MAR-2000; 2000EP-00200757.
XX
PA (VHAE-) VAN HAERINGEN LAB BV.
XX
PI Van Haringen H, Van Haringen WA;
XX
PS WPI; 2001-572636/65.
XX
DR Analyzing genomic DNA in a sample, useful for analyzing genes of
XX organisms (e.g. a species or individual) or identifying endangered
XX animals or plants, by using oligonucleotide primers comprising universal
XX variable fragments.
XX
PS Disclosure; Page 3; 23pp; English.
XX
CC The patent discloses a method and associated kit for analysing genomic
CC DNA in a sample. The method comprises conducting a nucleic acid
CC amplification on the genomic DNA in the sample using both first and
CC second oligonucleotide primer to produce DNA fragments based on repeat
CC sequences on at least one end of the genomic DNA. The first primer is a
CC 5' variation generator including a repeat sequence and at least one non-
CC repeat nucleotide. The second oligonucleotide primer is a 3' fragment
CC generator starting within such a genetic distance that amplification of
CC the genomic DNA can be performed and preferably includes inosine. The
CC method is useful for the genetic analysis of an individual organism,
CC particularly of a species or individual. It is also useful for the rapid
CC and straight forward identification of endangered animals or plants. The
CC present DNA sequence is an AC repeat of 5' variation generator
XX
SQ Sequence 6 BP; 3 A; 3 C; 0 G; 0 T; 0 U; 0 Other;
XX
Query Match 83.3%; Score 5; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGTG 5
Db 5 GTGTG 1
RESULT 3
ADR33261/c
ID ADR33261 standard; DNA; 6 BP.
XX
AC ADR33261;
XX

```

DT 04-NOV-2004 (first entry)
DE Human nicking agent target DNA #802.
XX
KW ss; nicking agent; assay panel; diagnosis; expression pattern;
KW DNA fingerprinting; nosocomial infection; microbiological assay;
KW bacterial contamination; genome mapping; bioremediation.
XX
OS Homo sapiens.
XX WO2004067765-A2.
XX
XX 12-AUG-2004.
XX
XX 29-JAN-2004; 2004WO-US002720.
XX
XX 29-JAN-2003; 2003US-0443811P.
XX
XX (KECK-) KECK GRADUATE INST.
XX
XX Van Ness J, Galas DJ, Van Ness LK;
XX WPI; 2004-581010/56.
XX
XX Identifying nucleic acid sample source, useful for identifying bacterial
XX strains involved in nosocomial infections, comprises treating the nucleic
XX acid sample with components comprising a nicking agent under nicking
XX conditions.
XX
XX Example 1; Page 84; 238pp; English.
XX
XX The invention relates to a method of treating a nucleic acid sample with
XX components under nicking conditions, where the components comprise a
XX nicking agent, and the conditions cause the nicking agent to nick the
XX nucleic acid sample to thus produce a family of initiating
XX oligonucleotide fragments, and subjecting one or more members of the
XX family of initiating oligonucleotide fragments to a characterization
XX process to thus provide results. The method is useful for creating an
XX assay panel of diagnostic oligonucleotides that can identify any organism
XX or individual. The method is useful for characterizing other DNA
XX molecules e.g., cDNA, and for characterizing cDNA expression patterns.
XX The method, kit or composition is useful for identifying the source
XX organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
XX non-human animal or human. The method is particularly useful for rapidly
XX fingerprinting DNA to identifying prokaryotic and eukaryotic species,
XX subspecies, and especially strains or individuals of the subspecies. It
XX is especially useful for identifying different bacterial strains involved
XX in e.g., nosocomial infections. Furthermore, the method is useful for
XX diagnosing bacterial disease in plants and humans, monitoring for
XX bacterial content and/or contamination in the environment, monitoring
XX food for bacterial contamination, monitoring quality assurance/control of
XX bacterial contamination, monitoring microbiological assays, tracing bacterial
XX contamination and/or outbreaks of bacterial infections, genome mapping,
XX monitoring bioremediation sites, and for monitoring agricultural sites
XX for test crops, bacteria and recombinant molecules. This sequence
XX corresponds to nucleic acid used in the method of the invention.
XX
XX Sequence 6 BP; 4 A; 2 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 83.3%; Score 5; DB 13; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 9.7e+08;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 TGTGT 6
XX |||||
XX Db 5 TGTGT 1
XX
XX RESULT 4
XX ADR33262/c
XX ID ADR33262 standard; DNA; 6 BP.
XX

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AC ADR33262;
XX
XX 04-NOV-2004 (first entry)
XX
XX Human nicking agent target DNA #803.
XX
XX ss; nicking agent; assay panel; diagnosis; expression pattern;
XX DNA fingerprinting; nosocomial infection; microbiological assay;
XX bacterial contamination; genome mapping; bioremediation.
XX
XX Homo sapiens.
XX WO2004067765-A2.
XX
XX 12-AUG-2004.
XX
XX 29-JAN-2004; 2004WO-US002720.
XX
XX 29-JAN-2003; 2003US-0443811P.
XX
XX (KECK-) KECK GRADUATE INST.
XX
XX Van Ness J, Galas DJ, Van Ness LK;
XX WPI; 2004-581010/56.
XX
XX Identifying nucleic acid sample source, useful for identifying bacterial
XX strains involved in nosocomial infections, comprises treating the nucleic
XX acid sample with components comprising a nicking agent under nicking
XX conditions.
XX
XX Example 1; Page 84; 238pp; English.
XX
XX The invention relates to a method of treating a nucleic acid sample with
XX components under nicking conditions, where the components comprise a
XX nicking agent, and the conditions cause the nicking agent to nick the
XX nucleic acid sample to thus produce a family of initiating
XX oligonucleotide fragments, and subjecting one or more members of the
XX family of initiating oligonucleotide fragments to a characterization
XX process to thus provide results. The method is useful for creating an
XX assay panel of diagnostic oligonucleotides that can identify any organism
XX or individual. The method is useful for characterizing other DNA
XX molecules e.g., cDNA, and for characterizing cDNA expression patterns.
XX The method, kit or composition is useful for identifying the source
XX organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
XX non-human animal or human. The method is particularly useful for rapidly
XX fingerprinting DNA to identifying prokaryotic and eukaryotic species,
XX subspecies, and especially strains or individuals of the subspecies. It
XX is especially useful for identifying different bacterial strains involved
XX in e.g., nosocomial infections. Furthermore, the method is useful for
XX diagnosing bacterial disease in plants and humans, monitoring for
XX bacterial content and/or contamination in the environment, monitoring
XX food for bacterial contamination, monitoring quality assurance/control of
XX bacterial contamination, monitoring microbiological assays, tracing bacterial
XX contamination and/or outbreaks of bacterial infections, genome mapping,
XX monitoring bioremediation sites, and for monitoring agricultural sites
XX for test crops, bacteria and recombinant molecules. This sequence
XX corresponds to nucleic acid used in the method of the invention.
XX
XX Sequence 6 BP; 4 A; 2 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 83.3%; Score 5; DB 13; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 9.7e+08;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 TGTGT 6
XX |||||
XX Db 5 TGTGT 1
XX
XX RESULT 5
XX AAQ78699
XX

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ID AAQ78699 standard; DNA; 6 BP.
XX
AC AAQ78699;
XX
DT 25-MAR-2003 (revised)
DT 06-JUN-1995 (first entry)
XX
DE Pistil gene promoter consensus sequence.
XX
KW Pistil; anther; gene expression; female sterile; male sterile;
KW S-locus glycoprotein; SLG; S-locus related gene; SLR1; promoter;
KW transgenic plant; crop improvement; da.
XX
OS Brassica sp.
XX
PN WO9425613-A1.
XX
PD 10-NOV-1994.
XX
PF 03-MAY-1994; 94WO-US004557.
XX
PR 03-MAY-1993; 93US-00054362.
XX
PA (CORR ) CORNELL RES FOUND INC.
XX
PI Nasrallah ME, Nasrallah JB, Thorsness MK;
XX
XX WPI; 1994-358288/44.
XX
PT Isolated DNA elements directing pistil- or anther-specific gene
PT expression - used to cause female and male sterility in plants.
XX
PS Disclosure; Page 32; 54pp; English.
XX
CC Comparison of the promoter regions of Brassica sp. S-locus glycoprotein
CC SLG13, SLG2, SLG8 and S-locus related SLR1 genes (given in AAQ78703-06)
CC identified consensus sequences, which can be used as minimal promoter
CC elements for pistil- or anther-specific gene expression in plants. The
CC pistil-specific element has at least 70% homology to the consensus
CC elements given in AAQ78698-700. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
XX Sequence 6 BP; 0 A; 0 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 73.3%; Score 4.4; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 9.7e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGTGT 6
DB 1 GTTTGT 6

RESULT 6
ABN73213/c
ID ABN73213 standard; cDNA; 6 BP.
XX
AC ABN73213;
XX
XX 03-JUL-2002 (first entry)
DT
DE Bovine embryonic germ (EG) cell cDNA EST 000128a CONTIG 73.
XX
DE Bovine; Bos taurus; EST; expressed sequence tag; totipotence;
KW Bovine development; gene; ss.
XX
OS Bos taurus.
XX
PN WO200194550-A2.
XX
PD 13-DEC-2001.
XX
PF 07-JUN-2001; 2001WO-US018576.

AAQ78699 standard; DNA; 6 BP.
06-JUN-2001; 2001US-00876143.
(INFI-) INFIGEN INC.
Eilertsen KJ, Pfister-Genskow M, Childs L;
WPI; 2002-351289/38.
An expressed sequence tag (EST), the expression of which, or its
complementary sequence, in a cell identifies the cell as a
developmentally competent or incompetent cell.
Example 16; Page 129; 584pp; English.
The present invention describes an expressed sequence tag (EST), where
the EST is an isolated, enriched, or purified nucleic acid sequence
representing all or part of a gene, the expression of which, or its
complementary sequence, in a cell identifies the cell as a
developmentally competent or incompetent cell. Molecules which induce
developmental competence in a cell line are useful for inducing
totipotence in one or more cells. Molecules which induce developmental
incompetence in a cell line are useful for preventing a full term
pregnancy in an animal and inhibiting totipotence. The molecules are also
useful for treating a disease in an animal by inducing development of one
or more cells of the animal into a specific cell type. The present
sequence represents a bovine EST which is given in the exemplification of
the present invention
Sequence 6 BP; 4 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 73.3%; Score 4.4; DB 6; Length 6;
Best Local Similarity 83.3%; Pred. No. 9.7e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGTGT 6
DB 6 GTTTT 1

RESULT 7
AAS96420/c
ID AAS96420 standard; DNA; 5 BP.
XX
AC AAS96420;
XX
DT 26-FEB-2002 (first entry)
DE Kozak sequence containing PCR primer.
XX
KW Cell cycle protein; CCP; ss; cell cycle regulation; herbicide;
KW plant growth regulator; plant development; abiotic stress; biotic stress;
KW nutrient deprivation; pathogen attack; crop yield; PCR primer.
XX
OS Unidentified.
XX
PN WO200185946-A2.
XX
PD 15-NOV-2001.
XX
PP 14-MAY-2001; 2001WO-IB001307.
XX
PR 12-MAY-2000; 2000US-0204045P.
XX
PA (CROP-) CROPDISEIGN NV.
XX
PI Inze D, Boudolf V, De Veylder L, Acosta JAT, Magyar Z;
XX
XX WPI; 2002-062249/08.
XX
XX New cell cycle protein and nucleic acid molecule encoding it useful for
PT regulating cell cycle progression in plants and for identifying

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modulators which are useful as herbicides or plant growth regulators.

Example 2; Page 298; 316pp; English.

The invention relates to a novel cell cycle protein (CCP) and the polynucleotides encoding them. CCP is useful for identifying a compound which modulates the activity of the polypeptide and which binds to the polypeptide and an anti-CCP antibody is useful for detecting the presence of CCP in a sample. A CCP modulator is useful for modulating the cell cycle or growth of a plant such as Arabidopsis thaliana, rice, wheat, maize, tomato, alfalfa, oilseed rape, soybean, sunflower and canola. CCP nucleic acid and polypeptide molecules are useful as modulating agents in regulating cell cycle progression in plants. CCP is useful to treat disorders characterised by insufficient or excessive production of CCP or protein or production of CCP protein forms which have decreased or aberrant activity. Compounds that bind to or modulate the activity of CCP polypeptide are useful as herbicides or plant growth regulators. The polynucleotide is useful for modifying cell fate, plant development, plant morphology, biochemistry and/or physiology, the length of the G1, S, G2 and/or M phase of the cell cycle of a plant, initiation, promotion, stimulation or enhancement of cell division, DNA replication, seed set, seed size, seed development, tuber, fruit, leaf formation, shoot and root initiation and/or development, nodule function, dwarfism in plants, senescence, tolerance or resistance to stress. CCP, the polynucleotide and the anti-CCP antibody are useful in agriculture to modulate the protein levels or activity of a protein involved in the cell cycle due to environmental conditions, including abiotic stress such as cold, nutrient deprivation, heat, drought, salt stress, or biotic stress such as pathogen attack, to modulate e.g. enhance crop yields, and attenuate plant architecture, plant quality traits, plant reproduction and seed development, endoreduplication in storage cells, storage tissues and/or storage organs of plants or its parts. CCP is useful as an immunogen to generate antibodies. CCP protein is useful to screen for naturally occurring CCP substrates. The polynucleotide is useful for expressing CCP protein, to detect CCP mRNA, or a genetic lesion in a CCP gene and to modulate CCP activity. The present sequence is a PCR primer used to isolate a nucleic acid encoding a CCP protein of the invention

Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTG 5
|||
DB 5 TGTG 2

RESULT 8
AAQ58436
ID AAQ58436 standard; DNA; 6 BP.
XX AAQ58436;
AC AAQ58436;

DT 20-SEP-1994 (first entry)
XX Sequencing primer #8.

KW Polymerase chain reaction; primer; PCR; detection; amplify;
KW base sequence; Alu sequence; promoter; RNA polymerase; ss.
XX Synthetic.
XX JP06022798-A.
XX 01-FEB-1994.
XX 07-JUL-1992; 92JP-00180095.
XX 07-JUL-1992; 92JP-00180095.
XX (HITA) HITACHI LTD.

XX WPI; 1994-071011/09.
XX Nucleic acid base sequence determination - using set of primers each
PT config. sequence complementary to repeated sequence in genome but
PT differing at 3'-end.
XX Disclosure; Page 6; 9pp; Japanese.

XX The sequences given in AAQ58429-48 are primers which were used in the
CC method of the invention for the determination of the base sequence of
CC nucleic acids. The primers contain sequences which are complementary to
CC sequences which commonly appear in the genome, eg. an Alu sequence, but
CC contain differences from the genomic sequences at their 3' end. The
CC primers may also be complementary to a promoter region recognised by RNA
CC polymerase. These primers may be used to efficiently determine the base
CC sequence of numerous regions of long DNA simultaneously

XX Sequence 6 BP; 1 A; 0 C; 2 G; 2 T; 0 U; 1 Other;
SQ Query Match 66.7%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTG 5
|||
DB 2 TGTG 5

RESULT 9
ABK72534
ID ABK72534 standard; DNA; 6 BP.
XX ABK72534;
AC ABK72534;

DT 13-AUG-2002 (first entry)
XX Human OPAL gene, exon/intron junction #1.

DE Human; ophthalmological; OPAL; autosomal dominant optic atrophy; ADOA;
KW gene; ds.
XX Homo sapiens.
OS WO200227022-A2.
PN 04-APR-2002.
PD 26-SEP-2001; 2001WO-GB004284.
XX 26-SEP-2000; 2000GB-00023555.
PR (UNLO) UNIV COLLEGE LONDON.
XX (UYEY-) UNIV EYE HOSPITAL.
PA Bhattacharya S, Wisinger B, Alexander C, Votruba M;
XX WPI; 2002-416484/44.

XX Novel human normal or mutant OPAL (the predominant locus for autosomal
PT dominant optic atrophy (ADOA)) polypeptides and the OPAL gene, useful in
PT the diagnosis and treatment of autosomal dominant optic atrophy ADOA.
XX Disclosure; Fig 12; 75pp; English.

XX The invention relates to an isolated human normal or mutant OPAL (the
CC predominant locus for autosomal dominant optic atrophy (ADOA))
CC polypeptide (I), characterised by a molecular weight of about 112 kDa,
CC and substantially free of other human proteins. Also described is the
CC (II) encoding (I). (I) and (II) are useful as a medicament, for the
CC treatment of a medical condition resulting from a defect in the OPAL
CC gene, which results in autosomal dominant optic atrophy. The nucleic acid
CC and antibodies to (I) are useful in a variety of hybridisation and

CC immunological assays to screen for, and to detect the presence of, either
 CC a normal or a defective OPAL gene or gene product. ABK72533-ABK72593
 CC represent the human OPAL gene and intron/exon splice junctions
 XX

SQ Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTG 5
 Db 2 TGTG 5

RESULT 10
 ID ABS78161 standard; DNA; 6 BP.

AC ABS78161;
 XX
 DT 13-DEC-2002 (first entry)

XX Angiogenesis inhibitory oligonucleotide #645.

XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
 KW rubosis; Osler-Weber Syndrome; myocardial angiogenesis;
 KW plaque neovascularisation; telangiectasia; haemophilic joint;
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
 KW scleroderma; hypertrophic scar.

OS Synthetic.

XX WO200253141-A2.

PD 11-JUL-2002.

XX 14-DEC-2001; 2001WO-US048458.

XX 14-DEC-2000; 2000US-0255534P.

PA (COLE-) COLEY PHARM GROUP INC.

XX Bratzler RL;

DR WPI; 2002-566690/60.

PT Inhibiting angiogenesis in a subject, involves administering at least one
 PT antiangiogenic nucleic acid molecule to the subject.

XX Claim 2; Page 31; 276pp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising
 CC administering at least one antiangiogenic nucleic acid molecule. Also
 CC included is a kit comprising a first container housing the antiangiogenic
 CC nucleic acids, and instructions for administering them to a subject
 CC having a condition characterised by unwanted angiogenesis. The method is
 CC useful for inhibiting angiogenesis associated with solid tumour growth,
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
 CC rubosis, Osler-Weber Syndrome, myocardial angiogenesis, plaque
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
 CC acid of the invention

SQ Sequence 6 BP; 1 A; 1 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 6; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGT 4
 Db 3 GTGT 6

RESULT 11
 ACD99933
 ID ACD99933 standard; DNA; 6 BP.

XX ACD99933;

XX 25-SEP-2003 (first entry)

XX Immunostimulatory nucleic acid #619.

XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
 KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
 KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.

OS Synthetic.

PN US2003050268-A1.

PD 13-MAR-2003.

PF 29-MAR-2002; 2002US-00112653.

PR 29-MAR-2001; 2001US-0279642P.

XX (KRIE/) KRIEG A M.

PA (BERG/) BERG D J.

XX Krieg AM, Berg DJ;

XX WPI; 2003-521815/49.

PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
 PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
 PT disease by administering an immunostimulatory nucleic acid.

PS Disclosure; Page 25; 229pp; English.

XX The invention describes a method of treating non-allergic inflammatory
 CC disease comprising administering to a subject having or at risk of
 CC developing a non-allergic inflammatory disease an immunostimulatory
 CC nucleic acid for prevention or treatment of the disease. The method is
 CC useful for treating non-allergic inflammatory diseases, such as
 CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
 CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
 CC This sequence represents an immunostimulatory nucleic acid

SQ Sequence 6 BP; 1 A; 1 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 9; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGT 4
 Db 3 GTGT 6

RESULT 12
 ADE14140
 ID ADE14140 standard; DNA; 6 BP.

XX ADE14140;

XX 29-JAN-2004 (first entry)

XX DE Optineurin promoter motif, repeat element or regulatory region #249.
 XX DE Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
 KW SNP; glaucoma; progressive ocular hypertensive disorder;
 KW glaucoma related disorder; motif; repeat element; regulatory region.
 XX OS Homo sapiens.
 XX XX US2003190617-A1.
 XX XX 09-OCT-2003.
 XX PF 06-MAR-2002; 2002US-00091281.
 XX PR 06-MAR-2002; 2002US-00091281.
 XX XX (SIEE/) SI E.
 PA (RAYM/) RAYMOND V.
 PA (MORI/) MORISSETTE J.
 XX PI Raymond V, Morissette J, Si E;
 XX WPI; 2003-864168/80.
 XX DR New nucleic acid sequences of the optineurin gene are useful to detect
 XX PT polymorphisms particularly single nucleotide polymorphisms in the
 XX PT optineurin promoter to diagnose, prognose and treat glaucoma and related
 XX PT disorders.
 XX PS Claim 11; SEQ ID NO 251; 159pp; English.
 XX CC The invention relates to an isolated nucleic acid (N1) comprising at
 CC least 20 but not more than 1500 consecutive nucleotides of the optineurin
 CC promoter appearing as ADE13890. Also included are the optineurin promoter
 CC operably linked to a heterologous nucleic acid, a nucleic acid capable of
 CC detecting a single nucleotide polymorphism (SNP) in the optineurin
 CC promoter, a host cell comprising the promoter operably linked to a
 CC heterologous sequence, diagnosing or prognosing glaucoma in a sample
 CC obtained from a cell or bodily fluid (comprising detecting a polymorphism
 CC in a promoter region of the optineurin gene, associated with a glaucoma
 CC phenotype), detecting a SNP sequence variation in a sample containing
 CC DNA, detecting the presence of an optineurin promoter sequence variation
 CC in a sample containing DNA, determining the presence or increased
 CC susceptibility to glaucoma or to a progressive ocular hypertensive
 CC disorder resulting in loss of visual field in a patient (or the severity
 CC or progression of glaucoma in a patient, comprising providing
 CC amplification reaction primers that direct amplification of a selected
 CC nucleic acid region containing the variation within the optineurin
 CC promoter and amplifying the DNA) and detecting a polymorphism (comprising
 CC obtaining a sample containing human genomic DNA, providing a nucleic acid
 CC capable of detecting a SNP located within an optineurin promoter, and
 CC detecting the polymorphism). The invention is used to diagnose and
 CC prognose glaucoma and also to treat glaucoma related disorders. The
 CC present sequence is an optineurin promoter motif, repeat element or
 CC putative regulatory region.
 XX SQ Sequence 6 BP; 0 A; 0 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 66.7%; Score 4; DB 10; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TGTG 5
 ||||
 Db 1 TGTG 4
 RESULT 13
 ADE14096
 ID ADE14096 standard; DNA; 6 BP.
 XX AC ADE14096;

XX DT 29-JAN-2004 (first entry)
 XX DE Optineurin promoter motif, repeat element or regulatory region #205.
 DE Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
 KW SNP; glaucoma; progressive ocular hypertensive disorder;
 KW glaucoma related disorder; motif; repeat element; regulatory region.
 XX OS Homo sapiens.
 XX XX US2003190617-A1.
 XX XX 09-OCT-2003.
 XX PF 06-MAR-2002; 2002US-00091281.
 XX PR 06-MAR-2002; 2002US-00091281.
 XX XX (SIEE/) SI E.
 PA (RAYM/) RAYMOND V.
 PA (MORI/) MORISSETTE J.
 XX PI Raymond V, Morissette J, Si E;
 XX WPI; 2003-864168/80.
 XX DR New nucleic acid sequences of the optineurin gene are useful to detect
 XX PT polymorphisms particularly single nucleotide polymorphisms in the
 XX PT optineurin promoter to diagnose, prognose and treat glaucoma and related
 XX PT disorders.
 XX PS Claim 11; SEQ ID NO 207; 159pp; English.
 XX CC The invention relates to an isolated nucleic acid (N1) comprising at
 CC least 20 but not more than 1500 consecutive nucleotides of the optineurin
 CC promoter appearing as ADE13890. Also included are the optineurin promoter
 CC operably linked to a heterologous nucleic acid, a nucleic acid capable of
 CC detecting a single nucleotide polymorphism (SNP) in the optineurin
 CC promoter, a host cell comprising the promoter operably linked to a
 CC heterologous sequence, diagnosing or prognosing glaucoma in a sample
 CC obtained from a cell or bodily fluid (comprising detecting a polymorphism
 CC in a promoter region of the optineurin gene, associated with a glaucoma
 CC phenotype), detecting a SNP sequence variation in a sample containing
 CC DNA, detecting the presence of an optineurin promoter sequence variation
 CC in a sample containing DNA, determining the presence or increased
 CC susceptibility to glaucoma or to a progressive ocular hypertensive
 CC disorder resulting in loss of visual field in a patient (or the severity
 CC or progression of glaucoma in a patient, comprising providing
 CC amplification reaction primers that direct amplification of a selected
 CC nucleic acid region containing the variation within the optineurin
 CC promoter and amplifying the DNA) and detecting a polymorphism (comprising
 CC obtaining a sample containing human genomic DNA, providing a nucleic acid
 CC capable of detecting a SNP located within an optineurin promoter, and
 CC detecting the polymorphism). The invention is used to diagnose and
 CC prognose glaucoma and also to treat glaucoma related disorders. The
 CC present sequence is an optineurin promoter motif, repeat element or
 CC putative regulatory region.
 XX SQ Sequence 6 BP; 0 A; 0 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 66.7%; Score 4; DB 10; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TGTG 5
 ||||
 Db 1 TGTG 4
 RESULT 14
 ADE13916
 ID ADE13916 standard; DNA; 6 BP.

XX	AC	ADE13916;	
XX	AC	ADE14095 standard; DNA; 6 BP.	
XX	AC	ADE14095;	
DT	DT	29-JAN-2004 (first entry)	
XX	DE	Optineurin promoter motif, repeat element or regulatory region #25.	
XX	DE	Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;	
KW	KW	SNP; glaucoma; progressive ocular hypertensive disorder;	
KW	KW	glaucoma related disorder; motif; repeat element; regulatory region.	
XX	OS	Homo sapiens.	
XX	OS	US2003190617-A1.	
PN	PN	09-OCT-2003.	
XX	PD	09-OCT-2003.	
XX	PD	06-MAR-2002; 2002US-00091281.	
XX	PF	06-MAR-2002; 2002US-00091281.	
XX	PF	06-MAR-2002; 2002US-00091281.	
XX	PR	(SIEE/) SI E.	
XX	PA	(RAYM/) RAYMOND V.	
XX	PA	(MORI/) MORISSETTE J.	
XX	PI	Raymond V, Morissette J, Si E;	
XX	PI	WPI; 2003-864168/80.	
XX	DR	New nucleic acid sequences of the optineurin gene are useful to detect	
XX	PT	polymorphisms particularly single nucleotide polymorphisms in the	
XX	PT	optineurin promoter to diagnose, prognose and treat glaucoma and related	
XX	PT	disorders.	
XX	PS	Claim 11; SEQ ID NO 27; 159pp; English.	
XX	PS	The invention relates to an isolated nucleic acid (N1) comprising at	
XX	CC	least 20 but not more than 1500 consecutive nucleotides of the optineurin	
XX	CC	promoter appearing as ADE13890. Also included are the optineurin promoter	
XX	CC	operably linked to a heterologous nucleic acid, a nucleic acid capable of	
XX	CC	detecting a single nucleotide polymorphism (SNP) in the optineurin	
XX	CC	promoter, a host cell comprising the promoter operably linked to a	
XX	CC	heterologous sequence, diagnosing or prognosing glaucoma in a sample	
XX	CC	obtained from a cell or bodily fluid (comprising detecting a polymorphism	
XX	CC	phenotype), detecting a SNP sequence variation in a sample containing	
XX	CC	DNA, detecting the presence of an optineurin promoter sequence variation	
XX	CC	in a sample containing DNA, determining the presence or increased	
XX	CC	susceptibility to glaucoma or to a progressive ocular hypertensive	
XX	CC	disorder resulting in loss of visual field in a patient (or the severity	
XX	CC	or progression of glaucoma in a patient, comprising providing	
XX	CC	amplification reaction primers that direct amplification of a selected	
XX	CC	nucleic acid region containing the variation within the optineurin	
XX	CC	promoter and amplifying the DNA) and detecting a polymorphism (comprising	
XX	CC	obtaining a sample containing human genomic DNA, providing a nucleic acid	
XX	CC	capable of detecting a SNP located within an optineurin promoter, and	
XX	CC	detecting the polymorphism). The invention is used to diagnose and	
XX	CC	prognose glaucoma and also to treat glaucoma related disorders. The	
XX	CC	present sequence is an optineurin promoter motif, repeat element or	
XX	CC	putative regulatory region.	
XX	CC	Sequence 6 BP; 0 A; 0 C; 3 G; 3 T; 0 U; 0 Other;	
XX	SQ	Sequence 6 BP; 0 A; 0 C; 3 G; 3 T; 0 U; 0 Other;	
Query Match 66.7%; Score 4; DB 10; Length 6;			
Best Local Similarity 100.0%; Pred. No. 9.7e+08;			
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	2	TGTG 5	
DB	1	TGTG 4	
RESULT 15			
XX	AC	ADE14095	
XX	ID	ADE14095 standard; DNA; 6 BP.	
XX	AC	ADE14095;	
XX	AC	ADE14095;	
DT	DT	29-JAN-2004 (first entry)	
XX	DE	Optineurin promoter motif, repeat element or regulatory region #204.	
XX	DE	Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;	
KW	KW	SNP; glaucoma; progressive ocular hypertensive disorder;	
KW	KW	glaucoma related disorder; motif; repeat element; regulatory region.	
XX	OS	Homo sapiens.	
XX	OS	US2003190617-A1.	
PN	PN	09-OCT-2003.	
XX	PD	09-OCT-2003.	
XX	PD	06-MAR-2002; 2002US-00091281.	
XX	PF	06-MAR-2002; 2002US-00091281.	
XX	PF	06-MAR-2002; 2002US-00091281.	
XX	PR	(SIEE/) SI E.	
XX	PA	(RAYM/) RAYMOND V.	
XX	PA	(MORI/) MORISSETTE J.	
XX	PI	Raymond V, Morissette J, Si E;	
XX	PI	WPI; 2003-864168/80.	
XX	DR	New nucleic acid sequences of the optineurin gene are useful to detect	
XX	PT	polymorphisms particularly single nucleotide polymorphisms in the	
XX	PT	optineurin promoter to diagnose, prognose and treat glaucoma and related	
XX	PT	disorders.	
XX	PS	Claim 11; SEQ ID NO 206; 159pp; English.	
XX	PS	The invention relates to an isolated nucleic acid (N1) comprising at	
XX	CC	least 20 but not more than 1500 consecutive nucleotides of the optineurin	
XX	CC	promoter appearing as ADE13890. Also included are the optineurin promoter	
XX	CC	operably linked to a heterologous nucleic acid, a nucleic acid capable of	
XX	CC	detecting a single nucleotide polymorphism (SNP) in the optineurin	
XX	CC	promoter, a host cell comprising the promoter operably linked to a	
XX	CC	heterologous sequence, diagnosing or prognosing glaucoma in a sample	
XX	CC	obtained from a cell or bodily fluid (comprising detecting a polymorphism	
XX	CC	in a promoter region of the optineurin gene, associated with a glaucoma	
XX	CC	phenotype), detecting a SNP sequence variation in a sample containing	
XX	CC	DNA, detecting the presence of an optineurin promoter sequence variation	
XX	CC	in a sample containing DNA, determining the presence or increased	
XX	CC	susceptibility to glaucoma or to a progressive ocular hypertensive	
XX	CC	disorder resulting in loss of visual field in a patient (or the severity	
XX	CC	or progression of glaucoma in a patient, comprising providing	
XX	CC	amplification reaction primers that direct amplification of a selected	
XX	CC	nucleic acid region containing the variation within the optineurin	
XX	CC	promoter and amplifying the DNA) and detecting a polymorphism (comprising	
XX	CC	obtaining a sample containing human genomic DNA, providing a nucleic acid	
XX	CC	capable of detecting a SNP located within an optineurin promoter, and	
XX	CC	detecting the polymorphism). The invention is used to diagnose and	
XX	CC	prognose glaucoma and also to treat glaucoma related disorders. The	
XX	CC	present sequence is an optineurin promoter motif, repeat element or	
XX	CC	putative regulatory region.	
XX	CC	Sequence 6 BP; 0 A; 0 C; 3 G; 3 T; 0 U; 0 Other;	
XX	SQ	Sequence 6 BP; 0 A; 0 C; 3 G; 3 T; 0 U; 0 Other;	
Query Match 66.7%; Score 4; DB 10; Length 6;			
Best Local Similarity 100.0%; Pred. No. 9.7e+08;			
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	2	TGTG 5	
DB	1	TGTG 4	

RESULT 16
ADE14265
ID ADE14265 standard; DNA; 6 BP.
XX AC ADE14265;
XX DT 29-JAN-2004 (first entry)
XX DE Optineurin promoter motif, repeat element or regulatory region #374.
XX DE Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
XX KW SNP; glaucoma; progressive ocular hypertensive disorder;
XX KW glaucoma related disorder; motif; repeat element; regulatory region.
XX OS Homo sapiens.
XX PN US2003190617-A1.
XX PD 09-OCT-2003.
XX PF 06-MAR-2002; 2002US-00091281.
XX PR 06-MAR-2002; 2002US-00091281.
XX PA (SIEE/) SI E.
XX PA (RAYM/) RAYMOND V.
XX PA (MORI/) MORISSETTE J.
XX PI Raymond V, Morissette J, Si E;
XX WPI; 2003-864168/80.
XX PT New nucleic acid sequences of the optineurin gene are useful to detect
XX PT polymorphisms particularly single nucleotide polymorphisms in the
XX PT optineurin promoter to diagnose, prognose and treat glaucoma and related
XX PT disorders.
XX PS Claim 11; SEQ ID NO 376; 159pp; English.
XX CC The invention relates to an isolated nucleic acid (N1) comprising at
XX CC least 20 but not more than 1500 consecutive nucleotides of the optineurin
XX CC promoter appearing as ADE13890. Also included are the optineurin promoter
XX CC operably linked to a heterologous nucleic acid, a nucleic acid capable of
XX CC detecting a single nucleotide polymorphism (SNP) in the optineurin
XX CC promoter, a host cell comprising the promoter operably linked to a
XX CC heterologous sequence, diagnosing or prognosing glaucoma in a sample
XX CC obtained from a cell or bodily fluid (comprising detecting a polymorphism
XX CC in a promoter region of the optineurin gene, associated with a glaucoma
XX CC phenotype), detecting a SNP sequence variation in a sample containing
XX CC DNA, detecting the presence of an optineurin promoter sequence variation
XX CC in a sample containing DNA, determining the presence or increased
XX CC susceptibility to glaucoma or to a progressive ocular hypertensive
XX CC disorder resulting in loss of visual field in a patient (or the severity
XX CC or progression of glaucoma in a patient, comprising providing
XX CC amplification reaction primers that direct amplification of a selected
XX CC nucleic acid region containing the variation within the optineurin
XX CC promoter and amplifying the DNA) and detecting a polymorphism (comprising
XX CC obtaining a sample containing human genomic DNA, providing a nucleic acid
XX CC capable of detecting a SNP located within an optineurin promoter, and
XX CC detecting the polymorphism). The invention is used to diagnose and
XX CC prognose glaucoma and also to treat glaucoma related disorders. The
XX CC present sequence is an optineurin promoter motif, repeat element or
XX CC putative regulatory region.
XX CC Sequence 6 BP; 0 A; 0 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 66.7%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TTGTG 5
|||||
DB 1 TTGTG 4
RESULT 18
ADK14289/c
ID ADK14289 standard; DNA; 6 BP.
XX AC ADK14289;
XX DT 20-MAY-2004 (first entry)
XX DE Candida promoter motif URS1-like sequence SEQ ID NO:18.
XX DE Candida tropicalis; CYP gene promoter; modified CYP gene promoter;
XX KW yeast host cell; URS1; URS2; URS1-like; URS2-like;
XX KW beta oxidation pathway; omega oxidation pathway; gene; ds.
XX OS Candida sp.
Query Match 66.7%; Score 4; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TTGTG 5
|||||
DB 1 TTGTG 4
RESULT 17
ADE52744
ID ADE52744 standard; DNA; 6 BP.
XX AC ADE52744;
XX DT 29-JAN-2004 (first entry)
XX DE Oligonucleotide SEQ ID 110.
XX KW DNA-binding protein; interferon-activatable protein; ss.
XX OS Synthetic.
XX PN WO2003089466-A1.
XX PD 30-OCT-2003.
XX PF 18-APR-2003; 2003WO-JP004981.
XX PR 19-APR-2002; 2002JP-00117840.
XX PR 30-APR-2002; 2002JP-00128418.
XX PR 30-APR-2002; 2002JP-00128779.
XX PR 04-DEC-2002; 2002JP-00352469.
XX PA (RIKE) RIKEN KK.
XX PA (DNAP-) DNAFORM KK.
XX PA (MITU) MITSUBISHI CHEM CORP.
XX PI Hayashizaki Y, Kamiya M, Kubodera H;
XX WPI; 2004-011681/01.
XX PT Proteins with DNA binding activity and substances that affect their
XX PT activity or expression, useful for treating associated disorders.
XX PS Example 9; SEQ ID NO 110; 237pp; Japanese.
XX CC The present invention relates to novel proteins (ADE52648-ADE52660,
XX CC ADE52670 and ADE52672) and their coding sequences (ADE52635-ADE52647,
XX CC ADE52669 and ADE52671). The proteins have a DNA-binding activity or an
XX CC interferon-activatable protein (IAP)-like activity. The present
XX CC oligonucleotide is related to AML1a.
XX CC Sequence 6 BP; 0 A; 0 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 66.7%; Score 4; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TTGTG 5
|||||
DB 1 TTGTG 4
RESULT 18
ADK14289/c
ID ADK14289 standard; DNA; 6 BP.
XX AC ADK14289;
XX DT 20-MAY-2004 (first entry)
XX DE Candida promoter motif URS1-like sequence SEQ ID NO:18.
XX DE Candida tropicalis; CYP gene promoter; modified CYP gene promoter;
XX KW yeast host cell; URS1; URS2; URS1-like; URS2-like;
XX KW beta oxidation pathway; omega oxidation pathway; gene; ds.
XX OS Candida sp.
Query Match 66.7%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TTGTG 5
|||||
DB 1 TTGTG 4

XX WO2004016756-A2.
 PN
 XX
 PD 26-FEB-2004.
 XX
 XX 15-AUG-2003; 2003WO-US025545.
 XX
 XX 16-AUG-2002; 2002US-0403979P.
 PR
 PR 14-AUG-2003; 2003US-00640962.
 XX
 XX (COGN-) COGNIS CORP.
 PA
 XX
 XX Wilson RC, Craft DL, Zhang Y, Stavenhagen JB;
 PI
 XX
 XX WPI; 2004-203787/19.
 DR
 XX
 XX New modified Candida tropicalis CYP gene promoters comprising nucleotide
 PT sequence for a CYP gene promoter, useful for modulating expression of a
 PT protein of the beta or omega oxidation pathway in a yeast cell.
 PT
 XX
 PS Claim 4; SEQ ID NO 18; 99pp; English.
 XX
 XX The present invention describes modified Candida tropicalis CYP gene
 CC promoters comprising a nucleotide sequence for a CYP gene promoter. Also
 CC described: (1) a yeast host cell comprising the modified Candida
 CC tropicalis CYP gene promoter; and (2) a method for modulating expression
 CC of a protein of the beta or omega oxidation pathway in a yeast cell.
 CC comprising: (a) isolating a CYP gene promoter from C. tropicalis; (b)
 CC modifying the promoter by addition of one or more URS1, URS2, URS1-like
 CC or URS2-like sequences; (c) operably linking the modified promoter with a
 CC coding sequence for a protein of the omega or beta oxidation pathway; (d)
 CC transforming a yeast cell with the modified promoter operably linked to
 CC the coding sequence; and (e) growing the yeast under conditions
 CC favourable for expression of the coding sequence under the control of the
 CC modified promoter. The promoters are useful for modulating expression of
 CC a protein of the beta or omega oxidation pathway in a yeast cell. The
 CC present sequence is used in the exemplification of the present invention.
 XX
 XX Sequence 6 BP; 3 A; 2 C; 1 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 66.7%; Score 4; DB 12; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTGT 4
 DB ||||
 4 GTGT 1
 RESULT 19
 ADK14312/c
 ID ADK14312 standard; DNA; 6 BP.
 XX
 AC ADK14312;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Candida promoter motif URS2-like sequence SEQ ID NO:41.
 XX
 XX Candida tropicalis; CYP gene promoter; modified CYP gene promoter;
 KW yeast host cell; URS1; URS2; URS1-like; URS2-like;
 KW beta oxidation pathway; omega oxidation pathway; gene; ds.
 XX
 OS Candida sp.
 XX
 PN WO2004016756-A2.
 XX
 XX 26-FEB-2004.
 PD
 XX
 XX 15-AUG-2003; 2003WO-US025545.
 XX
 XX 16-AUG-2002; 2002US-0403979P.
 PR
 PR 14-AUG-2003; 2003US-00640962.
 XX
 PR

XX (COGN-) COGNIS CORP.
 PA
 XX Wilson RC, Craft DL, Zhang Y, Stavenhagen JB;
 PI
 XX
 XX WPI; 2004-203787/19.
 DR
 XX
 XX New modified Candida tropicalis CYP gene promoters comprising nucleotide
 PT sequence for a CYP gene promoter, useful for modulating expression of a
 PT protein of the beta or omega oxidation pathway in a yeast cell.
 PT
 XX
 PS Claim 9; SEQ ID NO 41; 99pp; English.
 XX
 XX The present invention describes modified Candida tropicalis CYP gene
 CC promoters comprising a nucleotide sequence for a CYP gene promoter. Also
 CC described: (1) a yeast host cell comprising the modified Candida
 CC tropicalis CYP gene promoter; and (2) a method for modulating expression
 CC of a protein of the beta or omega oxidation pathway in a yeast cell
 CC comprising: (a) isolating a CYP gene promoter from C. tropicalis; (b)
 CC modifying the promoter by addition of one or more URS1, URS2, URS1-like
 CC or URS2-like sequences; (c) operably linking the modified promoter with a
 CC coding sequence for a protein of the omega or beta oxidation pathway; (d)
 CC transforming a yeast cell with the modified promoter operably linked to
 CC the coding sequence; and (e) growing the yeast under conditions
 CC favourable for expression of the coding sequence under the control of the
 CC modified promoter. The promoters are useful for modulating expression of
 CC a protein of the beta or omega oxidation pathway in a yeast cell. The
 CC present sequence is used in the exemplification of the present invention.
 XX
 XX Sequence 6 BP; 2 A; 3 C; 1 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 66.7%; Score 4; DB 12; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTGT 4
 DB ||||
 4 GTGT 1
 RESULT 20
 ADL09233/c
 ID ADL09233 standard; DNA; 6 BP.
 XX
 AC ADL09233;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE SP6 promoter DNA fragment #12.
 XX
 KW amplification; primer; promoter; RNA polymerase; ds.
 XX
 OS Enterobacteria phage SP6.
 XX
 PN WO2004016757-A2.
 XX
 PD 26-FEB-2004.
 XX
 XX 15-AUG-2003; 2003WO-US025564.
 PF
 XX
 PR 16-AUG-2002; 2002US-0404075P.
 PR
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX Karin M, Park JM;
 PI
 XX WPI; 2004-203788/19.
 DR
 XX
 XX Producing a nucleic acid sequence comprises amplifying double stranded
 PT DNA sequence in the presence of first and second primers to produce a
 PT first nucleic acid molecule having the double stranded DNA sequence in a
 PT head to head orientation.
 XX

PS Disclosure; SEQ ID NO 49; 55pp; English.

XX This invention describes a novel method for producing a nucleic acid
 CC sequence comprising amplifying the double stranded DNA sequence of
 CC interest in the presence of the first primer and the second primer to
 CC produce a first nucleic acid molecule comprising the double stranded DNA
 CC sequence of interest flanked by at least a portion of the first promoter
 CC in a head to head orientation. The method involves providing RNA
 CC polymerase that specifically binds to the first promoter and contacting
 CC the first nucleic acid molecule with the RNA polymerase to produce double
 CC stranded RNA that is complementary to the double stranded DNA sequence of
 CC interest. This method further comprises providing a third primer
 CC complementary to at least a portion of the first promoter and amplifying
 CC the first nucleic acid molecule produced in the presence of the third
 CC primer to produce a second nucleic acid molecule comprising the double
 CC stranded DNA sequence of interest flanked by the first promoter in a head
 CC to head orientation. The method further comprises providing RNA
 CC polymerase that specifically binds to the first promoter and contacting
 CC the second nucleic acid molecule with the RNA polymerase to produce
 CC double stranded RNA that is complementary to the double stranded DNA
 CC sequence of interest. The second strand of the double-stranded DNA
 CC sequence of interest comprises at least a portion of a second promoter.
 CC The second promoter is different from the first promoter. The first
 CC promoter comprises T7, T3 or SP6 promoter. The first strand of the double
 CC stranded DNA comprises a nucleotide sequence linked to the 3' end of the
 CC first promoter, and the first primer further comprises a second sequence
 CC complementary to the nucleotide sequence, where the second sequence is
 CC linked to the 3' end of the first sequence of the first primer. The first
 CC primer comprises a sequence complementary to T7, T3 or SP6 promoter. The
 CC first sequence comprises a second primer complementary to at least a
 CC portion of a promoter. The methods and kits are useful for producing
 CC nucleic acid sequences as powerful alternative tools for functional
 CC genomics.

XX SQ Sequence 6 BP; 2 A; 2 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 12; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGT 4
 DB 5 GGTGT 2

RESULT 21
 ADO05792/c
 ID ADO05792 standard; DNA; 6 BP.
 XX ADO05792;
 XX 15-JUL-2004 (first entry)
 XX Telomere-specific PNA-labelled probe repeat fragment, SEQ ID 6.
 DE PNA; peptide nucleic acid; telomere length assay; in vitro fertilization;
 XX telomere; quantitative fluorescent in situ hybridization; Q-FISH;
 KW aneuploidy; probe; ss.
 XX Synthetic.
 XX WO2004035597-A2.
 XX 29-APR-2004.
 XX 13-OCT-2003; 2003WO-US032672.
 PF 16-OCT-2002; 2002US-0419071P.
 PR 07-MAR-2003; 2003US-0452741P.
 XX (WOME-) WOMEN & INFANTS HOSPITAL RHODE ISLAND.
 PA Keefe DL;
 XX

XX WPI; 2004-348432/32.
 XX Determining the risk of reproductive failure or aneuploidy in an oocyte,
 PT useful for in vitro fertilization purposes, comprises measuring the
 PT telomere length of a chromosome obtained from the oocyte.
 XX Claim 49; Page 23; 47pp; English.
 XX The invention relates to determining the risk of reproductive failure or
 CC aneuploidy in a cell from a subject. The method involves obtaining at
 CC least one chromosome from the cell, measuring telomere length of the
 CC chromosome, and comparing the measured length of the telomere to the
 CC standardized average length of a control telomere to determine the risk
 CC of reproductive failure or aneuploidy in the cell. In determining the
 CC risk of reproductive failure or aneuploidy in a cell, the cell is an
 CC oocyte, an oocyte representative of a population of oocytes, a polar body
 CC from a fertilized oocyte, or a polar body from an unfertilized oocyte.
 CC Preferably, the cell is an oocyte. Selecting a fertilized oocyte with a
 CC low risk of reproductive failure or aneuploidy for in vitro fertilization
 CC comprises obtaining at least one chromosome from the polar body of the
 CC fertilized oocyte, measuring telomere length of the chromosome, and
 CC comparing the measured length of the telomere to the standardized average
 CC length of a control telomere to select a fertilized oocyte with a low
 CC risk of reproductive failure for in vitro fertilization. In the above
 CC methods, a labelled telomere-specific probe is hybridized to the
 CC chromosome prior to measuring telomere length of the chromosome. The
 CC probe is hybridized to telomere repeats. The probe is peptide nucleic
 CC acid (PNA)-labelled. The telomere is measured using quantitative
 CC fluorescent in situ hybridization (Q-FISH) analysis. In vitro
 CC fertilization comprises selecting a fertilized oocyte cited above and
 CC implanting the selected oocyte in the subject. The methods are useful for
 CC in vitro fertilization. The kit and methods may also be used for
 CC assessing the risk of reproductive failure and/or aneuploidy. Sequences
 CC ADO05788-ADO05795 represent specific examples of repeat fragments
 CC contained in the telomere-specific PNA-labelled probes.

XX SQ Sequence 6 BP; 2 A; 4 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 12; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTGT 5
 DB 6 TGTGT 3

RESULT 22
 ADR35664/c
 ID ADR35664 standard; DNA; 6 BP.
 XX ADR35664;
 XX 04-NOV-2004 (first entry)
 XX Human nicking agent DNA containing BstNBI restriction site #2084.
 DE ss; nicking agent; assay panel; diagnosis; expression pattern;
 XX DNA fingerprinting; nosocomial infection; microbiological assay;
 KW bacterial contamination; genome mapping; bioremediation.
 XX Homo sapiens.
 XX WO2004067765-A2.
 XX 12-AUG-2004.
 XX 29-JAN-2004; 2004WO-US002720.
 XX 29-JAN-2003; 2003US-0443811P.
 XX (KECK-) KECK GRADUATE INST.

XX PI Van Ness J, Galas DJ, Van Ness LK;
XX PA WPI; 2004-581010/56.
XX PT Identifying nucleic acid sample source, useful for identifying bacterial
XX PT strains involved in nosocomial infections, comprises treating the nucleic
XX PT acid sample with components comprising a nicking agent under nicking
XX PT conditions.
XX PS Example 3; Page 105-219; 238pp; English.
XX CC The invention relates to a method of treating a nucleic acid sample with
XX CC components under nicking conditions, where the components comprise a
XX CC nicking agent, and the conditions cause the nicking agent to nick the
XX CC nucleic acid sample to thus produce a family of initiating
XX CC oligonucleotide fragments, and subjecting one or more members of the
XX CC family of initiating oligonucleotide fragments to a characterization
XX CC process to thus provide results. The method is useful for creating an
XX CC assay panel of diagnostic oligonucleotides that can identify any organism
XX CC or individual. The method is useful for characterizing other DNA
XX CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
XX CC The method, kit or composition is useful for identifying the source
XX CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
XX CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
XX CC subspecies, and especially strains or individuals of the subspecies. It
XX CC is especially useful for identifying different bacterial strains involved
XX CC in e.g., nosocomial infections. Furthermore, the method is useful for
XX CC diagnosing bacterial disease in plants and humans, monitoring for
XX CC bacterial content and/or contamination in the environment, monitoring
XX CC food for bacterial contamination, monitoring quality assurance/quality control of
XX CC laboratory tests involving microbiological assays, tracing bacterial
XX CC contamination and/or outbreaks of bacterial infections, genome mapping,
XX CC monitoring bioremediation sites, and for monitoring agricultural sites
XX CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-
XX CC ADR37496 correspond to target nucleic acids containing an NBstNBI
XX CC restriction site and used in the method of the invention.
XX SQ Sequence 6 BP; 2 A; 2 C; 0 G; 1 T; 0 U; 1 Other;
Query Match 66.7%; Score 4; DB 13; Length 6;
Best Local Similarity 66.7%; Pred. No. 9.7e+08;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTGTGT 6
Db 6 GASTGT 1
RESULT 23
ID ADR35687 standard; DNA; 6 BP.
XX AC ADR35687;
XX DT 04-NOV-2004 (first entry)
XX DE Human nicking agent DNA containing BstNBI restriction site #2107.
XX KW ss; nicking agent; assay panel; diagnosis; expression pattern;
XX KW DNA fingerprinting; nosocomial infection; microbiological assay;
XX KW bacterial contamination; genome mapping; bioremediation.
XX OS Homo sapiens.
XX PN WO2004067765-A2.
XX PD 12-AUG-2004.
XX PF 29-JAN-2004; 2004WO-US002720.
XX

PR 29-JAN-2003; 2003US-0443811P.
XX PA (KECK-) KECK GRADUATE INST.
XX PI Van Ness J, Galas DJ, Van Ness LK;
XX PT WPI; 2004-581010/56.
XX DR Identifying nucleic acid sample source, useful for identifying bacterial
XX PT strains involved in nosocomial infections, comprises treating the nucleic
XX PT acid sample with components comprising a nicking agent under nicking
XX PT conditions.
XX PS Example 3; Page 105-219; 238pp; English.
XX CC The invention relates to a method of treating a nucleic acid sample with
XX CC components under nicking conditions, where the components comprise a
XX CC nicking agent, and the conditions cause the nicking agent to nick the
XX CC nucleic acid sample to thus produce a family of initiating
XX CC oligonucleotide fragments, and subjecting one or more members of the
XX CC family of initiating oligonucleotide fragments to a characterization
XX CC process to thus provide results. The method is useful for creating an
XX CC assay panel of diagnostic oligonucleotides that can identify any organism
XX CC or individual. The method is useful for characterizing other DNA
XX CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
XX CC The method, kit or composition is useful for identifying the source
XX CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
XX CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
XX CC subspecies, and especially strains or individuals of the subspecies. It
XX CC is especially useful for identifying different bacterial strains involved
XX CC in e.g., nosocomial infections. Furthermore, the method is useful for
XX CC diagnosing bacterial disease in plants and humans, monitoring for
XX CC bacterial content and/or contamination in the environment, monitoring
XX CC food for bacterial contamination, monitoring quality assurance/quality control of
XX CC laboratory tests involving microbiological assays, tracing bacterial
XX CC contamination and/or outbreaks of bacterial infections, genome mapping,
XX CC monitoring bioremediation sites, and for monitoring agricultural sites
XX CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-
XX CC ADR37496 correspond to target nucleic acids containing an NBstNBI
XX CC restriction site and used in the method of the invention.
XX SQ Sequence 6 BP; 1 A; 0 C; 2 G; 2 T; 0 U; 1 Other;
Query Match 66.7%; Score 4; DB 13; Length 6;
Best Local Similarity 66.7%; Pred. No. 9.7e+08;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTGTGT 6
Db 1 GASTGT 6
RESULT 24
ID ADR35663/c standard; DNA; 6 BP.
XX AC ADR35663;
XX DT 04-NOV-2004 (first entry)
XX DE Human nicking agent DNA containing BstNBI restriction site #2083.
XX KW ss; nicking agent; assay panel; diagnosis; expression pattern;
XX KW DNA fingerprinting; nosocomial infection; microbiological assay;
XX KW bacterial contamination; genome mapping; bioremediation.
XX OS Homo sapiens.
XX PN WO2004067765-A2.
XX PD 12-AUG-2004.
XX

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XX PF 29-JAN-2004; 2004WO-US002720.
XX PD 12-AUG-2004.
XX PF 29-JAN-2003; 2003US-0443811P.
XX PA (KECK-) KECK GRADUATE INST.
XX PI Van Ness J, Galas DJ, Van Ness LK;
XX DR WPI; 2004-581010/56.
XX PT Identifying nucleic acid sample source, useful for identifying bacterial
XX PT strains involved in nosocomial infections, comprises treating the nucleic
XX PT acid sample with components comprising a nicking agent under nicking
XX PS conditions.
XX PS Example 3; Page 105-219; 238pp; English.
XX CC The invention relates to a method of treating a nucleic acid sample with
XX CC components under nicking conditions, where the components comprise a
XX CC nicking agent, and the conditions cause the nicking agent to nick the
XX CC nucleic acid sample to thus produce a family of initiating
XX CC oligonucleotide fragments, and subjecting one or more members of the
XX CC family of initiating oligonucleotide fragments to a characterization
XX CC process to thus provide results. The method is useful for creating an
XX CC assay panel of diagnostic oligonucleotides that can identify any organism
XX CC or individual. The method is useful for characterizing other DNA
XX CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
XX CC The method, kit or composition is useful for identifying the source
XX CC of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
XX CC non-human animal or human. The method is particularly useful for rapidly
XX CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
XX CC subpecies, and especially strains or individuals of the subspecies. It
XX CC is especially useful for identifying different bacterial strains involved
XX CC in e.g., nosocomial infections. Furthermore, the method is useful for
XX CC diagnosing bacterial disease in plants and humans, monitoring for
XX CC bacterial content and/or contamination in the environment, monitoring
XX CC food for bacterial contamination, monitoring quality assurance/processes for
XX CC bacterial contamination, monitoring quality assurance/quality control of
XX CC laboratory tests involving microbiological assays, tracing bacterial
XX CC contamination and/or outbreaks of bacterial infections, genome mapping,
XX CC monitoring bioremediation sites, and for monitoring agricultural sites
XX CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-
XX CC ADR37496 correspond to target nucleic acids containing an NBstNBI
XX CC restriction site and used in the method of the invention.
XX SQ Sequence 6 BP; 2 A; 2 C; 0 G; 1 T; 0 U; 1 Other;
Query Match 66.7%; Score 4; DB 13; Length 6;
Best Local Similarity 66.7%; Pred. No. 9.7e+08;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTGTGT 6
Db 6 GASTGT 1
RESULT 25
ADR35667
ID ADR35667 standard; DNA; 6 BP.
XX AC ADR35667;
XX DT 04-NOV-2004 (first entry)
XX DE Human nicking agent DNA containing BstNBI restriction site #2087.
XX KW ss; nicking agent; assay panel; diagnosis; expression pattern;
XX KW DNA fingerprinting; nosocomial infection; microbiological assay;
XX KW bacterial contamination; genome mapping; bioremediation.
XX OS Homo sapiens.
XX

PN WO2004067765-A2.
PD 12-AUG-2004.
PF 29-JAN-2004; 2004WO-US002720.
PR 29-JAN-2003; 2003US-0443811P.
PX (KECK-) KECK GRADUATE INST.
PY Van Ness J, Galas DJ, Van Ness LK;
PZ WPI; 2004-581010/56.
PT Identifying nucleic acid sample source, useful for identifying bacterial
PT strains involved in nosocomial infections, comprises treating the nucleic
PT acid sample with components comprising a nicking agent under nicking
PT conditions.
PT Example 3; Page 105-219; 238pp; English.
PT CC The invention relates to a method of treating a nucleic acid sample with
PT CC components under nicking conditions, where the components comprise a
PT CC nicking agent, and the conditions cause the nicking agent to nick the
PT CC nucleic acid sample to thus produce a family of initiating
PT CC oligonucleotide fragments, and subjecting one or more members of the
PT CC family of initiating oligonucleotide fragments to a characterization
PT CC process to thus provide results. The method is useful for creating an
PT CC assay panel of diagnostic oligonucleotides that can identify any organism
PT CC or individual. The method is useful for characterizing other DNA
PT CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
PT CC The method, kit or composition is useful for identifying the source
PT CC of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
PT CC non-human animal or human. The method is particularly useful for rapidly
PT CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
PT CC subpecies, and especially strains or individuals of the subspecies. It
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PT CC in e.g., nosocomial infections. Furthermore, the method is useful for
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PT CC bacterial content and/or contamination in the environment, monitoring
PT CC food for bacterial contamination, monitoring quality assurance/processes for
PT CC bacterial contamination, monitoring quality assurance/quality control of
PT CC laboratory tests involving microbiological assays, tracing bacterial
PT CC contamination and/or outbreaks of bacterial infections, genome mapping,
PT CC monitoring bioremediation sites, and for monitoring agricultural sites
PT CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-
PT CC ADR37496 correspond to target nucleic acids containing an NBstNBI
PT CC restriction site and used in the method of the invention.
PT SQ Sequence 6 BP; 1 A; 0 C; 2 G; 2 T; 0 U; 1 Other;
Query Match 66.7%; Score 4; DB 13; Length 6;
Best Local Similarity 66.7%; Pred. No. 9.7e+08;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTGTGT 6
Db 1 GASTGT 6
RESULT 26
ADR35668
ID ADR35668 standard; DNA; 6 BP.
XX AC ADR35668;
XX DT 04-NOV-2004 (first entry)
XX DE Human nicking agent DNA containing BstNBI restriction site #2088.
XX KW ss; nicking agent; assay panel; diagnosis; expression pattern;
XX KW DNA fingerprinting; nosocomial infection; microbiological assay;
XX KW bacterial contamination; genome mapping; bioremediation.
XX

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KW ss; nicking agent; assay panel; diagnosis; expression pattern;
KW DNA fingerprinting; nosocomial infection; microbiological assay;
KW bacterial contamination; genome mapping; bioremediation.
XX
OS Homo sapiens.
XX
PN WO2004067765-A2.
XX
PD 12-AUG-2004.
XX
PF 29-JAN-2004; 2004WO-US002720.
XX
PR 29-JAN-2003; 2003US-0443811P.
XX
PA (KECK-) KECK GRADUATE INST.
XX
PI Van Ness J, Galas DJ, Van Ness LK;
XX WPI; 2004-581010/56.
XX
PT Identifying nucleic acid sample source, useful for identifying bacterial
PT strains involved in nosocomial infections, comprises treating the nucleic
PT acid sample with components comprising a nicking agent under nicking
PT conditions.
XX
PS Example 3; Page 105-219; 238pp; English.
XX
CC The invention relates to a method of treating a nucleic acid sample with
CC components under nicking conditions, where the components comprise a
CC nicking agent, and the conditions cause the nicking agent to nick the
CC nucleic acid sample to thus produce a family of initiating
CC oligonucleotide fragments, and subjecting one or more members of the
CC family of initiating oligonucleotide fragments to a characterization
CC process to thus provide results. The method is useful for creating an
CC assay panel of diagnostic oligonucleotides that can identify any organism
CC or individual. The method is useful for characterizing other DNA
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CC The method, kit or composition is useful for identifying the source
CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC non-human animal or human. The method is particularly useful for rapidly
CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
CC subspecies, and especially strains or individuals of the subspecies. It
CC is especially useful for identifying different bacterial strains involved
CC in e.g., nosocomial infections. Furthermore, the method is useful for
CC diagnosing bacterial disease in plants and humans, monitoring for
CC bacterial content and/or contamination in the environment, monitoring
CC food for bacterial contamination, monitoring quality assurance/quality control of
CC laboratory tests involving microbiological assays, tracing bacterial
CC contamination and/or outbreaks of bacterial infections, genome mapping,
CC monitoring bioremediation sites, and for monitoring agricultural sites
CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-
CC ADR37496 correspond to target nucleic acids containing an NBstNBI
CC restriction site and used in the method of the invention.
XX
SQ Sequence 6 BP; 1 A; 0 C; 2 G; 2 T; 0 U; 1 Other;
    Query Match          66.7%; Score 4; DB 13; Length 6;
    Best Local Similarity 66.7%; Pred. No. 9.7e+08;
    Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGTGT 6
Db | :|||
   1 GASTGT 6

RESULT 27
ADR35665/c
ID ADR35665 standard; DNA; 6 BP.
XX
AC ADR35665;
XX
DT 04-NOV-2004 (first entry)
XX
DE Human nicking agent DNA containing BstNBI restriction site #2085.
XX

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KW ss; nicking agent; assay panel; diagnosis; expression pattern;
KW DNA fingerprinting; nosocomial infection; microbiological assay;
KW bacterial contamination; genome mapping; bioremediation.
XX
OS Homo sapiens.
XX
PN WO2004067765-A2.
XX
PD 12-AUG-2004.
XX
PF 29-JAN-2004; 2004WO-US002720.
XX
PR 29-JAN-2003; 2003US-0443811P.
XX
PA (KECK-) KECK GRADUATE INST.
XX
PI Van Ness J, Galas DJ, Van Ness LK;
XX WPI; 2004-581010/56.
XX
PT Identifying nucleic acid sample source, useful for identifying bacterial
PT strains involved in nosocomial infections, comprises treating the nucleic
PT acid sample with components comprising a nicking agent under nicking
PT conditions.
XX
PS Example 3; Page 105-219; 238pp; English.
XX
CC The invention relates to a method of treating a nucleic acid sample with
CC components under nicking conditions, where the components comprise a
CC nicking agent, and the conditions cause the nicking agent to nick the
CC nucleic acid sample to thus produce a family of initiating
CC oligonucleotide fragments, and subjecting one or more members of the
CC family of initiating oligonucleotide fragments to a characterization
CC process to thus provide results. The method is useful for creating an
CC assay panel of diagnostic oligonucleotides that can identify any organism
CC or individual. The method is useful for characterizing other DNA
CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC The method, kit or composition is useful for identifying the source
CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC non-human animal or human. The method is particularly useful for rapidly
CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
CC subspecies, and especially strains or individuals of the subspecies. It
CC is especially useful for identifying different bacterial strains involved
CC in e.g., nosocomial infections. Furthermore, the method is useful for
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CC bacterial content and/or contamination in the environment, monitoring
CC food for bacterial contamination, monitoring quality assurance/quality control of
CC laboratory tests involving microbiological assays, tracing bacterial
CC contamination and/or outbreaks of bacterial infections, genome mapping,
CC monitoring bioremediation sites, and for monitoring agricultural sites
CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-
CC ADR37496 correspond to target nucleic acids containing an NBstNBI
CC restriction site and used in the method of the invention.
XX
SQ Sequence 6 BP; 1 A; 0 C; 2 G; 2 T; 0 U; 1 Other;
    Query Match          66.7%; Score 4; DB 13; Length 6;
    Best Local Similarity 66.7%; Pred. No. 9.7e+08;
    Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGTGT 6
Db | :|||
   1 GASTGT 6

RESULT 28
ADR35666/c
ID ADR35666 standard; DNA; 6 BP.
XX
AC ADR35666;
XX
DT 04-NOV-2004 (first entry)
XX

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XX DE Human nicking agent DNA containing BstNBI restriction site #2086.
XX DT ss; nicking agent; assay panel; diagnosis; expression pattern;
XX DE DNA fingerprinting; nosocomial infection; microbiological assay;
XX KW bacterial contamination; genome mapping; bioremediation.
XX OS Homo sapiens.
XX PN WO2004067765-A2.
XX PD 12-AUG-2004.
XX PF 29-JAN-2004; 2004WO-US002720.
XX PR 29-JAN-2003; 2003US-0443811P.
XX PA (KECK-) KECK GRADUATE INST.
XX PI Van Ness J, Galas DJ, Van Ness LK;
XX DR WPI; 2004-581010/56.
XX PT Identifying nucleic acid sample source, useful for identifying bacterial
XX PT strains involved in nosocomial infections, comprises treating the nucleic
XX PT acid sample with components comprising a nicking agent under nicking
XX PS conditions.
XX PS Example 3; Page 105-219; 238pp; English.
XX CC The invention relates to a method of treating a nucleic acid sample with
XX CC components under nicking conditions, where the components comprise a
XX CC nicking agent, and the conditions cause the nicking agent to nick the
XX CC nucleic acid sample to thus produce a family of initiating
XX CC oligonucleotide fragments, and subjecting one or more members of the
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XX CC assay panel of diagnostic oligonucleotides that can identify any organism
XX CC or individual. The method is useful for characterizing other DNA
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XX CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
XX CC subspecies, and especially strains or individuals of the subspecies. It
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XX CC in e.g., nosocomial infections. Furthermore, the method is useful for
XX CC diagnosing bacterial disease in plants and humans, monitoring for
XX CC bacterial content and/or contamination in the environment, monitoring
XX CC food for bacterial contamination, monitoring quality assurance/quality control of
XX CC bacterial contamination, monitoring quality assurance/quality control of
XX CC laboratory tests involving microbiological assays, tracing bacterial
XX CC contamination and/or outbreaks of bacterial infections, genome mapping,
XX CC monitoring bioremediation sites, and for monitoring agricultural sites
XX CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-
XX CC ADR37496 correspond to target nucleic acids containing an NBstNBI
XX CC restriction site and used in the method of the invention.
XX SQ Sequence 6 BP; 2 A; 2 C; 0 G; 1 T; 0 U; 1 Other;
XX
XX Query Match 66.7%; Score 4; DB 13; Length 6;
XX Best Local Similarity 66.7%; Pred. No. 9.7e+08;
XX Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 GTGTGT 6
XX | :|||
XX 6 GASTGT 1
XX
XX Db
XX
XX RESULT 29
XX ADR35669
XX ID ADR35669 standard; DNA; 6 BP.
XX

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AC ADR35669;
XX 04-NOV-2004 (first entry)
XX Human nicking agent DNA containing BstNBI restriction site #2089.
XX DE ss; nicking agent; assay panel; diagnosis; expression pattern;
XX KW DNA fingerprinting; nosocomial infection; microbiological assay;
XX KW bacterial contamination; genome mapping; bioremediation.
XX OS Homo sapiens.
XX PN WO2004067765-A2.
XX PD 12-AUG-2004.
XX PF 29-JAN-2004; 2004WO-US002720.
XX PR 29-JAN-2003; 2003US-0443811P.
XX PA (KECK-) KECK GRADUATE INST.
XX PI Van Ness J, Galas DJ, Van Ness LK;
XX DR WPI; 2004-581010/56.
XX PT Identifying nucleic acid sample source, useful for identifying bacterial
XX PT strains involved in nosocomial infections, comprises treating the nucleic
XX PT acid sample with components comprising a nicking agent under nicking
XX PS conditions.
XX PS Example 3; Page 105-219; 238pp; English.
XX CC The invention relates to a method of treating a nucleic acid sample with
XX CC components under nicking conditions, where the components comprise a
XX CC nicking agent, and the conditions cause the nicking agent to nick the
XX CC nucleic acid sample to thus produce a family of initiating
XX CC oligonucleotide fragments, and subjecting one or more members of the
XX CC family of initiating oligonucleotide fragments to a characterization
XX CC process to thus provide results. The method is useful for creating an
XX CC assay panel of diagnostic oligonucleotides that can identify any organism
XX CC or individual. The method is useful for characterizing other DNA
XX CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
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XX CC of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
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XX CC fingerprinting DNA to identifying prokaryotic and eukaryotic species. It
XX CC is especially useful for identifying different bacterial strains involved
XX CC in e.g., nosocomial infections. Furthermore, the method is useful for
XX CC diagnosing bacterial disease in plants and humans, monitoring for
XX CC bacterial content and/or contamination in the environment, monitoring
XX CC food for bacterial contamination, monitoring quality assurance/quality control of
XX CC bacterial contamination, monitoring quality assurance/quality control of
XX CC laboratory tests involving microbiological assays, tracing bacterial
XX CC contamination and/or outbreaks of bacterial infections, genome mapping,
XX CC monitoring bioremediation sites, and for monitoring agricultural sites
XX CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-
XX CC ADR37496 correspond to target nucleic acids containing an NBstNBI
XX CC restriction site and used in the method of the invention.
XX SQ Sequence 6 BP; 1 A; 0 C; 2 G; 2 T; 0 U; 1 Other;
XX
XX Query Match 66.7%; Score 4; DB 13; Length 6;
XX Best Local Similarity 66.7%; Pred. No. 9.7e+08;
XX Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 GTGTGT 6
XX | :|||
XX 1 GASTGT 6
XX
XX Db
XX
XX RESULT 30

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AAZ10696/c
ID AAZ10696 standard; DNA; 5 BP.
XX
AC AAZ10696;
XX
DT 23-NOV-1999 (first entry)
XX
XX Oligonucleotide sequence that increases p53 activity in a cell.
DE
XX p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
KW UV-induced hyperproliferative disease; psoriasis; vitiligo;
KW atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
KW skin cancer; ss.
XX
OS Synthetic.
XX
PN GB2336157-A.
XX
PD 13-OCT-1999.
XX
PF 24-MAR-1999; 99GB-00006758.
XX
PR 26-MAR-1998; 98US-00048927.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Gilchrist BA, Yaar M, Eller M;
XX
DR WPI; 1999-543520/46.
XX
PT DNA fragments useful for increasing p53 activity in a cell and reducing
PT susceptibility to UV-induced hyperproliferative diseases.
XX
PS Claim 11; Page 30; 44pp; English.
XX
CC AAZ10692-97 represent DNA fragments that are used for increasing p53
CC activity in a cell. The oligonucleotides are UV mimetics and protect
CC cells against subsequent exposure to UV-irradiation or chemicals. The
CC oligonucleotides are useful for increasing p53 activity in a cell,
CC reducing the susceptibility to UV-induced hyperproliferative diseases,
CC treating psoriasis, vitiligo, atopic dermatitis, allergic rhinitis,
CC conjunctivitis, and UV-induced dermatoses, reducing photoaging and
CC reducing susceptibility to skin cancer
XX
SQ Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 56.7%; Score 3.4; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. NO. 1.2e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGTG 5
Db 5 GRATG 1

Search completed: July 20, 2005, 22:58:57
Job time : 197.4 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:25:43 ; Search time 1348.8 Seconds
(without alignments)
169.325 Million cell updates/sec

Title: US-09-735-363A-10

Perfect score: 6

Sequence: 1 ggtgtg 6

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 1216

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gssi: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	6	100.0	6	6	CA851767 D17C12 E2
C 2	4.4	73.3	6	7	CF309881 ABF--04-E
C 3	4	66.7	6	7	CF302557 7LEAF--08
C 4	3.4	56.7	5	9	CL423849 01S0750-0
C 5	3.4	56.7	5	9	CL685110 PRI0140b
C 6	3.4	56.7	6	7	CF312755 ABF--08-K
C 7	3.4	56.7	6	7	CF332957 JMT--01-K
C 8	3.4	56.7	6	9	CL680271 PRI0128C
C 9	3	50.0	3	9	CL423861 01S0750-0
C 10	3	50.0	4	7	CF318871 HD--09-C1
C 11	3	50.0	4	7	CF324308 HDN--06-D
C 12	3	50.0	4	7	CO785960 B285A-B0
C 13	3	50.0	5	7	CF297897 7LEAF--01
C 14	3	50.0	5	7	CF300956 7LEAF--05
C 15	3	50.0	5	7	CF302927 7LEAF--08
C 16	3	50.0	5	7	CF307842 ABF--01-G
C 17	3	50.0	5	7	CF318944 HD--09-E0
C 18	3	50.0	5	7	CF323326 HDN--03-I
C 19	3	50.0	5	7	CF333993 JMT--03-B
C 20	3	50.0	5	7	CF930992 CF--05-R
C 21	3	50.0	6	6	CA850905 D07H12 O2
C 22	3	50.0	6	6	CA851633 D15H03 O1
C 23	3	50.0	6	7	CF323984 HDN--05-E
C 24	3	50.0	6	7	CF339252 RCL1--04-

25	3	50.0	6	9	CL687157	CL687157 PRI0146a
26	2.4	40.0	4	7	CF318085	CF318085 HD--07-P2
27	2.4	40.0	4	8	BZ382195	BZ382195 SALK 1179
28	2.4	40.0	5	6	CA850981	CA850981 D08H03 P1
29	2.4	40.0	5	7	CF314074	CF314074 HD--02-H0
C 30	2.4	40.0	5	7	CF327578	CF327578 NACL--02-
C 31	2.4	40.0	5	7	CL667999	CL667999 PRI0156C
32	2.4	40.0	5	9	CL680087	CL680087 PRI0127d
C 33	2.4	40.0	6	6	CA851592	CA851592 D15D09 G2
C 34	2.4	40.0	6	6	CA853780	CA853780 B12B09 se
C 35	2.4	40.0	6	7	CF310635	CF310635 ABF--05-G
C 36	2.4	40.0	6	7	CF338772	CF338772 RCL1--02-
C 37	2.4	40.0	6	9	CL679615	CL679615 PRI0126C
C 38	2.4	40.0	6	9	CL682618	CL682618 PRI0134C
C 39	2.4	40.0	6	9	CL694328	CL694328 PRI0163d
C 40	2	33.3	2	7	CF301411	CF301411 7LEAF--06
C 41	2	33.3	2	7	CF306288	CF306288 HDAL--03-
C 42	2	33.3	2	7	CF331310	CF331310 NACL--07-
C 43	2	33.3	2	7	CF333014	CF333014 JMT--01-L
C 44	2	33.3	2	7	CO792627	CO792627 NT015C D1
C 45	2	33.3	2	9	CL661289	CL661289 PRI0135b
C 46	2	33.3	2	9	CL670560	CL670560 PRI0162b
C 47	2	33.3	2	9	CL682684	CL682684 PRI0134C
C 48	2	33.3	2	9	CL688205	CL688205 PRI0148d
C 49	2	33.3	2	9	CL872635	CL872635 abe83c10
C 50	2	33.3	2	9	CL874640	CL874640 abe83c10
C 51	2	33.3	2	9	CL876415	CL876415 abf13c11
C 52	2	33.3	2	9	CL883717	CL883717 abf63c08
C 53	2	33.3	3	1	AL043149	AL043149 DKFP2434E
C 54	2	33.3	3	6	CA850938	CA850938 D08D06 H1
C 55	2	33.3	3	6	CA851961	CA851961 D19E05 I1
C 56	2	33.3	3	7	CF305942	CF305942 HDAL--02-
C 57	2	33.3	3	7	CF308858	CF308858 ABF--02-N
C 58	2	33.3	3	7	CF310006	CF310006 ABF--04-H
C 59	2	33.3	3	7	CF311628	CF311628 ABF--06-O
C 60	2	33.3	3	7	CF313258	CF313258 HD--01-F0
C 61	2	33.3	3	7	CF315632	CF315632 HD--04-K0
C 62	2	33.3	3	7	CF317717	CF317717 HD--07-I0
C 63	2	33.3	3	7	CF338538	CF338538 RCL1--01-
C 64	2	33.3	3	7	CF339357	CF339357 RCL1--04-
C 65	2	33.3	3	7	CF339421	CF339421 RCL1--04-
C 66	2	33.3	3	7	CF339646	CF339646 RCL1--05-
C 67	2	33.3	3	7	CF340077	CF340077 RCL1--06-
C 68	2	33.3	3	7	CF372478	CF372478 CSECS052H
C 69	2	33.3	3	7	CK575874	CK575874 IST WIS 9
C 70	2	33.3	3	7	CK632435	CK632435 AM1-AP000
C 71	2	33.3	3	7	CO793948	CO793948 NT019B A0
C 72	2	33.3	3	7	CO819398	CO819398 CSECS153H
C 73	2	33.3	3	7	CV179297	CV179297 CSECS016C
C 74	2	33.3	3	9	CL656746	CL656746 PRI0127b
C 75	2	33.3	3	9	CL664603	CL664603 PRI0147C
C 76	2	33.3	3	9	CL668376	CL668376 PRI0157C
C 77	2	33.3	3	9	CL669749	CL669749 PRI0160b
C 78	2	33.3	3	9	CL679295	CL679295 PRI0125C
C 79	2	33.3	3	9	CL884066	CL884066 abf65h10
C 80	2	33.3	4	1	AL039425	AL039425 DKFP2434L
C 81	2	33.3	4	1	AL045617	AL045617 DKEFP2434O
C 82	2	33.3	4	6	CA850965	CA850965 D08F10 L2
C 83	2	33.3	4	6	CA850974	CA850974 D08G08 N2
C 84	2	33.3	4	7	CF300707	CF300707 7LEAF--05
C 85	2	33.3	4	7	CF306914	CF306914 HD--07-L0
C 86	2	33.3	4	7	CF317847	CF317847 HDN--05-M
C 87	2	33.3	4	7	CF324158	CF324158 JMT--01-N
C 88	2	33.3	4	7	CF333086	CF333086 JMT--04-P
C 89	2	33.3	4	7	CF335346	CF335346 JMT--07-B
C 90	2	33.3	4	7	CF336880	CF336880 RCL1--01-
C 91	2	33.3	4	7	CF338536	CF338536 RCL1--07-
C 92	2	33.3	4	7	CF340391	CF340391 RCL1--08-
C 93	2	33.3	4	7	CF340642	CF340642 RCL1--08-
C 94	2	33.3	4	7	CF340653	CF340653 RCL1--08-
C 95	2	33.3	4	8	BZ424869	BZ424869 100020550
C 96	2	33.3	4	9	CL655267	CL655267 PRI0122d
C 97	2	33.3	4	9	CL655267	CL655267 PRI0122d

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98      2 33.3 4 9 CL670570 CL670570 PRI0162C
99      2 33.3 4 9 CL889653 CL889653 abf96d10-
c 100 2 33.3 5 1 AL042985 AL042985 DKFZp434N

ALIGNMENTS

RESULT 1
CA851767/c
LOCUS
DEFINITION
D17C12.E24.06.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
cDNA clone D17C12 5', mRNA sequence.
ACCESSION
CA851767
KEYWORDS
SOURCE
ORGANISM
Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 6)
REFERENCE
Alkharouf,N.W., Khan,R. and Matthews,B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
JOURNAL
COMMENT
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.

FEATURES
source
1. .6
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D17C12"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."

ORIGIN
Query Match 100.0%; Score 6; DB 6; Length 6;
Best Local Similarity 100.0%; Pred.No. 6.3e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGTGT 6
Db |||||
6 GTGTGT 1

RESULT 2
CF309881/c
LOCUS
DEFINITION
ABF--04-E05.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--04-E05, mRNA sequence.
ACCESSION
CF309881
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 6)
REFERENCE
CF309881
ABF--04-E05.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--04-E05, mRNA sequence.
ACCESSION
CF309881
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 6)
REFERENCE

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AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
of Bioscience and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .6
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--04-E05"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

ORIGIN
Query Match 73.3%; Score 4.4; DB 7; Length 6;
Best Local Similarity 83.3%; Pred.No. 6.3e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGTGT 6
Db |||||
6 GTTGT 1

RESULT 3
CF302557/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--08-D07, mRNA
sequence.
ACCESSION
CF302557
VERSION
CF302557.1 GI:33674318
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 6)
REFERENCE
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
of Bioscience and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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1. .6
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--08-D07"
/tissue_type="leaf"

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/dev stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN
Query Match      66.7%; Score 4; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGT 4
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Db 6 GTGT 3

RESULT 4
CL423849/c
LOCUS
DEFINITION
CL423849
VERSION
KEYWORDS
SOURCE
ORGANISM
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 5)
Latshaw,S., Tan,B.-C., Settles,A.M. and McCarty,D.R.
AUTHORS
TITLE
Sequence tagged transposon insertions from the UniformMu maize
JOURNAL
COMMENT
Contact: Donald R. McCarty
Plant Molecular and Cellular Biology Program
University of Florida
PO 110690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1928 x322
Email: drmc@ufl.edu
Sequence flanking probable Mu insertion site in UniformMu
line: 01S0750-04, Primer set: C
Class: transposon insertion site.
FEATURES
source
1..5
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="W22 (ACR, bz1-m9)"
/cultivar="UniformMu"
/db_xref="taxon:4577"
/clone="01S0750-04C1-A12"
/notes="Vector: TOPO-PCR4; DNA flanking Mu transposon
insertions in Mu inactive lines were extracted from the
UniformMu maize population by the thermo asymmetric
interlaced PCR (TAIL) protocol using primers specific for
the Mu terminal inverted repeat and a set of 16 arbitrary
primers. Amplicons were size enriched using Sepharose 400
spin columns and cloned into the TOPO PCR4 vector."

ORIGIN
Query Match      56.7%; Score 3.4; DB 9; Length 5;
Best Local Similarity 80.0%; Pred. No. 7.6e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGT 5
    ||||
Db 5 GAGTG 1

RESULT 5
CL685110
LOCUS
DEFINITION
PRI0140b.D09.2 - PRI0140b.BR (S) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 5)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AUTHORS
TITLE
AppaB: an AcedB database for the nematode satellite organism
JOURNAL
COMMENT
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
FEATURES
source
1..5
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/notes="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Query Match      56.7%; Score 3.4; DB 9; Length 5;
Best Local Similarity 80.0%; Pred. No. 7.6e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGT 5
    ||||
Db 1 GCGTG 5

RESULT 6
CF312755
LOCUS
DEFINITION
ABF--08-K07.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--08-K07, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoidae; Oryzaeae; Oryza.
1 (bases 1 to 6)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
COMMENT
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

```

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FEATURES
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      /organism="Oryza sativa (japonica cultivar-group)"
      /mol_type="mRNA"
      /cultivar="Nackdong"
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      /clone="ABF-08-K07"
      /tissue_type="leaf"
      /dev_stage="14 days after germination"
      /lab_host="E.coli DH10B"
      /clone_lib="ABF3-overexpressing transgenic rice plasmid
      cDNA library (ABF)"
      /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
      for 2hrs. Oligo-capped mRNA was reverse transcribed and
      then used for PCR. mRNA was prepared from ABA-responsive
      element binding transcription factor 3 overexpression
      line."

ORIGIN
  Query Match
  Best Local Similarity 56.7%; Score 3.4; DB 7; Length 6;
  Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGTG 5
   ||||
Db 2 GGTGT 6

RESULT 7
CF332957/c
LOCUS
DEFINITION
  CF332957
  6 bp mRNA linear EST 18-AUG-2003
  library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
  JMT--01-K14, mRNA sequence.
ACCESSION
  CF332957
VERSION
  CF332957.1 GI:33814152
KEYWORDS
  EST.
SOURCE
  Oryza sativa (japonica cultivar-group)
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzaceae; Oryza.
  REFERENCE
    1 (bases 1 to 6)
    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
    Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
    Large-scale Sequencing Analysis of Rice ESTs
    Unpublished (2003)
    Contact: Nahm B.H.
    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
    of Bioscience and Bioinformatics, Myongji University
    Yongin, Kyonggi, Korea
    Tel: 82 31 330 6193
    Fax: 82 31 321 6355
    Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
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    1..6
      /organism="Oryza sativa (japonica cultivar-group)"
      /mol_type="mRNA"
      /cultivar="Nackdong"
      /db_xref="taxon:39947"
      /clone="JMT-01-K14"
      /tissue_type="leaf"
      /dev_stage="14 days after germination"
      /lab_host="E.coli DH10B"
      /clone_lib="AtJMT-overexpressing transgenic rice plasmid
      cDNA library (JMT)"
      /note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
      was reverse transcribed and then used for PCR. mRNA was
      prepared from Arabidopsis Jasmonate Carboxyl
      methyltransferase overexpression line."

ORIGIN
  Query Match
  Best Local Similarity 56.7%; Score 3.4; DB 7; Length 6;
  Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGTG 5
   ||||
Db 2 GGTGT 6

RESULT 8
CL680271
LOCUS
DEFINITION
  CL680271
  6 bp DNA linear GSS 09-JUL-2004
  PRI0128c.E04.2 - PRI0128c.BR (6) Mixed stage fosmid library of P.
  pacificus var. California Pristionchus pacificus genomic, genomic
  survey sequence.
ACCESSION
  CL680271
VERSION
  CL680271.1 GI:50187114
KEYWORDS
  GSS.
SOURCE
  Pristionchus pacificus
  ORGANISM
    Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
    Neodiplogasteridae; Pristionchus.
  REFERENCE
    1 (bases 1 to 6)
    Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
    AppaDB: an AcedB database for the nematode satellite organism
    Pristionchus pacificus
    Nucleic Acids Res. 32 (1), D421-D422 (2004)
    Contact: Sommer RJ
    Evolutionary Biology
    Max-Planck-Institute for Developmental Biology
    Spemannstr. 37-39, Tuebingen D-72076, Germany
    Tel: 00497071601371
    Fax: 00497071601498
    Email: raif.sommer@tuebingen.mpg.de
    This library was generated at Caltech, Pasadena, USA and end
    sequenced at Vancouver, Canada.
    Seq primer: T7
    Class: fosmid ends.
  FEATURES
    source
      Location/Qualifiers
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          /mol_type="genomic DNA"
          /strains="California"
          /db_xref="taxon:54126"
          /clone_lib="Mixed stage fosmid library of P. pacificus
          var. California"
          /note="Vector: pEpifos-5 Fosmid vector"
  ORIGIN
    Query Match
    Best Local Similarity 80.0%; Score 3.4; DB 9; Length 6;
    Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGTGT 6
   ||||
Db 2 TCGGT 6

RESULT 9
CL423861/c
LOCUS
DEFINITION
  CL423861
  3 bp DNA linear GSS 16-MAR-2004
  01S0750-04C1-C02 UniformMu MutAIL Library Zea mays genomic clone
  01S0750-04C1-C02, genomic survey sequence.
ACCESSION
  CL423861
VERSION
  CL423861.1 GI:45501905
KEYWORDS
  GSS.
SOURCE
  Zea mays
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
    clade; Panicoidae; Andropogoneae; Zea.
  REFERENCE
    1 (bases 1 to 3)
    Latehaw,S., Tan,B.-C., Settles,A.M. and McCarty,D.R.
    Sequence tagged transposon insertions from the UniformMu maize

```



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ORIGIN
Query Match          50.0%; Score 3; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.6e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 TGT 4
      |||
Db      3 TGT 1

RESULT 15
LOCUS CF302927
DEFINITION 7LEAF--08-N23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
          sativa (japonica cultivar-group) cDNA clone 7LEAF--08-N23, mRNA
          sequence.
ACCESSION CF302927
VERSION CF302927.1 GI:33674688
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzeae; Oryza.
          1 (bases 1 to 5)
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
          Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
          source
          1..5
          /organism="Oryza sativa (japonica cultivar-group)"
          /mol_type="mRNA"
          /cultivar="Nackdong"
          /db_xref="taxon:39947"
          /clone="ABF--01-G18"
          /tissue_type="leaf"
          /dev_stage="14 days after germination"
          /lab_host="E.coli DH10B"
          /clone_lib="ABF3-overexpressing transgenic rice plasmid
          cDNA library (ABF)"
          /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
          for 2hrs. Oligo-capped mRNA was reverse transcribed and
          then used for PCR. mRNA was prepared from ABA-responsive
          element binding transcription factor 3 overexpression
          line."

ORIGIN
Query Match          50.0%; Score 3; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.6e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 TGT 4
      |||
Db      3 TGT 1

RESULT 17
LOCUS CF318944
DEFINITION HD--09-E08.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
          library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
          HD--09-E08, mRNA sequence.
ACCESSION CF318944
VERSION CF318944.1 GI:33690705
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzeae; Oryza.
          1 (bases 1 to 5)
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
          Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
          source
          1..5
          /organism="Oryza sativa (japonica cultivar-group)"
          /mol_type="mRNA"
          /cultivar="Nackdong"
          /db_xref="taxon:39947"
          /clone="7LEAF--08-N23"
          /tissue_type="leaf"
          /dev_stage="7 days after germination"
          /lab_host="E.coli DH10B"
          /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
          /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
          with oligoribonucleotides and then used as templates for
          RT-PCR."

ORIGIN
Query Match          50.0%; Score 3; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.6e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 TGT 4
      |||
Db      3 TGT 5

RESULT 16
LOCUS CF307842/c
DEFINITION ABF--01-G18.g1 ABF3-overexpressing transgenic rice plasmid cDNA
          library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
          ABF--01-G18, mRNA sequence.
ACCESSION CF307842
VERSION CF307842.1 GI:33679603
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzeae; Oryza.
          1 (bases 1 to 5)
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
          Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
          source
          1..5
          /organism="Oryza sativa (japonica cultivar-group)"
          /mol_type="mRNA"

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 5)
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
          Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
          source
          1..5
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          /cultivar="Nackdong"
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          /clone="ABF--01-G18"
          /tissue_type="leaf"
          /dev_stage="14 days after germination"
          /lab_host="E.coli DH10B"
          /clone_lib="ABF3-overexpressing transgenic rice plasmid
          cDNA library (ABF)"
          /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
          for 2hrs. Oligo-capped mRNA was reverse transcribed and
          then used for PCR. mRNA was prepared from ABA-responsive
          element binding transcription factor 3 overexpression
          line."

ORIGIN
Query Match          50.0%; Score 3; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.6e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 TGT 4
      |||
Db      3 TGT 1

RESULT 17
LOCUS CF318944
DEFINITION HD--09-E08.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
          library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
          HD--09-E08, mRNA sequence.
ACCESSION CF318944
VERSION CF318944.1 GI:33690705
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzeae; Oryza.
          1 (bases 1 to 5)
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
          Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
          source
          1..5
          /organism="Oryza sativa (japonica cultivar-group)"
          /mol_type="mRNA"

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/cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="HD--09-E08"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

ORIGIN

Query Match 50.0%; Score 3; DB 7; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.6e+09;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGT 4
 |||
 Db 3 TGT 5

RESULT 18

CF323326/c

LOCUS

DEFINITION HDN--03-120.g1 OshDAC1-overexpressing transgenic rice lambda phage
 cDNA library II (HDN) Oryza sativa (japonica cultivar-group) cDNA

ACCESSION CF323326

VERSION CF323326.1

KEYWORDS GI:33794892

SOURCE EST

ORIGIN Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 5)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 321 6355

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..5

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="HDN--03-120"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli SOLR"

/clone_lib="OshDAC1-overexpressing transgenic rice lambda

phage cDNA library II (HDN)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:

XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at

5' end with EcoRI and 3' end with XhoI site. mRNA was

derived from rice Histone Deacetylase overexpression

line."

ORIGIN

Query Match 50.0%; Score 3; DB 7; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.6e+09;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTG 3
 |||
 Db 5 GTG 3

RESULT 19

CF333993

LOCUS

DEFINITION JMT--03-B22.g1 AtJMT-overexpressing transgenic rice plasmid
 library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone

JMT--03-B22, mRNA sequence.

ACCESSION CF333993

VERSION CF333993.1

KEYWORDS GI:33816290

SOURCE EST

ORIGIN Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 5)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 321 6355

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..5

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="JMT--03-B22"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="AtJMT-overexpressing transgenic rice plasmid

cDNA library (JMT)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA

was reverse transcribed and then used for PCR. mRNA was

prepared from Arabidopsis Jasmonate Carboxyl

methyltransferase overexpression line."

ORIGIN

Query Match 50.0%; Score 3; DB 7; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.6e+09;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGT 4
 |||
 Db 2 TGT 4

RESULT 20

CF930992/c

LOCUS

DEFINITION CF--05-R-N09 Bos taurus CF-24-HW cDNA library Bos taurus cDNA clone
 CF--05-R-N09(5'), mRNA sequence.

ACCESSION CF930992

VERSION CF930992.1

KEYWORDS GI:38280813

SOURCE EST

ORIGIN Bos taurus (cow)

Bos taurus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovinae; Bos.

1 (bases 1 to 5)

AUTHORS Yoon,D.H., Lee,S.H., Lee,J.H., Sang,B.C. and Oh,S.J.

TITLE Gene Expression Profiling of the Bovine adipose tissues
JOURNAL Unpublished (2003)
COMMENT Contact: Dr. Du-Hak Yoon
National Livestock Research Institute, RDA
564 Omoekchun-dong, Suwon, 441-350, Korea
Tel: 82 31 290 1593
Fax: 82 31 290 1792
Email: dhyoon@rda.go.kr
Insert Length: 5 Std Error: 0.00
Seq primer: ATTAACCTCACTAAG
POLYA=No.

FEATURES

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Location/Qualifiers
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="CF-05-R-N09(5')"
/sex="four males mixed"
/tissue_type="adipose tissue"
/cell_type="adipocyte"
/dev_stage="24 months old"
/lab_host="X11-BlueWRF strain"
/clone_lib="Bos taurus CF-24-HW cDNA library"
/note="Vector: Uni-ZAPXR; Site_1: EcoRI; Site_2: Xho I"

ORIGIN

Query Match 50.0%; Score 3; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.6e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTG 3
|||
DB 4 GTG 2

RESULT 21

CA850905
LOCUS D07H12.024.16.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
DEFINITION cDNA clone D07H12 5', mRNA sequence.

ACCESSION CA850905
VERSION CA850905.1 GI:33387698
KEYWORDS Glycine max (soybean)
SOURCE Glycine max (soybean)

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 6)
Alkharouf, N.W., Khan, R. and Matthews, B.F.
Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode

JOURNAL Unpublished (2002)
COMMENT Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350, USA

Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.

FEATURES

source
1. .6
Location/Qualifiers
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D07H12"
/tissue_type="Roots"
/dev_stage="Seedlings"

/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA

ORIGIN

Query Match 50.0%; Score 3; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.3e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTG 3
|||
DB 1 GTG 3

RESULT 22

CA851633/c
LOCUS D15H03.015.16.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
DEFINITION cDNA clone D15H03 5', mRNA sequence.

ACCESSION CA851633
VERSION CA851633.1 GI:33388426
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 6)
Alkharouf, N.W., Khan, R. and Matthews, B.F.

AUTHORS Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode

JOURNAL Unpublished (2002)

COMMENT Contact: Alkharouf, N.W.

Soybean Genomics and Improvement Laboratory (SGIL)

US Department of Agriculture (USDA), ARS, PSI

Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350, USA

Tel: 301 504 5750

Fax: 301 504 5728

Email: alkharon@ba.ars.usda.gov.

FEATURES

source
1. .6
Location/Qualifiers
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D15H03"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."

ORIGIN

Query Match 50.0%; Score 3; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.3e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGT 4
|||
DB 6 TGT 4

RESULT 23

CF323984/c
LOCUS HDN--05-E22.g1 OSHDAC1-overexpressing transgenic rice lambda phage
DEFINITION cDNA library II (HDN) Oryza sativa (japonica cultivar-group) cDNA clone HDN--05-E22, mRNA sequence.

ACCESSION CF323984
VERSION CF323984.1 GI:33796236
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1. (bases 1 to 6)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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1. .6
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"

/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HDN--05-E22"
/issue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OshDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

ORIGIN

Query Match 50.0%; Score 3; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.3e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTG 3
|||
Db 4 GTG 2

RESULT 24

CF339252
LOCUS
DEFINITION
RCL1--04-E20.g1 Regenerated callus lambda phage cDNA library (RCL1)
Oryza sativa (japonica cultivar-group) cDNA clone RCL1--04-E20,
mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1. (bases 1 to 6)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

1. .6
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"

/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="RCL1--04-E20"
/issue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
/note="Vector: pBluescript SK(+); Site_1: SstI; Site_2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

ORIGIN

Query Match 50.0%; Score 3; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.3e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGT 4
|||
Db 4 TGT 6

RESULT 25

CL687157
LOCUS
DEFINITION
PR10146a_E04.2 - PR10146a.BR (6) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM

Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.

REFERENCE 1 (bases 1 to 6)

Authors Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AppADB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: raif.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.

Seq primer: T7

Class: fosmid ends.
Location/Qualifiers

1. .6
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"

ORIGIN

Query Match 50.0%; Score 3; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.3e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGT 4
|||
Db 2 TGT 4

```

RESULT 26
CF318065
LOCUS
DEFINITION
HD--07-P21-g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD-07-P21, mRNA sequence.
CF318065
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erihartoideae; Oryzeae; Oryza.
1 (bases 1 to 4)
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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1..4
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--07-P21"
/tissue_type="callus"
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/lab_host="E.coli DH10B"
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cDNA library (HD)"
/notes="Vector: pCRA-TOPO; Site:1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
ORIGIN
Query Match 40.0%; Score 2.4; DB 7; Length 4;
Best Local Similarity 75.0%; Pred. No. 9.5e+09;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTCT 4
Db 1 GTTT 4
RESULT 27
CF3182195
LOCUS
DEFINITION
SALK_117983.27.80.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_117983.27.80.x, genomic
survey sequence.
CF3182195
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 4)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
FEATURES
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/notes="Arabidopsis thaliana TDNA insertion lines"
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna\_protocols.html
ORIGIN
Query Match 40.0%; Score 2.4; DB 8; Length 4;
Best Local Similarity 75.0%; Pred. No. 9.5e+09;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTCT 4
Db 1 GTAT 4
RESULT 28
CA850981
LOCUS
DEFINITION
D08H03_P15_16.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
cDNA clone D08H03 5', mRNA sequence.
CA850981
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 5)
Alkharouf, N.W., Khan, R. and Matthews, B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.
FEATURES
source
1..5
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/organism="Glycine max"
/mol_type="mRNA"
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/db_xref="taxon:3847"
/clone="D08H03"
/tissue_type="Roots"
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/clone lib="cdna Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."

ORIGIN

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Best Local Similarity 75.0%; Pred. No. 7.6e+09;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGT 4
|||
Db 1 GTAT 4

RESULT 29

CF314074

LOCUS

DEFINITION HD--02-H09.g1 OshDACL1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone

CF314074

CF314074.1

GI:33685835

EST.

SOURCE

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 5)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..5

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

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/lab_host="E.coli DH10B"

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/note="Vector: pCR4-TOPO; Site:1: EcoRI; Callus was

treated with ABA(20um) for 1hr. Oligo-capped mRNA was

reverse transcribed and then used for PCR. mRNA was

derived from rice Histone Deacetylase overexpression

line."

ORIGIN

Query Match 40.0%; Score 2.4; DB 7; Length 5;
Best Local Similarity 75.0%; Pred. No. 7.6e+09;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGTG 5
|||
Db 1 TCTG 4

RESULT 30

CF327578/c

LOCUS

DEFINITION NACL--02-B23.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--02-B23, mRNA

CF327578

5 bp mRNA linear EST 18-AUG-2003

NACL--02-B23.b1 Rice callus plasmid cDNA library (NACL) Oryza

sativa (japonica cultivar-group) cDNA clone NACL--02-B23, mRNA

sequence.
CF327578
CF327578.1 GI:33803408
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 5)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

1..5
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/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="NACL--02-B23"
/tissue_type="callus"
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/note="Vector: pCR4-TOPO; Site:1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN

Query Match 40.0%; Score 2.4; DB 7; Length 5;
Best Local Similarity 75.0%; Pred. No. 7.6e+09;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGT 4
|||
Db 4 GAGT 1

Search completed: July 21, 2005, 01:54:29
Job time : 1361.8 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:43:13 ; Search time 57 Seconds
(without alignments)
172.240 Million cell updates/sec

Title: US-09-735-363A-10

Perfect score: 6

Sequence: 1 g9tgt 6

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2678

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	5	83.3	5	3	US-09-180-903-4
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4	5	83.3	6	1	US-08-367-175A-24
5	5	83.3	6	2	US-08-471-994-8
6	5	83.3	6	3	US-08-154-364-8
7	5	83.3	6	3	US-08-154-364-14
8	5	83.3	6	3	US-09-180-903-9
9	5	83.3	6	3	US-09-281-481A-22
10	5	83.3	6	4	US-09-958-221A-2
11	5	83.3	6	5	PCT-US94-06456-7
12	5	83.3	6	5	PCT-US94-06456-36
13	4.4	73.3	6	2	US-08-485-158A-2
14	4.2	70.0	6	2	US-08-420-629-3
15	4	66.7	4	3	US-09-180-903-3
16	4	66.7	6	1	US-08-381-097A-12
17	4	66.7	6	1	US-08-459-064B-22
18	4	66.7	6	2	US-08-460-421A-22
19	4	66.7	6	2	US-08-372-652-10
20	4	66.7	6	4	US-09-086-663A-77
21	4	66.7	6	4	US-09-830-401-2
22	4	66.7	6	5	PCT-US95-16311-10
23	3.4	56.7	5	3	US-08-855-372B-20
24	3.4	56.7	5	3	US-08-855-372B-21
25	3.4	56.7	5	3	US-08-855-372B-23
26	3.4	56.7	5	3	US-09-048-927-4
27	3.4	56.7	5	3	US-09-498-851-20
C 1	5	83.3	5	1	US-08-717-526-56
2	5	83.3	5	3	US-09-180-903-4
3	5	83.3	5	3	US-09-180-903-5
4	5	83.3	6	1	US-08-367-175A-24
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7	5	83.3	6	3	US-08-154-364-14
8	5	83.3	6	3	US-09-180-903-9
9	5	83.3	6	3	US-09-281-481A-22
10	5	83.3	6	4	US-09-958-221A-2
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21	4	66.7	6	4	US-09-830-401-2
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27	3.4	56.7	5	3	US-09-498-851-20

Sequence 21, Appl	5	3	US-09-498-851-21	56.7	3.4	28
Sequence 23, Appl	5	3	US-09-498-851-23	56.7	3.4	29
Sequence 46, Appl	5	4	US-09-305-839-46	56.7	3.4	C 30
Sequence 35, Appl	5	5	PCT-US91-03680-35	56.7	3.4	C 31
Sequence 35, Appl	6	1	US-07-630-288A-35	56.7	3.4	32
Sequence 53, Appl	6	1	US-08-153-051B-53	56.7	3.4	33
Sequence 52, Appl	6	1	US-08-060-952C-52	56.7	3.4	34
Sequence 35, Appl	6	1	US-08-468-049-35	56.7	3.4	35
Sequence 70, Appl	6	2	US-08-151-477A-53	56.7	3.4	36
Sequence 34, Appl	6	3	US-09-107-708-4	56.7	3.4	C 38
Sequence 34, Appl	6	3	US-08-793-634B-34	56.7	3.4	39
Sequence 4, Appl	6	3	US-09-449-581-4	56.7	3.4	C 40
Sequence 52, Appl	6	3	US-08-464-011B-52	56.7	3.4	41
Sequence 43, Appl	6	3	US-09-268-544B-43	56.7	3.4	C 42
Sequence 70, Appl	6	4	US-09-378-535-70	56.7	3.4	43
Sequence 3, Appl	6	4	US-09-830-401-3	56.7	3.4	44
Sequence 12, Appl	6	4	US-09-244-438-12	56.7	3.4	C 45
Sequence 14, Appl	6	5	PCT-US95-04092-14	56.7	3.4	46
Sequence 4, Appl	6	4	US-09-336-552A-4	53.3	3.2	C 47
Sequence 44, Appl	4	3	US-08-630-019A-44	50.0	3	C 48
Sequence 3, Appl	4	3	US-09-248-093-3	50.0	3	C 49
Sequence 2, Appl	5	1	US-08-242-402-2	50.0	3	C 50
Sequence 3, Appl	5	1	US-08-270-180-3	50.0	3	C 51
Sequence 47, Appl	5	1	US-08-068-945A-47	50.0	3	C 52
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Sequence 47, Appl	5	1	US-08-153-051B-47	50.0	3	54
Sequence 20, Appl	5	1	US-08-060-952C-20	50.0	3	55
Sequence 47, Appl	5	1	US-08-442-806-47	50.0	3	C 56
Sequence 47, Appl	5	2	US-08-151-477A-47	50.0	3	57
Sequence 10, Appl	5	2	US-08-319-052-10	50.0	3	C 58
Sequence 12, Appl	5	2	US-08-319-052-12	50.0	3	59
Sequence 44, Appl	5	3	US-08-819-867-44	50.0	3	60
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Sequence 22, Appl	5	3	US-08-855-372B-22	50.0	3	62
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Sequence 21, Appl	5	3	US-08-846-301A-21	50.0	3	C 65
Sequence 32, Appl	5	3	US-08-793-634B-32	50.0	3	66
Sequence 10, Appl	5	3	US-08-442-108B-10	50.0	3	C 67
Sequence 12, Appl	5	3	US-08-442-108B-12	50.0	3	68
Sequence 20, Appl	5	3	US-08-464-011B-20	50.0	3	69
Sequence 20, Appl	5	3	US-09-638-509C-20	50.0	3	C 70
Sequence 22, Appl	5	3	US-09-638-509C-22	50.0	3	C 71
Sequence 22, Appl	5	3	US-09-498-851-22	50.0	3	72
Sequence 3, Appl	5	4	US-09-723-685-3	50.0	3	73
Sequence 4, Appl	5	4	US-09-723-685-4	50.0	3	C 74
Sequence 7, Appl	5	4	US-09-763-565-7	50.0	3	75
Sequence 44, Appl	5	4	US-09-378-535-44	50.0	3	76
Sequence 3, Appl	5	5	PCT-US95-05141-3	50.0	3	C 77
Sequence 1, Appl	6	1	US-07-847-743B-1	50.0	3	C 78
Sequence 10, Appl	6	1	US-08-011-398B-10	50.0	3	79
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Sequence 13, Appl	6	1	US-08-365-189-13	50.0	3	C 81
Sequence 625, App	6	1	US-08-171-389-625	50.0	3	C 82
Sequence 1, Appl	6	1	US-08-456-201-1	50.0	3	C 83
Sequence 1, Appl	6	1	US-08-211-682-1	50.0	3	C 84
Sequence 6, Appl	6	1	US-08-211-682-6	50.0	3	85
Sequence 13, Appl	6	1	US-08-211-682-9	50.0	3	86
Sequence 25, Appl	6	1	US-07-596-783-25	50.0	3	C 87
Sequence 25, Appl	6	1	US-08-484-499-25	50.0	3	C 88
Sequence 25, Appl	6	1	US-08-123-936-625	50.0	3	C 89
Sequence 25, Appl	6	1	US-08-475-221B-25	50.0	3	C 90
Sequence 25, Appl	6	1	US-08-476-876-25	50.0	3	C 91
Sequence 1, Appl	6	1	US-08-309-644A-1	50.0	3	92
Sequence 2, Appl	6	1	US-08-445-909A-2	50.0	3	C 93
Sequence 5, Appl	6	1	US-08-445-909A-5	50.0	3	C 94
Sequence 10, Appl	6	1	US-08-464-051-10	50.0	3	C 95
Sequence 10, Appl	6	1	US-08-464-051-10	50.0	3	96
Sequence 1, Appl	6	2	US-08-330-161-1	50.0	3	C 97
Sequence 1, Appl	6	2	US-08-456-241-1	50.0	3	C 98
Sequence 10, Appl	6	2	US-08-462-498-10	50.0	3	C 99
Sequence 10, Appl	6	2	US-08-462-498-10	50.0	3	100

ALIGNMENTS

RESULT 1
US-08-717-526-56/c
; Sequence 56, Application US/08717526
; Patent No. 5786147
; GENERAL INFORMATION:
; APPLICANT: MABILAT, CLAUDE
; APPLICANT: RAOULT, DIDIER
; TITLE OF INVENTION: DETECTION OF ENTEROBACTERIA
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE
; STREET: 700 SOUTH WASHINGTON STREET
; CITY: ALEXANDRIA
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/717,526
; FILING DATE: 17-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BERRIDGE, WILLIAM P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 38732
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6400
; TELEFAX: 703-836-2787
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-717-526-56

Query Match 83.3%; Score 5; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTGT 6
Db 5 TGTGT 1

RESULT 2
US-09-180-903-4
; Sequence 4, Application US/09180903
; Patent No. 6316190
; GENERAL INFORMATION:
; APPLICANT: Rein, Alan
; Casas-Finet, Jose
; Fisher, Robert
; Fivash, Matthew
; Henderson, Louis E.
; TITLE OF INVENTION: Oligonucleotides Which Specifically Bind
; Retroviral Nucleocapsid Proteins
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California

; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/180,903
; FILING DATE: 12-Jul-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,128
; FILING DATE: 20-MAY-1996
; APPLICATION NUMBER: WO PCT/US97/08936
; FILING DATE: 13-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Choi, Kathleen L.
; REGISTRATION NUMBER: 43,433
; REFERENCE/DOCKET NUMBER: 015280-279100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-180-903-4

Query Match 83.3%; Score 5; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTGT 6
Db 1 TGTGT 5

RESULT 3
US-09-180-903-5
; Sequence 5, Application US/09180903
; Patent No. 6316190
; GENERAL INFORMATION:
; APPLICANT: Rein, Alan
; Casas-Finet, Jose
; Fisher, Robert
; Fivash, Matthew
; Henderson, Louis E.
; TITLE OF INVENTION: Oligonucleotides Which Specifically Bind
; Retroviral Nucleocapsid Proteins
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/180,903
; FILING DATE: 12-Jul-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,128

;/ FILING DATE: 20-MAY-1996
;/ APPLICATION NUMBER: WO PCT/US97/08936
;/ FILING DATE: 19-MAY-1997
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Choi, Kathleen L.
;/ REGISTRATION NUMBER: 43,433
;/ REFERENCE/DOCKET NUMBER: 015280-279100US
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (415) 576-0200
;/ TELEFAX: (415) 576-0300
;/ INFORMATION FOR SEQ ID NO: 5:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 5 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: DNA
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-180-903-5

Query Match 83.3%; Score 5; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTG 5
DB 1 GTGTG 5

RESULT 4
US-08-367-175A-24
;/ Sequence 24, Application US/08367175A
;/ Patent No. 5631115
;/ GENERAL INFORMATION:
;/ APPLICANT: OHTSUKA, Eiko
;/ APPLICANT: KOIZUMI, Makoto
;/ TITLE OF INVENTION: Looped, hairpin ribozyme
;/ NUMBER OF SEQUENCES: 27
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: FRISHAUF, HOLTZ, GOODMAN,
;/ ADDRESSEE: LANGER & CHICK, P.C.
;/ STREET: 767 Third Avenue
;/ CITY: New York
;/ STATE: New York
;/ COUNTRY: U.S.A.
;/ ZIP: 10017-2023
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.24
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/367,175A
;/ FILING DATE: 29 Dec. 1994
;/ CLASSIFICATION: 435
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: GOODMAN, Herbert
;/ REGISTRATION NUMBER: 17081
;/ REFERENCE/DOCKET NUMBER: 920081
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (212)319-4900
;/ TELEFAX: (212)319-5101
;/ TELEX: 236268
;/ INFORMATION FOR SEQ ID NO: 24:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 6 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: mRNA
;/ HYPOTHETICAL: N
;/ ANTI-SENSE: N
US-08-367-175A-24

Query Match 83.3%; Score 5; DB 1; Length 6;
Best Local Similarity 60.0%; Pred. No. 2.5e+08;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTG 5
DB 1 GUGUG 5

RESULT 5
US-08-471-994-8
;/ Sequence 8, Application US/08471994
;/ Patent No. 5861245
;/ GENERAL INFORMATION:
;/ APPLICANT: McClelland, Michael
;/ APPLICANT: Welsh, John T.
;/ APPLICANT: Sorge, Joseph A.
;/ TITLE OF INVENTION: ARBITRARILY PRIMED POLYMERASE CHAIN
;/ REACTION METHOD FOR FINGERPRINTING GENOMES
;/ NUMBER OF SEQUENCES: 13
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Pennie & Edmonds
;/ STREET: 1155 Avenue of the Americas
;/ CITY: New York
;/ STATE: New York
;/ COUNTRY: United States of America
;/ ZIP: 10036
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/471,994
;/ FILING DATE: 06-JUN-1995
;/ CLASSIFICATION: 435
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Halluin, Albert P.
;/ REGISTRATION NUMBER: 25,227
;/ REFERENCE/DOCKET NUMBER: 8142-103
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 415-854-3660
;/ TELEFAX: 415-854-3694
;/ TELEX: 66141 PENNIE
;/ INFORMATION FOR SEQ ID NO: 8:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 6 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: unknown
;/ TOPOLOGY: unknown
;/ MOLECULE TYPE: DNA (genomic)
US-08-471-994-8

Query Match 83.3%; Score 5; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTG 5
DB 2 GTGTG 6

RESULT 6
US-08-154-364-8
;/ Sequence 8, Application US/08154364
;/ Patent No. 6207810
;/ GENERAL INFORMATION:
;/ APPLICANT: McClelland, Michael
;/ APPLICANT: Welsh, John T.
;/ APPLICANT: Sorge, Joseph A.
;/ TITLE OF INVENTION: ARBITRARILY PRIMED
;/ POLYMERASE CHAIN

```

RESULT 7
US-08-1456-364-14
; Sequence 14, Application US/08154364
; Patent No. 6207810
; GENERAL INFORMATION:
; APPLICANT: McCelland, Michael
; APPLICANT: Welsh, John T.
; APPLICANT: Sorge, Joseph A.
; TITLE OF INVENTION: ARBITRARILY PRIMED
; TITLE OF INVENTION: POLYMERASE CHAIN
; TITLE OF INVENTION: REACTION METHOD FOR FINGER PRINTING
; TITLE OF INVENTION: GENOMES
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Limbach and Limbach
; STREET: 2001 Ferry Building
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release 1.0,
; SOFTWARE: Version 1.25

```

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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/154,364
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bortner, Scott R.
; REGISTRATION NUMBER: 34,298
; REFERENCE/DOCKET NUMBER: STRG-20142 USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-433-4150
; TELEFAX: 414-433-8716
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-154-364-14

Query Match      83.3%; Score 5; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY      1 GTGTG 5
        |||||
Db       2 GTGTG 6

RESULT 8
US-09-180-903-9
; Sequence 9, Application US/09180903
; Patent No. 6316190
; GENERAL INFORMATION:
; APPLICANT: Rein, Alan
; Casas-Finet, Jose
; Fisher, Robert
; Fivash, Matthew
; Henderson, Louis B.
; TITLE OF INVENTION: Oligonucleotides Which Specifically Bind
;                               Retroviral Nucleocapsid Proteins
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/180,903
; FILING DATE: 12-Jul-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,128
; FILING DATE: 20-MAY-1996
; APPLICATION NUMBER: WO PCT/US97/08936
; FILING DATE: 19-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Choi, Kathleen L.
; REGISTRATION NUMBER: 43,433
; REFERENCE/DOCKET NUMBER: 015280-279100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 9:

```

SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-180-903-9

Query Match 83.3%; Score 5; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTG 5
DB 2 GTGTG 6

RESULT 9
US-09-281-481A-22
; Sequence 22, Application US/09281481A
; Patent No. 6383747
; GENERAL INFORMATION:
; APPLICANT: DANKINS, Roger L. and ABRAHAM, Lawrence J.
; TITLE OF INVENTION: GENETIC ANALYSIS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY SCOTT MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/281,481A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/893,971
; FILING DATE: 16-JUL-1997
; APPLICATION NUMBER: US 232,229
; FILING DATE: 29-APR-1994
; APPLICATION NUMBER: PX9279 (AU)
; FILING DATE: 01-NOV-1991
; APPLICATION NUMBER: PCT/AU92/00583
; FILING DATE: 30-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DIGIGLIO, FRANK S
; REFERENCE/DOCKET NUMBER: 9279
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: +516 742 4343
; TELEFAX: +516 742 4366
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-281-481A-22

Query Match 83.3%; Score 5; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTG 5
DB 2 GTGTG 6

RESULT 10
US-09-958-221A-2/c
; Sequence 2, Application US/09958221A
; Patent No. 6886160
; GENERAL INFORMATION:
; APPLICANT: Haeringen van, Willem A.
; APPLICANT: Haeringen van, Hendrik
; TITLE OF INVENTION: UNIVERSAL VARIABLE FRAGMENTS
; FILE REFERENCE: 92750/64
; CURRENT APPLICATION NUMBER: US/09/958,221A
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: EP 00200757.3
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: PCT/NL01/00177
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-958-221A-2

Query Match 83.3%; Score 5; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTG 5
DB 5 GTGTG 1

RESULT 11
PCT-US94-06456-7
; Sequence 7, Application PC/TUS9406456
; GENERAL INFORMATION:
; APPLICANT: Beutel, Bruce A.
; APPLICANT: Coppola, George R.
; APPLICANT: Sherman, Michael I.
; TITLE OF INVENTION: Oligonucleotides Which Inhibit HIV Protease Function
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC - DOS
; SOFTWARE: DW4.V2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06456
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,873
; FILING DATE: 09-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliott M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 23550-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:

```
;
; LENGTH: 6 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
PCT-US94-06456-7

Query Match      83.3%; Score 5; DB 5; Length 6;
Best Local Similarity 60.0%; Pred. No. 2.5e+08;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTG 5
Db 2 GUGUG 6

RESULT 12
PCT-US94-06456-36
; Sequence 36, Application PC/TUS9406456
; GENERAL INFORMATION:
; APPLICANT: Beutel, Bruce A.
; APPLICANT: Coppola, George R.
; APPLICANT: Sherman, Michael I.
; TITLE OF INVENTION: Oligonucleotides Which Inhibit HIV Protease Function
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC - DOS
; SOFTWARE: DW4.V2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06456
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,873
; FILING DATE: 09-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliott M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 23550-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
; FEATURE:
PCT-US94-06456-36

Query Match      83.3%; Score 5; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTG 5
Db 2 GTGTG 6

RESULT 13
US-08-485-158A-2
; Sequence 2, Application US/08485158A
; Patent No. 5859328
; GENERAL INFORMATION:
; APPLICANT: Nasrallah, June B.
; APPLICANT: Nasrallah, Mikhail E.
; APPLICANT: Thoresness, Mary K.
; TITLE OF INVENTION: ISOLATED DNA ELEMENTS THAT DIRECT
; TITLE OF INVENTION: PISTIL-SPECIFIC AND ANTHER-SPECIFIC GENE EXPRESSION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak, & Seas
; STREET: 2100 Pennsylvania Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,158A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mack, Susan J.
; REGISTRATION NUMBER: 30,951
; REFERENCE/DOCKET NUMBER: A-6217-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-485-158A-2

Query Match      73.3%; Score 4.4; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGTGT 6
Db 1 GTTGT 6

RESULT 14
US-08-420-629-3
; Sequence 3, Application US/08420629
; Patent No. 5891627
; GENERAL INFORMATION:
; APPLICANT: EVANS, GLEN A.
; APPLICANT: SELLERI, LUCIA
; APPLICANT: EUBANKS, JAMES H.
; TITLE OF INVENTION: POLYMORPHIC LOCUS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/420,629
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/773,099
FILING DATE: 09-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR., PH.D., JOHN R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD1512
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..6
US-08-420-629-3

Query Match 70.0%; Score 4.2; DB 2; Length 6;
Best Local Similarity 60.0%; Pred. No. 2.5e+08;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTGT 6
|:|:|
DB 1 TRTGT 5

RESULT 15
US-09-180-903-3
Sequence 3, Application US/09180903
Patent No. 6316190
GENERAL INFORMATION:
APPLICANT: Rein, Alan
Casaas-Finet, Jose
Fisher, Robert
Fivash, Matthew
Henderson, Louis E.
TITLE OF INVENTION: Oligonucleotides Which Specifically Bind
Retroviral Nucleocapsid Proteins
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/180,903
FILING DATE: 12-Jul-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,128
FILING DATE: 20-MAY-1996
APPLICATION NUMBER: WO PCT/US97/08936
FILING DATE: 19-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Choi, Kathleen L.
REGISTRATION NUMBER: 43,433
REFERENCE/DOCKET NUMBER: 015280-27910005
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-180-903-3

Query Match 66.7%; Score 4; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 3.8e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTG 5
|:|:|
DB 1 TGTG 4

RESULT 16
US-08-381-097A-12
Sequence 12, Application US/08381097A
Patent No. 5643890
GENERAL INFORMATION:
APPLICANT: Iverson, Patrick L.
APPLICANT: Mata, John E.
TITLE OF INVENTION: Synthetic Oligodeoxyribonucleotides
Which Mimic Telomeric Sequences for Use in the Treatment
of Cancer and Other Diseases
TITLE OF INVENTION: of Cancer and Other Diseases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zarely, McKee, Thomte, Voorhees, & Sease
STREET: 801 Grand Suite 3200
CITY: Des Moines
STATE: Iowa
COUNTRY: United States
ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,097A
FILING DATE: 31-JAN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heidi S
REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: unmc 63092
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-288-3667
TELEFAX: 515-288-1338
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-381-097A-12

Query Match 66.7%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTG 5
|:|:|
DB 1 TGTG 4

RESULT 17
US-08-459-064B-22/c
; Sequence 22, Application US/08459064B
; Patent No. 5747452
; GENERAL INFORMATION:
; APPLICANT: RUOSLAHTI, ERKKI I.
; APPLICANT: MORLA, ALEX
; TITLE OF INVENTION: A METHOD OF MODULATING TUMOR CELL MIGRATION
; TITLE OF INVENTION: USING FIBRONECTIN TYPE III PEPTIDES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES LLP
; STREET: 4370 LA JOLLA VILLAGE DRIVE, STE 700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,064B
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/829,462
; FILING DATE: 31-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/021,626
; FILING DATE: 16-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/340,812
; FILING DATE: 17-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHRYN A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 1543
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..6
US-08-459-064B-22

Query Match 66.7%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGT 4
|||
Db 4 GTGT 1

RESULT 18
US-08-460-421A-22/c
; Sequence 22, Application US/08460421A
; Patent No. 5837813
; GENERAL INFORMATION:
; APPLICANT: RUOSLAHTI, ERKKI I.
; APPLICANT: MORLA, ALEX
; TITLE OF INVENTION: FIBRONECTIN BINDING SITES AND METHODS OF
; TITLE OF INVENTION: MODULATING FIBRONECTIN EXTRACELLULAR MATRIX ASSEMBLY

NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES LLP
STREET: 4370 LA JOLLA VILLAGE DRIVE, STE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,421A
FILING DATE: 01-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/829,462
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021,626
FILING DATE: 16-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/340,812
FILING DATE: 17-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHRYN A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 1542
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
FEATURE:
NAME/KEY: CDS
LOCATION: 1..6
US-08-460-421A-22

Query Match 66.7%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGT 4
|||
Db 4 GTGT 1

RESULT 19
US-08-372-652-10
; Sequence 10, Application US/08372652
; Patent No. 5932699
; GENERAL INFORMATION:
; APPLICANT: Moore, David
; APPLICANT: Seol, Wongi
; APPLICANT: Choi, Hueng-Sik
; TITLE OF INVENTION: RETINOID X RECEPTOR-INTERACTING
; TITLE OF INVENTION: POLYPEPTIDES AND RELATED MOLECULES AND METHODS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street, Suite 3100
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/372,652
; FILING DATE: 13-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/246001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
US-08-372-652-10

Query Match 66.7%; Score 4; DB 2; Length 6;
Best Local Similarity 33.3%; Pred. No. 2.5e+08;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGTGT 6
|::|
Db 1 GURAGU 6

RESULT 20

US-09-086-663A-77/c
; Sequence 77, Application US/09086663A
; Patent No. 6518063
; GENERAL INFORMATION:
; APPLICANT: DUCY, PATRICIA
; TITLE OF INVENTION: OSF2/CBFA1 COMPOSITIONS AND METHODS OF USE
; FILE REFERENCE: UTSC:525
; CURRENT APPLICATION NUMBER: US/09/086,663A
; CURRENT FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/080,189
; PRIOR FILING DATE: 1998-03-24
; PRIOR APPLICATION NUMBER: 60/048,430
; PRIOR FILING DATE: 1997-05-29
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-086-663A-77

Query Match 66.7%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTG 5
|::|
Db 6 TGTG 3

RESULT 21

US-09-830-401-2
; Sequence 2, Application US/09830401
; Patent No. 6593088
; GENERAL INFORMATION:
; APPLICANT: SAITO, Isao

; APPLICANT: FUJIMOTO, Kenzo
; APPLICANT: MATSUDA, Shigeo
; TITLE OF INVENTION: REVERSIBLE PHOTOLIGATING NUCLEIC ACID AND PHOSPHORAMIDITE
; FILE REFERENCE: 2001-0514A/LC/00653
; CURRENT APPLICATION NUMBER: US/09/830,401
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: PCT/JP00/05715
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 1999-240685
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHESIZED DNA OLIGOMER
US-09-830-401-2

Query Match 66.7%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTG 5
|::|
Db 1 TGTG 4

RESULT 22

PCT-US95-16311-10
; Sequence 10, Application PC/TUS9516311
; GENERAL INFORMATION:
; APPLICANT: Moore, David
; APPLICANT: Seol, Wongi
; APPLICANT: Choi, Hwang-Sik
; TITLE OF INVENTION: RETINOID X RECEPTOR-INTERACTING
; POLYPEPTIDES AND RELATED MOLECULES AND METHODS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street, Suite 3100
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16311
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/372,652
; FILING DATE: 13-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/246001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
PCT-US95-16311-10

Query Match 66.7%; Score 4; DB 5; Length 6;
Best Local Similarity 33.3%; Pred. No. 2.5e+08; Indels 0;
Matches 2; Conservative 3; Mismatches 1; Gaps 0;

QY 1 GTGTGT 6
|::|:
Db 1 GURAGU 6

RESULT 23

US-08-855-372B-20
; Sequence 20, Application US/08855372B
; Patent No. 6090549

GENERAL INFORMATION:

; APPLICANT: Mirzabekov, Andrei D
; APPLICANT: Parinov, Sergei V
; APPLICANT: Barsky, Victor E
; APPLICANT: Kirillov, Eugene V
; APPLICANT: Dubiley, Svetlana A
; TITLE OF INVENTION: Use of Continuous/Contiguous Stacking Hybridization as a Diagnostic
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHERSKOV & FLAYNIK
; STREET: 20 N. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.50 inch, 1.4 MB storage
; COMPUTER: PC
; OPERATING SYSTEM: Microsoft Windows 98

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/855,372B
; FILING DATE: 13-MAY-97
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/587,332
; FILING DATE: 16-JAN-96

ATTORNEY/AGENT INFORMATION:

; NAME: Cherskov, Michael J.
; REGISTRATION NUMBER: 33,664
; REFERENCE/DOCKET NUMBER: ANL-IN-95-027
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 621-1330
; TELEFAX: (312) 621-0088

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

; LENGTH: 5 bases
; TYPE: nucleic acid
; STRANDEDNESS: No. 6090549 Applicable
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: Yes
US-08-855-372B-20

Query Match 56.7%; Score 3.4; DB 3; Length 5;
Best Local Similarity 80.0%; Pred. No. 3e+08;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGTG 5
|||
Db 1 GATG 5

RESULT 24

US-08-855-372B-21

; Sequence 21, Application US/08855372B
; Patent No. 6090549

GENERAL INFORMATION:

; APPLICANT: Mirzabekov, Andrei D
; APPLICANT: Parinov, Sergei V

; APPLICANT: Barsky, Victor E
; APPLICANT: Kirillov, Eugene V
; APPLICANT: Dubiley, Svetlana A
; TITLE OF INVENTION: Use of Continuous/Contiguous Stacking Hybridization as a Diagnostic
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHERSKOV & FLAYNIK
; STREET: 20 N. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.50 inch, 1.4 MB storage
; COMPUTER: PC
; OPERATING SYSTEM: Microsoft Windows 98

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/855,372B
; FILING DATE: 13-MAY-97
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/587,332
; FILING DATE: 16-JAN-96

ATTORNEY/AGENT INFORMATION:

; NAME: Cherskov, Michael J.
; REGISTRATION NUMBER: 33,664
; REFERENCE/DOCKET NUMBER: ANL-IN-95-027
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 621-1330
; TELEFAX: (312) 621-0088

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

; LENGTH: 5 bases
; TYPE: nucleic acid
; STRANDEDNESS: No. 6090549 Applicable
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: Yes
US-08-855-372B-21

Query Match 56.7%; Score 3.4; DB 3; Length 5;
Best Local Similarity 80.0%; Pred. No. 3e+08;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGTGT 6
|||
Db 1 TGTAT 5

RESULT 25

US-08-855-372B-23

; Sequence 23, Application US/08855372B
; Patent No. 6090549

GENERAL INFORMATION:

; APPLICANT: Mirzabekov, Andrei D
; APPLICANT: Parinov, Sergei V
; APPLICANT: Barsky, Victor E
; APPLICANT: Kirillov, Eugene V
; APPLICANT: Dubiley, Svetlana A
; TITLE OF INVENTION: Use of Continuous/Contiguous Stacking Hybridization as a Diagnostic
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHERSKOV & FLAYNIK
; STREET: 20 N. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.50 inch, 1.4 MB storage
; COMPUTER: PC
; OPERATING SYSTEM: Microsoft Windows 98

SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/855,372B
; FILING DATE: 13-MAY-97
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/587,332
; FILING DATE: 16-JAN-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Cherskov, Michael J.
; REGISTRATION NUMBER: 33,664
; REFERENCE/DOCKET NUMBER: ANL-IN-95-027
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 621-1330
; TELEFAX: (312) 621-0088
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 bases
; TYPE: nucleic acid
; STRANDEDNESS: No. 6090549 Applicable
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: Yes
US-08-855-372B-23

Query Match 56.7%; Score 3.4; DB 3; Length 5;
Best Local Similarity 80.0%; Pred. No. 3e+08;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGTGT 6
|||
Db 1 TATGT 5

RESULT 26
US-09-048-927-4
; Sequence 4, Application US/09048927
; Patent No. 6147056
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Yaar, Mina
; APPLICANT: Eller, Mark
; TITLE OF INVENTION: Use of Locally Applied DNA Fragments
; FILE REFERENCE: BU94-68A2
; CURRENT APPLICATION NUMBER: US/09/048,927
; CURRENT FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/952,697
; EARLIER FILING DATE: 1996-06-03
; EARLIER APPLICATION NUMBER: 08/467,012
; EARLIER FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA Fragment
US-09-048-927-4

Query Match 56.7%; Score 3.4; DB 3; Length 5;
Best Local Similarity 80.0%; Pred. No. 3e+08;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGTG 5
|||
Db 1 GTATG 5

RESULT 27
US-09-498-851-20
; Sequence 20, Application US/09498851
; Patent No. 6440671
; GENERAL INFORMATION:
; APPLICANT: Mirzabekov, Andrei D

; APPLICANT: Parinov, Sergei V
; APPLICANT: Barsky, Victor E
; APPLICANT: Kirillov, Eugene V
; APPLICANT: Dubiley, Svetlana A
; TITLE OF INVENTION: Use of Continuous/Contiguous
; TITLE OF INVENTION: Stacking Hybridization as a Diagnostic Tool.
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHERSKOV & FLAYNIK
; STREET: 20 N. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.50 inch, 1.4 MB storage
; COMPUTER: PC
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,851
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/855,372
; FILING DATE: 13-MAY-97
; APPLICATION NUMBER: U.S. 08/587,332
; FILING DATE: 16-JAN-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Cherskov, Michael J.
; REGISTRATION NUMBER: 33,664
; REFERENCE/DOCKET NUMBER: ANL-IN-95-027
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 621-1330
; TELEFAX: (312) 621-0088
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 bases
; TYPE: nucleic acid
; STRANDEDNESS: No. 6440671 Applicable
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: yes
US-09-498-851-20

Query Match 56.7%; Score 3.4; DB 3; Length 5;
Best Local Similarity 80.0%; Pred. No. 3e+08;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGTG 5
|||
Db 1 GTATG 5

RESULT 28
US-09-498-851-21
; Sequence 21, Application US/09498851
; Patent No. 6440671
; GENERAL INFORMATION:
; APPLICANT: Mirzabekov, Andrei D
; APPLICANT: Parinov, Sergei V
; APPLICANT: Barsky, Victor E
; APPLICANT: Kirillov, Eugene V
; APPLICANT: Dubiley, Svetlana A
; TITLE OF INVENTION: Use of Continuous/Contiguous
; TITLE OF INVENTION: Stacking Hybridization as a Diagnostic Tool.
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHERSKOV & FLAYNIK
; STREET: 20 N. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.50 inch, 1.4 MB storage
COMPUTER: PC
OPERATING SYSTEM: Microsoft Windows 98
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,851
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/855,372
FILING DATE: 13-MAY-97
APPLICATION NUMBER: U.S. 08/587,332
FILING DATE: 16-JAN-96
ATTORNEY/AGENT INFORMATION:
NAME: Cherskov, Michael J.
REGISTRATION NUMBER: 33,664
REFERENCE/DOCKET NUMBER: ANL-IN-95-027
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 621-1330
TELEFAX: (312) 621-0088
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 bases
TYPE: nucleic acid
STRANDEDNESS: No. 6440671 Applicable
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: yes
US-09-498-851-21

Query Match 56.7%; Score 3.4; DB 3; Length 5;
Best Local Similarity 80.0%; Pred. No. 3e+08;
Matches 4; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 TGTGT 6
Db 1 TGTAT 5

RESULT 29
US-09-498-851-23
Sequence 23, Application US/09498851
Patent No. 6440671
GENERAL INFORMATION:
APPLICANT: Mirzabekov, Andrei D
APPLICANT: Parinov, Sergei V
APPLICANT: Barsky, Victor E
APPLICANT: Kirillov, Eugene V
APPLICANT: Dubiley, Svetlana A
TITLE OF INVENTION: Use of Continuous/Contiguous
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHERSKOV & FLAYNIK
STREET: 20 N. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.50 inch, 1.4 MB storage
COMPUTER: PC
OPERATING SYSTEM: Microsoft Windows 98
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,851
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/855,372
FILING DATE: 13-MAY-97
APPLICATION NUMBER: U.S. 08/587,332
FILING DATE: 16-JAN-96
ATTORNEY/AGENT INFORMATION:

NAME: Cherskov, Michael J.
REGISTRATION NUMBER: 33,664
REFERENCE/DOCKET NUMBER: ANL-IN-95-027
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 621-1330
TELEFAX: (312) 621-0088
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 bases
TYPE: nucleic acid
STRANDEDNESS: No. 6440671 Applicable
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: yes
US-09-498-851-23

Query Match 56.7%; Score 3.4; DB 3; Length 5;
Best Local Similarity 80.0%; Pred. No. 3e+08;
Matches 4; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 TGTGT 6
Db 1 TATGT 5

RESULT 30
US-09-305-839-46/c
Sequence 46, Application US/09305839
Patent No. 6514935
GENERAL INFORMATION:
APPLICANT: Lee, Mu-En
APPLICANT: Yet, Shaw-Fang
TITLE OF INVENTION: Methods of Treating Hypertension
FILE REFERENCE: 21508-064
CURRENT APPLICATION NUMBER: US/09/305,839
CURRENT FILING DATE: 1999-05-05
PRIOR APPLICATION NUMBER: 08/818,655
PRIOR FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 46
LENGTH: 5
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: artif: peptide
US-09-305-839-46

Query Match 56.7%; Score 3.4; DB 4; Length 5;
Best Local Similarity 80.0%; Pred. No. 3e+08;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGTG 5
Db 5 GGGTG 1

Search completed: July 21, 2005, 04:29:16
Job time : 63 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 21, 2005, 00:00:54 ; Search time 710.6 Seconds
(without alignments)
53.568 Million cell updates/sec

Title: US-09-735-363A-10

Perfect score: 6

Sequence: 1 gtgtgt 6

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7173243 seqs, 3172129809 residues

Total number of hits satisfying chosen parameters: 6704

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
- 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	6	100.0	6	9	US-09-735-363A-71
3	6	100.0	6	9	US-09-879-668-2
4	6	100.0	6	15	US-10-280-274-2
5	6	100.0	6	17	US-10-297-008-11
6	6	100.0	6	18	US-10-420-513A-1
7	6	100.0	6	21	US-10-963-286-15
Sequence 10, Appl					
Sequence 71, Appl					
Sequence 2, Appl					
Sequence 2, Appl					
Sequence 11, Appl					
Sequence 15, Appl					

83.3	5	8	9	US-09-735-363A-9	6	9	US-09-735-363A-9	Sequence 9, Appl
83.3	5	9	9	US-09-735-363A-70	6	9	US-09-735-363A-70	Sequence 70, Appl
83.3	5	10	5	US-09-879-668-1	6	9	US-09-879-668-1	Sequence 1, Appl
83.3	5	C	11	US-09-958-221A-2	6	10	US-09-958-221A-2	Sequence 2, Appl
83.3	5	C	12	US-10-280-274-1	6	15	US-10-280-274-1	Sequence 1, Appl
83.3	5	C	13	US-10-678-849-2	6	21	US-10-678-849-2	Sequence 2, Appl
83.3	5	C	14	US-10-963-286-14	6	21	US-10-963-286-14	Sequence 14, Appl
73.3	4	C	15	US-10-190-312A-339	6	16	US-10-190-312A-339	Sequence 339, App
73.3	4	C	16	US-10-190-312A-344	6	16	US-10-190-312A-344	Sequence 344, App
66.7	4	17	4	US-09-735-363A-54	4	9	US-09-735-363A-54	Sequence 54, Appl
66.7	4	18	4	US-09-735-363A-59	4	9	US-09-735-363A-59	Sequence 59, Appl
66.7	4	19	4	US-10-172-620-6	5	14	US-10-172-620-6	Sequence 6, Appl
66.7	4	20	4	US-09-735-363A-39	6	9	US-09-735-363A-39	Sequence 39, Appl
66.7	4	C	21	US-09-887-469-2	6	9	US-09-887-469-2	Sequence 2, Appl
66.7	4	22	4	US-09-888-326-49	6	10	US-09-888-326-49	Sequence 49, Appl
66.7	4	23	4	US-09-776-479-645	6	11	US-09-776-479-645	Sequence 645, App
66.7	4	24	4	US-09-776-479-645	6	11	US-09-776-479-645	Sequence 645, App
66.7	4	25	4	US-09-887-469-2	6	11	US-09-887-469-2	Sequence 2, Appl
66.7	4	26	4	US-10-112-653-619	6	14	US-10-112-653-619	Sequence 619, App
66.7	4	27	4	US-10-017-995-645	6	14	US-10-017-995-645	Sequence 645, App
66.7	4	28	4	US-10-336-265-2	6	15	US-10-336-265-2	Sequence 2, Appl
66.7	4	C	29	US-10-336-265-5	6	15	US-10-336-265-5	Sequence 5, Appl
66.7	4	30	4	US-10-091-281-27	6	16	US-10-091-281-27	Sequence 27, Appl
66.7	4	31	4	US-10-091-281-206	6	16	US-10-091-281-206	Sequence 206, App
66.7	4	32	4	US-10-091-281-207	6	16	US-10-091-281-207	Sequence 207, App
66.7	4	33	4	US-10-091-281-251	6	16	US-10-091-281-251	Sequence 251, App
66.7	4	34	4	US-10-091-281-376	6	16	US-10-091-281-376	Sequence 376, App
66.7	4	C	35	US-10-109-363-7	6	16	US-10-109-363-7	Sequence 7, Appl
66.7	4	C	36	US-10-190-312A-311	6	16	US-10-190-312A-311	Sequence 311, App
66.7	4	37	4	US-10-314-578-645	6	17	US-10-314-578-645	Sequence 645, App
66.7	4	38	4	US-10-417-038-186	6	18	US-10-417-038-186	Sequence 186, App
66.7	4	C	39	US-10-413-357A-79	6	20	US-10-413-357A-79	Sequence 79, Appl
66.7	4	40	4	US-10-831-778-645	6	20	US-10-831-778-645	Sequence 645, App
66.7	4	C	41	US-10-824-158A-79	6	21	US-10-824-158A-79	Sequence 79, Appl
66.7	4	C	42	US-10-912-932A-125	6	21	US-10-912-932A-125	Sequence 125, App
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56.7	3	4	5	US-09-735-363A-79	6	9	US-09-735-363A-79	Sequence 79, Appl
56.7	3	4	5	US-09-879-668-3	6	9	US-09-879-668-3	Sequence 3, Appl
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56.7	3	4	5	US-09-879-668-10	6	9	US-09-879-668-10	Sequence 10, Appl
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56.7	3	4	5	US-09-798-883B-55	6	10	US-09-798-883B-55	Sequence 55, Appl
56.7	3	4	5	US-09-326-885-55	6	10	US-09-326-885-55	Sequence 55, Appl
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56.7	3	4	C	US-10-133-888-10	6	13	US-10-133-888-10	Sequence 10, Appl

C 81 3.4 56.7 6 13 US-10-027-632-51938 Sequence 51938, A
C 82 3.4 56.7 6 13 US-10-027-632-53495 Sequence 53495, A
C 83 3.4 56.7 6 13 US-10-027-632-178012 Sequence 178012, A
C 84 3.4 56.7 6 14 US-10-092-908-18 Sequence 18, Appl
C 85 3.4 56.7 6 14 US-10-127-645-2 Sequence 2, Appl
C 86 3.4 56.7 6 14 US-10-127-645-4 Sequence 4, Appl
C 87 3.4 56.7 6 15 US-10-280-274-3 Sequence 3, Appl
C 88 3.4 56.7 6 15 US-10-280-274-4 Sequence 4, Appl
C 89 3.4 56.7 6 15 US-10-280-274-5 Sequence 5, Appl
C 90 3.4 56.7 6 15 US-10-280-274-6 Sequence 6, Appl
C 91 3.4 56.7 6 15 US-10-280-274-10 Sequence 10, Appl
C 92 3.4 56.7 6 15 US-10-280-274-11 Sequence 11, Appl
C 93 3.4 56.7 6 15 US-10-264-280-1 Sequence 1, Appl
C 94 3.4 56.7 6 15 US-10-264-280-3 Sequence 3, Appl
C 95 3.4 56.7 6 15 US-10-264-280-5 Sequence 5, Appl
C 96 3.4 56.7 6 15 US-10-264-280-7 Sequence 7, Appl
C 97 3.4 56.7 6 15 US-10-255-535-12 Sequence 12, Appl
C 98 3.4 56.7 6 16 US-10-041-860-101 Sequence 101, App
C 99 3.4 56.7 6 16 US-10-041-860-112 Sequence 112, App
C 100 3.4 56.7 6 16 US-10-041-860-131 Sequence 131, App

ALIGNMENTS

RESULT 1

US-09-735-363A-10
; Sequence 10, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-10

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Best Local Similarity 100.0%; Pred. No. 1e+09; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTGT 6
Db 1 GTGTGT 6

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US-09-735-363A-71
; Sequence 71, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925

; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 71
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-71
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Best Local Similarity 100.0%; Pred. No. 1e+09; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGTGT 6
Db 1 GTGTGT 6
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US-09-879-668-2
; Sequence 2, Application US/09879668
; Patent No. US20020091095A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Fillion, Mario C.
; TITLE OF INVENTION: Modulation of Fas and FasL Expression
; FILE REFERENCE: 02811-0241 42368-256931
; CURRENT APPLICATION NUMBER: US/09/879,668
; CURRENT FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: PCT/CA00/01467
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/228,925
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: US 60/266,229
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 09/735,363
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/170,325
; PRIOR FILING DATE: 1999-12-13
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide
US-09-879-668-2

Query Match 100.0%; Score 6; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTGT 6
Db 1 GTGTGT 6

RESULT 4

US-10-280-274-2
; Sequence 2, Application US/10280274
; Publication No. US2003011976A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Fillion, Mario C.
; TITLE OF INVENTION: Modulation of Fas and FasL Expression
; FILE REFERENCE: 02811-0242 42368-279803
; CURRENT APPLICATION NUMBER: US/10/280,274
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: PCT/CA00/01467
; PRIOR FILING DATE: 2000-12-12

; PRIOR APPLICATION NUMBER: US 09/879,668
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: US 60/228,925
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: US 60/266,229
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 09/735,363
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/170,325
; PRIOR FILING DATE: 1999-12-13
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide
US-10-280-274-2

Query Match 100.0%; Score 6; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGTGT 6
Db 1 GTGTGT 6

RESULT 5

US-10-297-008-11/c
; Sequence 11, Application US/10297008
; Publication No. US20030211581A1
; GENERAL INFORMATION:
; APPLICANT: The University of Virginia Patent Foundation
; APPLICANT: Herr, John
; APPLICANT: Reddi, Prabhakara P
; TITLE OF INVENTION: An Insulator Element having Enhancer-Blocking Properties
; FILE REFERENCE: 00567-02
; CURRENT APPLICATION NUMBER: US/10/297,008
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 60/208,371
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-297-008-11

Query Match 100.0%; Score 6; DB 17; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGTGT 6
Db 6 GTGTGT 1

RESULT 6

US-10-420-513A-1
; Sequence 1, Application US/10420513A
; Publication No. US20040058883A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Filion, Mario C.
; TITLE OF INVENTION: Oligonucleotide Compositions and Their Use for the Modulation of
; FILE REFERENCE: 02811-0301 (42368-283135)
; CURRENT APPLICATION NUMBER: US/10/420,513A
; PRIOR FILING DATE: 2003-04-22
; PRIOR APPLICATION NUMBER: US 60/374,540

; PRIOR FILING DATE: 2002-04-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-420-513A-1

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Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGTGT 6
Db 1 GTGTGT 6

RESULT 7

US-10-963-286-15
; Sequence 15, Application US/10963286
; Publication No. US20050095634A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Joffre B.
; APPLICANT: CRONIN, Maureen T.
; APPLICANT: KIEFER, Michael C.
; APPLICANT: LI, Xitong
; APPLICANT: CLARK, Kim
; TITLE OF INVENTION: QRT-PCR ASSAY SYSTEM FOR GENE EXPRESSION
; FILE REFERENCE: 39740-0014A
; CURRENT APPLICATION NUMBER: US/10/963,286
; CURRENT FILING DATE: 2004-10-11
; PRIOR APPLICATION NUMBER: US 60/512,556
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-963-286-15

Query Match 100.0%; Score 6; DB 21; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGTGT 6
Db 1 GTGTGT 6

RESULT 8

US-09-735-363A-9
; Sequence 9, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Filion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 9
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-9

Query Match 83.3%; Score 5; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09; Length 6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTG 5
Db 2 GTGTG 6

RESULT 9

US-09-735-363A-70
; Sequence 70, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 70
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-70

Query Match 83.3%; Score 5; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09; Length 6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTG 5
Db 2 GTGTG 6

RESULT 10

US-09-879-668-1
; Sequence 1, Application US/09879668
; Patent No. US20020091095A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Fillion, Mario C.
; TITLE OF INVENTION: Modulation of Fas and FasL Expression
; FILE REFERENCE: 02811-0241 42368-256931
; CURRENT APPLICATION NUMBER: US/09/879,668
; CURRENT FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: PCT/CA00/01467
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/228,925
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: US 60/266,229
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 09/735,363
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/170,325
; PRIOR FILING DATE: 1999-12-13
; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide
US-09-879-668-1

Query Match 83.3%; Score 5; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09; Length 6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTG 5
Db 2 GTGTG 6

RESULT 11

US-09-958-221A-2/c
; Sequence 2, Application US/09958221A
; Publication No. US20030017471A1
; GENERAL INFORMATION:
; APPLICANT: Haeringen van, Willem A.
; APPLICANT: Haeringen van, Hendrik
; TITLE OF INVENTION: UNIVERSAL VARIABLE FRAGMENTS
; FILE REFERENCE: 92750/64
; CURRENT APPLICATION NUMBER: US/09/958,221A
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: EP 00200757.3
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: PCT/NL01/00177
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-958-221A-2

Query Match 83.3%; Score 5; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09; Length 6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGTG 5
Db 5 GTGTG 1

RESULT 12

US-10-280-274-1
; Sequence 1, Application US/10280274
; Publication No. US20030119776A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Fillion, Mario C.
; TITLE OF INVENTION: Modulation of Fas and FasL Expression
; FILE REFERENCE: 02811-0242 42368-279803
; CURRENT APPLICATION NUMBER: US/10/280,274
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: PCT/CA00/01467
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 09/879,668
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: US 60/228,925
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: US 60/266,229
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 09/735,363
; PRIOR FILING DATE: 2000-12-12

; PRIOR APPLICATION NUMBER: US 60/170,325
; PRIOR FILING DATE: 1999-12-13
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1:
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide
US-10-280-274-1

Query Match 83.3%; Score 5; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGTG 5
|
|
|
|
Db 2 GTGTG 6

RESULT 13

US-10-676-849-2/c
; Sequence 2, Application US/10676849
; Publication No. US2005009038A1
; GENERAL INFORMATION:
; APPLICANT: Haeringen van, Willem A.
; APPLICANT: Haeringen van, Hendrik
; TITLE OF INVENTION: UNIVERSAL VARIABLE FRAGMENTS
; FILE REFERENCE: 92750/64
; CURRENT APPLICATION NUMBER: US/10/676,849
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US/09/958,221
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: EP 00200757.3
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: PCT/NL01/00177
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-10-676-849-2

Query Match 83.3%; Score 5; DB 21; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGTG 5
|
|
|
|
Db 5 GTGTG 1

RESULT 14

US-10-963-286-14/c
; Sequence 14, Application US/10963286
; Publication No. US2005009563A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Joffre B.
; APPLICANT: CRONIN, Maureen T.
; APPLICANT: KIEFER, Michael C.
; APPLICANT: Li, Xitong
; APPLICANT: CLARK, Kim
; TITLE OF INVENTION: qRT-PCR ASSAY SYSTEM FOR GENE EXPRESSION
; FILE REFERENCE: 39740-0014A
; CURRENT APPLICATION NUMBER: US/10/963,286
; CURRENT FILING DATE: 2004-10-11
; PRIOR APPLICATION NUMBER: US 60/512,556

; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-963-286-14

Query Match 83.3%; Score 5; DB 21; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGTG 5
|
|
|
|
Db 5 GTGTG 1

RESULT 15

US-10-190-312A-339/c
; Sequence 339, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; FILE REFERENCE: 2183-4993.1
; CURRENT APPLICATION NUMBER: US/10/190,312A
; CURRENT FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/303,199
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 339
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements
US-10-190-312A-339

Query Match 73.3%; Score 4.4; DB 16; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGTGT 6
|
|
|
|
Db 6 GTGGGT 1

RESULT 16

US-10-190-312A-344/c
; Sequence 344, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; FILE REFERENCE: 2183-4993.1
; CURRENT APPLICATION NUMBER: US/10/190,312A
; CURRENT FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/303,199
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 344
; LENGTH: 6

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements
US-10-190-312A-344

Query Match      73.3%; Score 4.4; DB 16; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGTGT 6
   | | | | |
Db 6 GGGTGT 1

RESULT 17
US-09-735-363A-54
; Sequence 54, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 54
; LENGTH: 4
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-54

Query Match      66.7%; Score 4; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.5e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGT 4
   | | | |
Db 1 GTGT 4

RESULT 18
US-09-735-363A-59
; Sequence 59, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 59
; LENGTH: 4
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-59
```

```
Query Match      66.7%; Score 4; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.5e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTG 5
   | | | |
Db 1 TGTG 4

RESULT 19
US-10-172-620-6
; Sequence 6, Application US/10172620
; Publication No. US20030053995A1
; GENERAL INFORMATION:
; APPLICANT: Hung, Mien-Chie
; APPLICANT: Lin, Shiaw-Yih
; TITLE OF INVENTION: Methods and Compositions for Inhibiting EGF Receptor
; FILE REFERENCE: UTSC:720US
; CURRENT APPLICATION NUMBER: US/10/172,620
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/298,579
; PRIOR FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Muted ATRS Sequence
US-10-172-620-6

Query Match      66.7%; Score 4; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGT 4
   | | | |
Db 2 GTGT 5

RESULT 20
US-09-735-363A-39
; Sequence 39, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 39
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-39

Query Match      66.7%; Score 4; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTG 5
   | | | |
Db 2 TGTG 5
```



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; Sequence 2, Application US/09887469
; Publication No. US20040258714A9
; GENERAL INFORMATION:
; APPLICANT: Krempel, Christine D.
; APPLICANT: Collins, Peter L.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Buchholz, Ursula
; APPLICANT: Whitehead, Stephen S.
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS VACCINES EXPRESSING
; TITLE OF INVENTION: PROTECTIVE ANTIGENS FROM PROMOTOR-PROXIMAL-GENES
; FILE REFERENCE: 15280-424-IUS
; CURRENT APPLICATION NUMBER: US/09/887,469
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,708
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
; OTHER INFORMATION: Respiratory Syncytial Virus
US-09-887-469-2

Query Match          66.7%; Score 4; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TGTG 5
        ||||
Db       4 TGTG 1

RESULT 26
US-10-112-653-619
; Sequence 619, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Daniel J.
; APPLICANT: Berg, Arthur M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 619
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-619

Query Match          66.7%; Score 4; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TGTG 4
        ||||
Db       3 GTGT 6

RESULT 27
US-10-017-995-645
; Sequence 645, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
```

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; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 645
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-645

Query Match          66.7%; Score 4; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGT 4
        ||||
Db       3 GTGT 6

RESULT 28
US-10-336-265-2
; Sequence 2, Application US/10336265
; Publication No. US20030148988A1
; GENERAL INFORMATION:
; APPLICANT: Kool, Eric T.
; TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for
; TITLE OF INVENTION: the Elongation of Telomere Repeats
; FILE REFERENCE: 12665-0021.NPUS01
; CURRENT APPLICATION NUMBER: US/10/336,265
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 60/345,056
; PRIOR FILING DATE: 2002-01-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-336-265-2

Query Match          66.7%; Score 4; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TGTG 5
        ||||
Db       1 TGTG 4

RESULT 29
US-10-336-265-5/c
; Sequence 5, Application US/10336265
; Publication No. US20030148988A1
; GENERAL INFORMATION:
; APPLICANT: Kool, Eric T.
; TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for
; TITLE OF INVENTION: the Elongation of Telomere Repeats
; FILE REFERENCE: 12665-0021.NPUS01
; CURRENT APPLICATION NUMBER: US/10/336,265
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 60/345,056
; PRIOR FILING DATE: 2002-01-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 6
```

```
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; US-10-336-265-5

Query Match      66.7%; Score 4; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TGTG 5
Db      6 TGTG 3

RESULT 30
US-10-091-281-27
; Sequence 27, Application US/10091281
; Publication No. US20030190617A1
; GENERAL INFORMATION:
; APPLICANT: RAYMOND, VINCENT
; APPLICANT: SI, ERWIN
; APPLICANT: MORISETTE, JEAN
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 13587.338
; CURRENT APPLICATION NUMBER: US/10/091,281
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Putative HAML/AML1.01 motif
US-10-091-281-27

Query Match      66.7%; Score 4; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TGTG 5
Db      1 TGTG 4

Search completed: July 21, 2005, 07:13:12
Job time : 714.6 secs
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 21:46:09 ; Search time 187.4 Seconds
(without alignments)
189.533 Million cell updates/sec

Title: US-09-735-363a-25
Perfect score: 6
Sequence: 1 999tgg 6

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 1582

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : N_Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	6	100.0	6	13	ADR32691 Human nlc
C 2	5	83.3	5	8	ABZ75664 Helicase-
C 3	5	83.3	6	2	AAT96305 Fungal te
C 4	5	83.3	6	8	ABX50029 Telomere
C 5	5	83.3	6	12	ADJ35723 Stablisli
C 6	4.4	73.3	6	2	AAT04935 Anti-HIV
C 7	4.4	73.3	6	6	ABZ77547 Angiogene
C 8	4.4	73.3	6	6	ABK87320 Mammalian
C 9	4.4	73.3	6	9	ACD99345 Immunosti
C 10	4.4	73.3	6	10	ACA88957 Selection
C 11	4.4	73.3	6	12	ADJ35665 Stablisli
C 12	4.4	73.3	6	12	ADK14379 Candida p
C 13	4.4	73.3	6	13	ADR32931 Human nlc
C 14	4	66.7	5	2	AAT96299 Fungal te
C 15	4	66.7	5	3	Aaz93601 Transcrip
C 16	4	66.7	5	8	ABZ75666 Helicase-
C 17	4	66.7	5	8	ABX49997 Telomere
C 18	4	66.7	6	2	AAQ50333 Ribozyme
C 19	4	66.7	6	2	AAT80319 Oligo HCV
C 20	4	66.7	6	2	AAT80320 Oligo HCV

C 21	4	66.7	6	2	AAV61659 Fusarium
C 22	4	66.7	6	3	Aaz89322 Human UCP
C 23	4	66.7	6	4	AAS06241 PCR prime
C 24	4	66.7	6	6	ABK72534 Human OPA
C 25	4	66.7	6	6	ABs77550 Angiogene
C 26	4	66.7	6	6	ABs65903 Inhibitor
C 27	4	66.7	6	6	ABs65904 Inhibitor
C 28	4	66.7	6	6	ABK30087 Beta-lact
C 29	4	66.7	6	9	ACD99348 Immunosti
C 30	4	66.7	6	10	ADD71358 Human scl
C 31	4	66.7	6	10	ADe14140 Optineuri
C 32	4	66.7	6	10	ADe14096 Optineuri
C 33	4	66.7	6	10	ADe13916 Optineuri
C 34	4	66.7	6	10	ADe14095 Optineuri
C 35	4	66.7	6	10	ADe14265 Optineuri
C 36	4	66.7	6	10	ADe38298 Immune mo
C 37	4	66.7	6	10	ADe38299 Immune mo
C 38	4	66.7	6	10	ADe38306 Immune mo
C 39	4	66.7	6	10	ADe38277 Immune mo
C 40	4	66.7	6	10	ADe38273 Immune mo
C 41	4	66.7	6	10	ADe38281 Immune mo
C 42	4	66.7	6	10	ADe38307 Immune mo
C 43	4	66.7	6	12	ADe52744 Oligonucle
C 44	4	66.7	6	12	ADJ35342 Stablisli
C 45	4	66.7	6	12	ADJ35709 Stablisli
C 46	4	66.7	6	12	ADJ35456 Stablisli
C 47	4	66.7	6	12	ADJ35541 Stablisli
C 48	4	66.7	6	12	ADK14301 Candida p
C 49	4	66.7	6	12	ADK14312 Candida p
C 50	4	66.7	6	12	ADL98067 Deleted s
C 51	4	66.7	6	12	ADO05792 Telomere-
C 52	4	66.7	6	13	ADR37260 Human nlc
C 53	4	66.7	6	13	ADR32740 Human nlc
C 54	4	66.7	6	13	ADR32631 Human nlc
C 55	4	66.7	6	13	ADR32677 Human nlc
C 56	4	66.7	6	13	ADR37262 Human nlc
C 57	4	66.7	6	13	ADR32553 Human nlc
C 58	4	66.7	6	13	ADR32877 Human nlc
C 59	4	66.7	6	13	ADR37261 Human nlc
C 60	4	66.7	6	13	ADR37263 Human nlc
C 61	4	66.7	6	13	ADN33281 E. coli 2
C 62	4	66.7	6	13	ADN33272 E. coli 2
C 63	3.6	60.0	6	13	ADR37222 Human nlc
C 64	3.6	60.0	6	13	ADR37224 Human nlc
C 65	3.6	60.0	6	13	ADR37225 Human nlc
C 66	3.6	60.0	6	13	ADR37203 Human nlc
C 67	3.6	60.0	6	13	ADR37223 Human nlc
C 68	3.6	60.0	6	13	ADR37221 Human nlc
C 69	3.6	60.0	6	13	ADR37226 Human nlc
C 70	3.6	60.0	6	13	ADR37202 Human nlc
C 71	3.4	56.7	5	2	AAV72347 US5908745
C 72	3.4	56.7	5	2	AAV72349 US5908745
C 73	3.4	56.7	5	8	ABZ75669 Helicase-
C 74	3.4	56.7	5	10	ADH60372 Myctophid
C 75	3.4	56.7	6	2	AAQ61541 TDT promo
C 76	3.4	56.7	6	2	AAT80318 Oligo HCV
C 77	3.4	56.7	6	2	AAT80318
C 78	3.4	56.7	6	3	AAV45399 TDT promo
C 79	3.4	56.7	6	3	AAA62709 PNA clamp
C 80	3.4	56.7	6	4	AAF91656 Breast-ca
C 81	3.4	56.7	6	4	AAFI1686 Breast-ca
C 82	3.4	56.7	6	4	AAFI17580 AC repeat
C 83	3.4	56.7	6	6	ABK88579 Hepatitis
C 84	3.4	56.7	6	6	ABK88579
C 85	3.4	56.7	6	8	ABK87321 Mammalian
C 86	3.4	56.7	6	8	ABZ75668 Helicase-
C 87	3.4	56.7	6	12	ADJ35778 Stablisli
C 88	3.4	56.7	6	12	ADJ35353 Stablisli
C 89	3.4	56.7	6	12	ADJ35593 Stablisli
C 90	3.4	56.7	6	12	ADJ35427 Stablisli
C 91	3.4	56.7	6	12	ADJ35500 Stablisli
C 92	3.4	56.7	6	12	ADJ35463 Stablisli
C 93	3.4	56.7	6	12	ADJ35519 Stablisli
C 94	3.4	56.7	6	12	ADJ35391 Stablisli

c 94 3.4 56.7 6 12 ADJ35621 Stabilisi
c 95 3.4 56.7 6 12 ADO81155
Ado81155 Prion pro
c 96 3.4 56.7 6 13 ADR32491
Adr32491 Human nic
c 97 3.4 56.7 6 13 ADR32878
Adr32878 Human nic
c 98 3.4 56.7 6 13 ADR32508
Adr32508 Human nic
c 99 3.2 53.3 6 1 AAN92488
Aan92488 Sequence
c 100 3.2 53.3 6 1 AAN92488
Aan92488 Sequence

ALIGNMENTS

RESULT 1
ADR32691/c
ID ADR32691 standard; DNA; 6 BP.
XX
AC ADR32691;
XX
DT 04-NOV-2004 (first entry)
XX
DE Human nicking agent target DNA #232.
DE
DE
KW ss; nicking agent; assay panel; diagnosis; expression pattern;
KW DNA fingerprinting; nosocomial infection; microbiological assay;
KW bacterial contamination; genome mapping; bioremediation.
XX
OS Homo sapiens.
XX
XX WO2004067765-A2.
XX
XX 12-AUG-2004.
XX
XX 29-JAN-2004; 2004WO-US002720.
XX
XX 29-JAN-2003; 2003US-0443811P.
XX
XX (KECK-) KECK GRADUATE INST.
XX
XX Van Ness J, Galas DJ, Van Ness LX;
XX
XX WPI; 2004-581010/56.
XX
XX
XX Identifying nucleic acid sample source, useful for identifying bacterial
XX strains involved in nosocomial infections, comprises treating the nucleic
XX acid sample with components comprising a nicking agent under nicking
XX conditions.
XX
XX Example 1; Page 75; 238pp; English.

The invention relates to a method of treating a nucleic acid sample with
components under nicking conditions, where the components comprise a
nicking agent, and the conditions cause the nicking agent to nick the
nucleic acid sample to thus produce a family of initiating
oligonucleotide fragments, and subjecting one or more members of the
family of initiating oligonucleotide fragments to a characterization
process to thus provide results. The method is useful for creating an
assay panel of diagnostic oligonucleotides that can identify any organism
or individual. The method is useful for characterizing other DNA
molecules e.g., cDNA, and for characterizing cDNA expression patterns.
The method, kit or composition is useful for identifying the source
organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
non-human animal or human. The method is particularly useful for rapidly
fingerprinting DNA to identifying prokaryotic and eukaryotic species,
subspecies, and especially strains or individuals of the subspecies. It
is especially useful for identifying different bacterial strains involved
in e.g., nosocomial infections. Furthermore, the method is useful for
diagnosing bacterial disease in plants and humans, monitoring for
bacterial content and/or contamination in the environment, monitoring
food for bacterial contamination, monitoring manufacturing processes for
bacterial contamination, monitoring quality assurance/quality control of
laboratory tests involving microbiological assays, tracing bacterial
contamination and/or outbreaks of bacterial infections, genome mapping,
monitoring bioremediation sites, and for monitoring agricultural sites

CC for test crops, bacteria and recombinant molecules. This sequence
CC corresponds to nucleic acid used in the method of the invention.
XX
SQ Sequence 6 BP; 1 A; 5 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 100.0%; Score 6; DB 13; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTGG 6
Db 6 GGGTGG 1

RESULT 2
ABZ75664/c
ID ABZ75664 standard; DNA; 5 BP.
XX
AC ABZ75664;
XX
DT 15-MAY-2003 (first entry)
XX
DE Helicase-like transcription factor (HLTF) binding oligonucleotide.
XX
KW HLTF; carcinogenesis; hyperproliferative lesion; cytostatic; virucide;
KW helicase-like transcription factor; telomerase reverse transcriptase;
KW dermatological; gynaecological; TERT; gene therapy; cancer; ss.
XX
OS Synthetic.
XX
XX WO2003002068-A2.
XX
XX 09-JAN-2003.
XX
XX 27-JUN-2002; 2002WO-US020757.
XX
XX 27-JUN-2001; 2001US-0301384P.
XX
XX (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX
XX Androphy EJ, Doshi N, Delayew A;
XX
XX WPI; 2003-210197/20.
XX
XX Inhibiting carcinogenesis of a cell, especially useful for treating a
XX human papilloma virus-mediated hyperproliferative lesion (warts) or
XX cancer, by reducing the activity of helicase-like transcription factor in
XX the cell.
XX
XX Claim 15; Page 24; 36pp; English.

The invention relates to inhibiting carcinogenesis of a cell, or
inhibiting growth of a cell in a human papillomavirus (HPV)-mediated
hyperproliferative lesion. The method involves reducing the amount of
helicase-like transcription factor (HLTF) in the cell or inhibiting the
binding of endogenous HLTF to telomerase reverse transcriptase (TERT)
promoter. The method is useful for inhibiting carcinogenesis of a cell,
or inhibiting growth of a cell in an HPV-mediated hyperproliferative
lesion. The method is particularly useful for treating cancer (especially
cervical cancer), or hyperproliferative lesions (warts) caused by HPV.
The method is also useful for diagnosing a neoplasm, or detecting the
presence of a malignant tumour or a predisposition to developing the
tumour. Sequences ABZ75663-669 represent specific examples of
oligonucleotides that bind to endogenous HLTF, thereby preventing HLTF
from binding to an intact TERT promoter region
Sequence 5 BP; 1 A; 4 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 83.3%; Score 5; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGTG 5

```

Db      |||||
        5 GGCTG 1

RESULT 3
AAT96305
ID AAT96305 standard; DNA; 6 BP.
XX
AC AAT96305;
XX
DT 25-MAR-2003 (revised)
DT 08-APR-1998 (first entry)
XX
XX Fungal telomeric nucleic acid sequence.
DE
XX Detection; eukaryotic pathogen; telomeric nucleic acid sequence;
KW telomerase activity; diagnosis; fungal infection; fungus; fungi;
KW malarial infection; malaria; ss.
XX
OS Saccharomyces cerevisiae.
XX
PN US5695932-A.
XX
PD 09-DEC-1997.
XX
PF 13-MAY-1993; 93US-00060952.
XX
PR 13-MAY-1992; 92US-00882438.
PR 24-MAR-1993; 93US-00038766.
XX
XX (UYCA-) UNIV CALIFORNIA SAN FRANCISCO.
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Blackburn EH, Shay J, Mceachern MJ, West MD, Wright W;
XX
DR WPI; 1998-041292/04.
XX
PT Detection of eukaryotic pathogens, especially fungal or Plasmodium spp. -
PT by detecting telomerase activity.
XX
PS Claim 5; Col 93-94; 82pp; English.
XX
XX The present sequence can be used in a novel method for detecting a
CC eukaryotic pathogen in a patient. The method comprises obtaining a sample
CC of somatic tissue or cells from the patient, determining if telomerase
CC activity is present and correlating this with the presence of the
CC pathogen. The method is useful for diagnosis of fungal infections,
CC especially a fungus of the genus Candida, Kluyveromyces, Saccharomyces,
CC Sporothrix, Coccidioides, Histoplasma, Blastomyces, Paracoccidioides,
CC Cryptococcus, Aspergillus, Mucor or Rhizopus, or malarial infections,
CC especially Plasmodium vivax, P. ovale, P. malariae or P. falciparum.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 6 BP; 0 A; 0 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 83.3%; Score 5; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTG 5
Db      |||||
        2 GGCTG 6

RESULT 4
ABX50029
ID ABX50029 standard; DNA; 6 BP.
XX
AC ABX50029;
XX
DT 12-FEB-2003 (first entry)
XX
DE Telomere length and/or telomerase activity related polynucleotide #52.

```

```

XX Cell proliferation; cell senescence; telomere length;
KW telomerase activity; cell replication; neoplasia; cancer;
KW age-related macular degeneration; Alzheimer's disease; atherosclerosis;
KW telomerase; telomerase inhibitor; immortalised cell; ss.
XX
OS Synthetic.
XX
PN US2002127634-A1.
XX
PD 12-SEP-2002.
XX
PF 05-JUN-1995; 95US-00463404.
XX
PR 13-MAY-1992; 92US-00882438.
PR 24-MAR-1993; 93US-00038766.
PR 13-MAY-1993; 93US-00060952.
XX
XX (WEST/) WEST M D.
PA (SHAY/) SHAY J.
PA (WRIG/) WRIGHT W.
PA (BLAC/) BLACKBURN E H.
XX
XX West MD, Shay J, Wright W, Blackburn EH;
XX
DR WPI; 2003-066896/06.
XX
PT Treating condition associated with cell senescence or increased rate of
PT cell proliferation, by administering to cell an agent that derepresses
PT telomerase in the senescing cells or that reduces loss of telomere
PT length.
XX
XX Disclosure; Page 50; 86pp; English.
XX
XX The invention describes a method use for treating increased rate of
CC proliferation of a cell or extending the ability of a cell to replicate,
CC or treating a disease associated with cell senescence. The method
CC comprises administering an agent to reduce loss of telomere length within
CC the cell during proliferation or replication, or to derepress telomerase
CC in the senescing cells. The method is useful for treating a condition
CC associated with an increased rate of proliferation of a cell extending
CC the ability of a cell to replicate, or for treating a disease or
CC condition associated with cell senescence e.g. neoplasia. A second method
CC disclosed in the invention is useful for treating a condition associated
CC with an elevated level of telomerase activity within a cell e.g. cancer.
CC Also disclosed is a method useful for diagnosis of a condition associated
CC with an increased rate of proliferation in a cell in an individual e.g.
CC age-related macular degeneration, astrocytes associated with Alzheimer's
CC disease and endothelial cells associated with atherosclerosis. This
CC sequence represents a polynucleotide used in the study of telomere length
CC and telomerase activity described in the invention
XX
SQ Sequence 6 BP; 0 A; 0 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 83.3%; Score 5; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTG 5
Db      |||||
        2 GGCTG 6

RESULT 5
ADJ35723/c
ID ADJ35723 standard; DNA; 6 BP.
XX
AC ADJ35723;
XX
DT 22-APR-2004 (first entry)
XX
DE Stabilising anti-repression, STAR, element dyad sequence #389.

```

KW STAR affiliated proteinaceous molecule; post translational modification;
 XX stabilising anti-repression; STAR; STAR element; ds; dyad.
 XX Unidentified.
 OS WO2003106674-A2.
 PN 24-DEC-2003.
 PD
 XX
 XX 30-MAY-2003; 2003WO-NL000410.
 PF
 XX 14-JUN-2002; 2002EP-00077344.
 PR
 XX (CHRO-) CHROMAGENICS BV.
 PA
 XX Otte AP, Kruckeberg AL, Satiijn DPE;
 PI WPI; 2004-082195/08.
 DR
 XX Producing proteinaceous molecules in cells by selecting a cell, providing
 PT a nucleic acid encoding a proteinaceous molecule with an stabilizing Anti
 PT -Repression sequence and expressing proteinaceous molecule.
 XX
 XX Disclosure; Page 103; 177pp; English.
 PS
 XX The invention relates to a method of producing a proteinaceous molecule
 CC (I) in a cell comprising selecting a cell for its suitability for
 CC producing (I), providing a nucleic acid encoding (I) with a nucleic acid
 CC comprising a Stabilising Anti-Repression (STAR) sequence, expressing the
 CC resulting nucleic acid in the cell and collecting (I). The method is
 CC useful for producing (I). A cell line (II) provided with a nucleic acid
 CC comprising a STAR sequence is useful for producing (I). (II) Enables
 CC production of affiliated proteinaceous molecule, as cell carries out
 CC proper post-translational modifications of produced proteins. The present
 CC sequence represents a stabilising anti-repression, STAR, element primer
 CC dyad sequence.
 XX
 XX Sequence 6 BP; 1 A; 5 C; 0 G; 0 T; 0 U; 0 Other;
 SQ Query Match 83.3%; Score 5; DB 12; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGTG 5
 DB |||||
 5 GGGTG 1

RESULT 6
 AAT04935
 ID AAT04935 standard; DNA; 6 BP.
 XX
 AC AAT04935;
 XX
 DT 10-MAY-1996 (first entry)
 XX
 DE Anti-HIV oligodeoxynucleotide.
 XX
 XX Anti-HIV; AIDS; ARC; treatment; ss.
 KW
 XX Synthetic.
 OS
 XX WO9526190-A1.
 PN
 XX 05-OCT-1995.
 PD
 XX 24-MAR-1995; 95WO-JP000543.
 PF
 XX 25-MAR-1994; 94JP-00092809.
 PR
 XX 25-MAR-1994; 94JP-00092810.
 XX
 XX (KAJI/) KAJI A.
 PA
 XX

PI Kaji A;
 XX WPI; 1995-351196/45.
 DR
 XX Anti HIV agents useful for the treatment of HIV, AIDS and ARC - comprise
 PT a phosphodiester linked oligonucleotide deriv.
 PT
 XX Example 3; Page 11; 19pp; Japanese.
 PS
 XX The oligodeoxynucleotides AAT04934/35 are anti-HIV agents, useful for
 CC treating HIV, AIDS and ARC. They are pref. given in a dosage of 1-100
 CC mg/day parenterally, or 0.1- 6g/day orally
 CC
 XX Sequence 6 BP; 0 A; 0 C; 6 G; 0 T; 0 U; 0 Other;
 SQ Query Match 73.3%; Score 4.4; DB 2; Length 6;
 Best Local Similarity 83.3%; Pred. No. 9.7e+08;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGGTGG 6
 DB |||||
 1 GGGGGG 6

RESULT 7
 ABS77547/c
 ID ABS77547 standard; DNA; 6 BP.
 XX
 AC ABS77547;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE Angiogenesis inhibitory oligonucleotide #31.
 XX
 KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
 KW rubosis; Osler-Webber Syndrome; myocardial angiogenesis;
 KW plaque neovascularisation; tetangiectasia; haemophilic joint;
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
 KW scleroderma; hypertrophic scar.
 XX
 OS Synthetic.
 XX
 XX WO200253141-A2.
 PN
 XX 11-JUL-2002.
 PD
 XX 14-DEC-2001; 2001WO-US048458.
 PF
 XX 14-DEC-2000; 2000US-0255534P.
 PR
 XX (COLE-) COLEY PHARM GROUP INC.
 XX
 PA Bratzler RL;
 PI
 XX WPI; 2002-566690/60.
 DR
 XX Inhibiting angiogenesis in a subject, involves administering at least one
 PT antiangiogenic nucleic acid molecule to the subject.
 PT
 XX Claim 2; Page 20; 276pp; English.
 PS
 XX The invention relates to inhibiting angiogenesis in a subject, comprising
 CC administering at least one antiangiogenic nucleic acid molecule. Also
 CC included is a kit comprising a first container housing the antiangiogenic
 CC nucleic acids, and instructions for administering them to a subject
 CC having a condition characterised by unwanted angiogenesis. The method is
 CC useful for inhibiting angiogenesis associated with solid tumour growth,
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
 CC

CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention
XX
SQ Sequence 6 BP; 0 A; 6 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 73.3%; Score 4.4; DB 6; Length 6;
Best Local Similarity 83.3%; Pred. No. 9.7e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTGG 6
DB 6 GGGGGG 1

RESULT 8
ABK87320
ID ABK87320 standard; DNA; 6 BP.

XX AC ABK87320;
XX
DT 24-SEP-2002 (first entry)
XX
DE Mammalian SPI recognition sequence #1.
XX
KW Nucleic acid detection; Spl; ss.

OS Mammalia.
XX
PN WO200244326-A2.

XX PD 06-JUN-2002.
XX
PF 26-NOV-2001; 2001WO-US044215.

XX PR 30-NOV-2000; 2000US-00728574.
XX
PA (STRA-) STRATAGENE.

XX PI Sorge JA, Whalen AM;
XX
XX WPI; 2002-508503/54.

XX
CC Detecting/measuring target nucleic acid, by forming cleavage structure by
CC incubating target nucleic acid with probe having binding moiety, cleaving
CC structure to release nucleic acid and detecting released fragments.

PS Disclosure; Page 75; 157pp; English.

XX
CC This invention relates to a novel method for detecting/measuring a target
CC nucleic acid. The method comprises forming a cleavage structure by
CC incubating the target sequence with a probe comprising a binding moiety
CC and a secondary structure that changes upon binding of the probe to the
CC target, cleaving the cleavage structure to release a nucleic acid
CC fragment, and detecting and/or measuring the fragment captured by binding
CC of the binding moiety to a capture element on a solid support. The method
CC of the invention is useful for detecting or measuring a target nucleic
CC acid and are useful for generating a signal indicative of the presence of
CC the target nucleic acid in a sample. Another method of the invention is
CC useful for simultaneously forming a cleavage structure, amplifying the
CC target nucleic acid in a sample and cleaving the cleavage structure. The
CC method does not require multiple steps, subsequent amplification process,
CC and allows for concurrent amplification and detection of target nucleic
CC acid in a sample. The present sequence represents the Mammalian SPI
CC recognition sequence shown in the specification
XX

SQ Sequence 6 BP; 0 A; 1 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 73.3%; Score 4.4; DB 6; Length 6;
Best Local Similarity 83.3%; Pred. No. 9.7e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTGG 6
DB 1 GGGCGG 6

RESULT 9
ACD99345/C
ID ACD99345 standard; DNA; 6 BP.

XX AC ACD99345;
XX
DT 25-SEP-2003 (first entry)

XX DE Immunostimulatory nucleic acid #31.

XX KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.

XX OS Synthetic.

XX PN US2003050268-A1.

XX PD 13-MAR-2003.

XX PF 29-MAR-2002; 2002US-00112653.

XX PR 29-MAR-2001; 2001US-0279642P.

XX PA (KRIE/) KRIEG A M.

XX PA (BERG/) BERG D J.

XX PI Krieg AM, Berg DJ;

XX DR WPI; 2003-521815/49.

XX
CC Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
CC allergic contact dermatitis, latex dermatitis or inflammatory bowel
CC disease by administering an immunostimulatory nucleic acid.

XX PS Disclosure; Page 9; 229pp; English.

XX
CC The invention describes a method of treating non-allergic inflammatory
CC disease comprising administering to a subject having or at risk of
CC developing a non-allergic inflammatory disease an immunostimulatory
CC nucleic acid for prevention or treatment of the disease. The method is
CC useful for treating non-allergic inflammatory diseases, such as
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC This sequence represents an immunostimulatory nucleic acid

SQ Sequence 6 BP; 0 A; 6 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 73.3%; Score 4.4; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 9.7e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTGG 6
DB 6 GGGGGG 1

RESULT 10
ACA88957
ID ACA88957 standard; DNA; 6 BP.

XX AC ACA88957;

XX DT 08-JUL-2003 (first entry)

XX DE Selection and amplification of genetic markers PCR related primer #68.

PT protein of the beta or omega oxidation pathway in a yeast cell.
 XX Example 2; SEQ ID NO 108; 99pp; English.
 XX The present invention describes modified Candida tropicalis CYP gene
 CC promoters comprising a nucleotide sequence for a CYP gene promoter. Also
 CC described: (1) a yeast host cell comprising the modified Candida
 CC tropicalis CYP gene promoter; and (2) a method for modulating expression
 CC of a protein of the beta or omega oxidation pathway in a yeast cell
 CC comprising: (a) isolating a CYP gene promoter from *C. tropicalis*; (b)
 CC modifying the promoter by addition of one or more URS1, URS2, URS1-like
 CC or URS2-like promoters; (c) operably linking the modified promoter with a
 CC coding sequence for a protein of the omega or beta oxidation pathway; (d)
 CC transforming a yeast cell with the modified promoter operably linked to
 CC the coding sequence; and (e) growing the yeast under conditions
 CC favourable for expression of the coding sequence under the control of the
 CC modified promoter. The promoters are useful for modulating expression of
 CC a protein of the beta or omega oxidation pathway in a yeast cell. The
 CC present sequence is used in the exemplification of the present invention.
 XX
 SQ Sequence 6 BP; 0 A; 0 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 73.3%; Score 4.4; DB 12; Length 6;
 Best Local Similarity 83.3%; Pred. No. 9.7e+08;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGGTGG 6
 |||||
 Db 1 GGGTTG 6
 |||||
 RESULT 13
 ID ADR32931/C
 AD ADR32931 standard; DNA; 6 BP.
 XX
 AC ADR32931;
 DT 04-NOV-2004 (first entry)
 XX
 DE Human nicking agent target DNA #472.
 DE
 KW ss; nicking agent; assay panel; diagnosis; expression pattern;
 KW DNA fingerprinting; nosocomial infection; microbiological assay;
 KW bacterial contamination; genome mapping; bioremediation.
 XX
 OS Homo sapiens.
 XX
 PN WO2004067765-A2.
 XX
 PD 12-AUG-2004.
 XX
 PF 29-JAN-2004; 2004WO-US002720.
 XX
 PR 29-JAN-2003; 2003US-0443811P.
 XX
 PA (KECK-) KECK GRADUATE INST.
 XX
 PI Van Ness J, Galas DJ, Van Ness LK;
 XX
 DR WPI; 2004-581010/56.
 XX
 XX Identifying nucleic acid sample source, useful for identifying bacterial
 PT strains involved in nosocomial infections, comprises treating the nucleic
 PT acid sample with components comprising a nicking agent under nicking
 PT conditions.
 XX
 XX Example 1; Page 79; 238pp; English.
 XX
 CC The invention relates to a method of treating a nucleic acid sample with
 CC components under nicking conditions, where the components comprise a
 CC nicking agent, and the conditions cause the nicking agent to nick the
 CC nucleic acid sample to thus produce a family of initiating
 CC oligonucleotide fragments, and subjecting one or more members of the

CC family of initiating oligonucleotide fragments to a characterization
 CC process to thus provide results. The method is useful for creating an
 CC assay panel of diagnostic oligonucleotides that can identify any organism
 CC or individual. The method is useful for characterizing other DNA
 CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
 CC The method, kit or composition is useful for identifying the source
 CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
 CC non-human animal or human. The method is particularly useful for rapidly
 CC fingerprinting DNA to identifying prokaryotic and eukaryotic species.
 CC subpecies, and especially strains or individuals of the subpecies. It
 CC is especially useful for identifying different bacterial strains involved
 CC in e.g., nosocomial infections. Furthermore, the method is useful for
 CC diagnosing bacterial disease in plants and humans, monitoring for
 CC bacterial content and/or contamination in the environment, monitoring
 CC food for bacterial contamination, monitoring quality assurance/quality control of
 CC laboratory tests involving microbiological assays, tracing bacterial
 CC contamination and/or outbreaks of bacterial infections, genome mapping,
 CC monitoring bioremediation sites, and for monitoring agricultural sites
 CC for test crops, bacteria and recombinant molecules. This sequence
 CC corresponds to nucleic acid used in the method of the invention.
 XX
 SQ Sequence 6 BP; 2 A; 4 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 73.3%; Score 4.4; DB 13; Length 6;
 Best Local Similarity 83.3%; Pred. No. 9.7e+08;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGGTGG 6
 |||||
 Db 6 GGTGG 1
 |||||
 RESULT 14
 AAT96299
 ID AAT96299 standard; DNA; 5 BP.
 XX
 AC AAT96299;
 DT 25-MAR-2003 (revised)
 DT 08-APR-1998 (first entry)
 XX
 DE Fungal telomeric nucleic acid sequence.
 XX
 KW Detection; eukaryotic pathogen; telomeric nucleic acid sequence;
 KW telomerase activity; diagnosis; fungal infection; fungus; fungi;
 KW malarial infection; malaria; ss.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN US5695932-A.
 XX
 PD 09-DEC-1997.
 XX
 PF 13-MAY-1993; 93US-00060952.
 XX
 PR 13-MAY-1992; 92US-00882438.
 PR 24-MAR-1993; 93US-00038766.
 XX
 PA (UYCA-) UNIV CALIFORNIA SAN FRANCISCO.
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Blackburn EH, Shay J, Meeachern MJ, West MD, Wright W;
 XX
 DR WPI; 1998-041292/04.
 XX
 XX Detection of eukaryotic pathogens, especially fungal or Plasmodium spp. -
 PT by detecting telomerase activity.
 PT
 PS Claim 5; Col 81-82; 82pp; English.
 XX
 XX The present sequence can be used in a novel method for detecting a sample
 CC eukaryotic pathogen in a patient. The method comprises obtaining a sample

CC of somatic tissue or cells from the patient, determining if telomerase
 CC activity is present and correlating this with the presence of the
 CC pathogen. The method is useful for diagnosis of fungal infections,
 CC especially a fungus of the genus Candida, Kluyveromyces, Saccharomyces,
 CC Sporothrix, Coccidioides, Histoplasma, Blastomyces, Paracoccidioides,
 CC Cryptococcus, Aspergillus, Mucor or Rhizopus, or malarial infections,
 CC especially Plasmodium vivax, P. ovale, P. malariae or P. falciparum.
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 5 BP; 0 A; 0 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.2e+09;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTGG 5
 ||||
 Db 2 GTGG 5

RESULT 15

AAZ93601/c

ID AAZ93601 standard; DNA; 5 BP.

XX AC

XX AAZ93601;

DT 24-JUL-2000 (first entry)

XX Transcription factor binding site of tobacco gene promoter sequence.
 DE Regulatory sequence; meristem; genetic engineering; gene expression;
 XX crop protection; transgenic plant; resistance; tobacco;
 KW transcription factor; alcohol dehydrogenase-1; Adhi; ss.
 XX Synthetic.

OS Nicotiana acuminata.

XX WO200012713-A1.

XX 09-MAR-2000.

PF 26-AUG-1999; 99WO-AU0000692.

PR 26-AUG-1998; 98AU-00005498.

XX (UYQU) UNIV QUEENSLAND.

PI Mudge SR, Birch RG;

DR WPI; 2000-237875/20.

PT Meristem-expressible nucleic acid sequences, useful for producing
 PT transgenic plants with improved characteristics such as resistance to
 PT pathogens.

PS Example 9; Page 51; 102pp; English.

XX Isolated regulatory sequences of plants that are operable in dividing
 CC cells, in particular the meristem cells of plants are useful in the
 CC genetic engineering of plants. The regulatory sequences can be used to
 CC control the expression of foreign genes placed under their control. Such
 CC methods are useful for producing transgenic plants with altered shape
 CC and/or size. The sequences are also useful for producing transgenic
 CC plants capable of rapid regeneration following harvest or plants having
 CC improved resistance to pathogens. This sequence has been shown to bind a
 CC factor involved in the activation of the maize alcohol dehydrogenase-1
 CC gene (adh1). It occurs three times in the meristem regulatory sequence of
 CC Tobacco described in GENESEQ record AAZ93567

XX Sequence 5 BP; 1 A; 3 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.2e+09;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GTGG 6
 ||||
 Db 4 GTGG 1

RESULT 16

ABZ75666

ID ABZ75666 standard; DNA; 5 BP.

XX AC

XX ABZ75666;

DT 15-MAY-2003 (first entry)

XX Helicase-like transcription factor (HLTF) binding oligonucleotide.
 DE HLTF; carcinogenesis; hyperproliferative lesion; cytostatic; virucide;
 KW helicase-like transcription factor; telomerase reverse transcriptase;
 KW dermatological; gynaecological; TERT; gene therapy; cancer; ss.
 XX Synthetic.

XX WO2003002068-A2.

XX 09-JAN-2003.

PF 27-JUN-2002; 2002WO-US020757.

PR 27-JUN-2001; 2001US-0301384P.

PA (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.

XX Androphy EU, Doshi N, Delayew A;

XX WPI; 2003-210197/20.

PT Inhibiting carcinogenesis of a cell, especially useful for treating a
 PT human papilloma virus-mediated hyperproliferative lesion (warts) or
 PT cancer, by reducing the activity of helicase-like transcription factor in
 PT the cell.

XX Claim 15; Page 24; 36pp; English.

XX The invention relates to inhibiting carcinogenesis of a cell, or
 CC inhibiting growth of a cell in a human papillomavirus (HPV)-mediated
 CC hyperproliferative lesion. The method involves reducing the amount of
 CC helicase-like transcription factor (HLTF) in the cell or inhibiting the
 CC binding of endogenous HLTF to telomerase reverse transcriptase (TERT)
 CC promoter. The method is useful for inhibiting carcinogenesis of a cell,
 CC or inhibiting growth of a cell in an HPV-mediated hyperproliferative
 CC lesion. The method is particularly useful for treating cancer (especially
 CC cervical cancer), or hyperproliferative lesions (warts) caused by HPV.
 CC The method is also useful for diagnosing a neoplasm, or detecting the
 CC presence of a malignant tumour or a predisposition to developing the
 CC tumour. Sequences ABZ75663-669 represent specific examples of
 CC oligonucleotides that bind to endogenous HLTF, thereby preventing HLTF
 CC from binding to an intact hTERT promoter region

XX Sequence 5 BP; 1 A; 0 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 8; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.2e+09;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GTGG 6
 ||||
 Db 2 GTGG 5

RESULT 17

ABX49997

ID ABX49997 standard; DNA; 5 BP.

XX AC ABX49997;
XX DT 12-FEB-2003 (first entry)
XX DE Telomere length and/or telomerase activity related polynucleotide #20.
XX KW Cell proliferation; cell senescence; telomere length;
XX KW telomerase activity; cell replication; neoplasia; cancer;
KW age-related macular degeneration; Alzheimer's disease; atherosclerosis;
KW telomerase; telomerase inhibitor; immortalised cell; ss.
XX OS Synthetic.
XX PN US2002127634-A1.
XX PD 12-SEP-2002.
XX PF 05-JUN-1995; 95US-00463404.
XX PR 13-MAY-1992; 92US-00882438.
PR 24-MAR-1993; 93US-00038766.
PR 13-MAY-1993; 93US-00060952.
XX PA (WEST/) WEST M D.
PA (SHAY/) SHAY J.
PA (WRIG/) WRIGHT W.
PA (BLAC/) BLACKBURN E H.
XX PI West MD, Shay J, Wright W, Blackburn EH;
XX DR WPI; 2003-066896/06.
XX PT Treating condition associated with cell senescence or increased rate of
PT cell proliferation, by administering to cell an agent that derepresses
PT telomerase in the senescing cells or that reduces loss of telomere
PT length.
XX PS Disclosure; Page 44; 86pp; English.
XX CC The invention describes a method use for treating increased rate of
CC proliferation of a cell or extending the ability of a cell to replicate,
CC or treating a disease associated with cell senescence. The method
CC comprises administering an agent to reduce loss of telomere length within
CC the cell during proliferation or replication, or to derepress telomerase
CC in the senescing cells. The method is useful for treating a condition
CC associated with an increased rate of proliferation of a cell extending
CC the ability of a cell to replicate, or for treating a disease or
CC condition associated with cell senescence e.g. neoplasia. A second method
CC disclosed in the invention is useful for treating a condition associated
CC with an elevated level of telomerase activity within a cell e.g. cancer.
CC Also disclosed is a method useful for diagnosis of a condition associated
CC with an increased rate of proliferation in a cell in an individual e.g.
CC age-related macular degeneration, astrocytes associated with Alzheimer's
CC disease and endothelial cells associated with atherosclerosis. This
CC sequence represents a polynucleotide used in the study of telomere length
XX and telomerase activity described in the invention
SQ Sequence 5 BP; 0 A; 0 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 66.7%; Score 4; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGTC 5
DB 2 GGTC 5
RESULT 18
AAQ50333
ID AAQ50333 standard; RNA; 6 BP.
XX

AC AAQ50333;
DT 25-MAR-2003 (revised)
DT 28-JAN-1994 (first entry)
DE Ribozyme facilitator molecule F3.
DE KW Substrate; cleavage; ribozyme; target; facilitator; hybridisation;
KW magnesium ion; mammal; pathogenic organism; virus; ss.
XX OS Synthetic.
XX PN WO9315194-A1.
XX PD 05-AUG-1993.
XX PF 04-FEB-1993; 93WO-US0000783.
XX PR 04-FEB-1992; 92US-00830713.
XX PA (WORC-) WORCESTER FOUND EXPERIMENTAL BIOLOGY.
XX PI Goodchild J;
XX DR WPI; 1993-258674/32.
XX PT Increasing catalytic activity of ribozyme(s) - comprises reacting target
PT RNA with ribozyme and facilitating oligo:nucleotide, useful for treating
PT e.g. viral infections.
XX PS Claim 8; Fig 1; 41pp; English.
XX CC The sequences given in AAQ45991-92 and AAQ50332-35 represent facilitator
CC molecules and ribozymes described in the invention. These ribozymes
CC comprise a target RNA molecule, (see also AAQ45990) and a facilitator
CC molecule which hybridises to a sequence in the target RNA spaced upto 5
CC nucleotides from the sequence to which the ribozyme itself binds. The use
CC of a facilitator oligonucleotide with a ribozyme reduces the amount of
CC magnesium ion that is required by the ribozyme to catalytically cleave
CC target RNA. The rate of cleavage of target RNA by a ribozyme is
CC dramatically enhanced when target RNA is reacted with the ribozyme in the
CC presence of a facilitator molecule. More than one facilitator molecule
CC may be used, with one binding 3' and the other 5' of the ribozyme
CC molecule. The ribozymes and facilitator molecules may be used in
CC conjunction, to treat mammals infected with pathogenic organisms, such as
CC viral infections. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 6 BP; 1 A; 1 C; 3 G; 1 T; 0 U; 0 Other;
Query Match 66.7%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGCT 4
DB 2 GGCT 5
RESULT 19
AAQ50319/C
ID AAQ50319 standard; DNA; 6 BP.
XX AC AAQ50319;
XX DT 16-OCT-1997 (first entry)
XX DE Oligo HCV-215, targetted to HCV mRNA position +235 to +240.
XX KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
KW inhibition; replication; expression; detection; chronic hepatitis;
KW acute hepatitis; hepatocarcinoma; ss.
XX OS Synthetic.

```

XX Key Location/Qualifiers
FH modified_base 1..6
FT /*tag= a
FT /note= "Comprises phosphorothioate linkages"
XX
XX WO96399500-A2.
XX
PD 12-DEC-1996.
XX
PF 04-JUN-1996; 96WO-EP002427.
XX
PR 06-JUN-1995; 95US-00471968.
XX
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
PA (HYBR-) HYBRIDON INC.
XX
PI Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
PI Roberts PC, Walther DM, Wolfe JL;
XX
WPI; 1997-043122/04.
XX
Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
the treatment and detection of HCV infection, esp. hepatitis and hepato-
carcinoma.
XX
Claim 1; Page 18; 100pp; English.
XX
The sequences given in AAT80211-382 represent synthetic oligonucleotides
which are complementary to a portion of the 5' untranslated region (UTR)
of hepatitis C virus (HCV). These sequences may be used in a
pharmaceutical composition for the control or prevention of HCV
infection. They may be used to inhibit replication or expression of HCV
or for detecting the presence of HCV in a sample. They may be used to
inhibit HCV replication in a cell and are therefore useful in the
treatment of HCV infections such as chronic and acute hepatitis and
hepatocarcinoma
XX
Sequence 6 BP; 1 A; 3 C; 2 G; 0 T; 0 U; 0 Other;
XX
Query Match 66.7%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGT 4
DB 4 GGGT 1
XX
RESULT 20
AAT80320
ID AAT80320 standard; DNA; 6 BP.
XX
AC AAT80320;
XX
DT 16-OCT-1997 (first entry)
XX
DE Oligo HCV-218, targeted to HCV mRNA position +240 to +245.
XX
KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
KW inhibition; replication; expression; detection; chronic hepatitis;
KW acute hepatitis; hepatocarcinoma; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..6
FT /*tag= a
FT /note= "Comprises phosphorothioate linkages"
XX
XX WO96399500-A2.
XX
PD 12-DEC-1996.
XX
PF 04-JUN-1996; 96WO-EP002427.
XX
PR 06-JUN-1995; 95US-00471968.
XX
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
PA (HYBR-) HYBRIDON INC.
XX
PI Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
PI Roberts PC, Walther DM, Wolfe JL;
XX
WPI; 1997-043122/04.
XX
Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
the treatment and detection of HCV infection, esp. hepatitis and hepato-
carcinoma.
XX
Claim 1; Page 18; 100pp; English.
XX
The sequences given in AAT80211-382 represent synthetic oligonucleotides
which are complementary to a portion of the 5' untranslated region (UTR)
of hepatitis C virus (HCV). These sequences may be used in a
pharmaceutical composition for the control or prevention of HCV
infection. They may be used to inhibit replication or expression of HCV
or for detecting the presence of HCV in a sample. They may be used to
inhibit HCV replication in a cell and are therefore useful in the
treatment of HCV infections such as chronic and acute hepatitis and
hepatocarcinoma
XX
Sequence 6 BP; 2 A; 0 C; 3 G; 1 T; 0 U; 0 Other;
XX
Query Match 66.7%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGT 4
DB 2 GGGT 5
XX
RESULT 21
AAV61659/c
ID AAV61659 standard; DNA; 6 BP.
XX
AC AAV61659;
XX
DT 03-DEC-1998 (first entry)
XX
DE Fusarium sp. 18S rRNA DNA fragment #3.
XX
KW 18S rRNA; detection; identification; fungus; ss.
XX
OS Fusarium sp.
XX
PN JP10234380-A.
XX
PD 08-SEP-1998.
XX
PF 28-FEB-1997; 97JP-00062104.
XX
PR 28-FEB-1997; 97JP-00062104.
XX
PA (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.
XX
WPI; 1998-535034/46.
XX
Use of oligo:nucleotide for detecting and identification of fungus of
Fusarium genus - as primer or probe to detect of identify microbes
rapidly and exactly.
XX
Claim 1; Page 6; 20pp; Japanese.
XX
AAV61657-V61664 are fragments of a Fusarium sp. 18S rRNA gene which are

```

CC used in a method for the detection and identification of a fungus of
 CC Fusarium genus. The process can be used to detect or identify microbes
 CC rapidly and exactly
 XX
 SQ Sequence 6 BP; 2 A; 4 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 66.7%; Score 4; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGT 4
 Db |||||
 4 GGGT 1

RESULT 22
 AAZ89322/C
 ID AAZ89322 standard; DNA; 6 BP.
 XX
 AC AAZ89322;
 XX
 DT 13-JUN-2000 (first entry)
 XX
 DE Human UCP3 promoter fragment #2.
 XX
 XX UCP3; uncoupling protein 3; human; promoter; fat cell; transcription;
 KW fat metabolism; ss.
 XX
 OS Homo sapiens.
 XX
 PN DE19838837-A1.
 XX
 PD 02-MAR-2000.
 XX
 PF 27-AUG-1998; 98DE-01038837.
 XX
 PR 27-AUG-1998; 98DE-01038837.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 PA (NOVO) NOVO-NORDISK AS.
 XX
 XX Esterbauer H, Oberkofler H, Patsch W;
 XX
 DR WPI; 2000-272214/24.
 XX
 PT Recombinant fat and muscle tissue specific uncoupling protein 3 promoters
 PT useful for identifying UCP3 modulators.
 XX
 PS Claim 2; Page 10; 38pp; German.
 XX
 CC This invention describes novel recombinant DNA molecules containing an
 CC uncoupling protein 3 (UCP-3) promoter DNA sequence active in fat cells
 CC but not functional in muscle cells or vice versa. The recombinant DNA
 CC molecules are useful for transcription of genes and, with host cells, to
 CC test for substances that can influence transcription. They can also be
 CC used to identify modulators of UCP3 promoters. UCP3 plays a role in fat
 CC metabolism and control of the promoter is useful in combating diseases
 CC with inappropriate fat tissue metabolism. This sequence represents a
 CC fragment of the human UCP-3 promoter which is used to illustrate the
 CC method of the invention
 XX
 SQ Sequence 6 BP; 1 A; 4 C; 0 G; 1 T; 0 U; 0 Other;
 Query Match 66.7%; Score 4; DB 3; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GGTC 5
 Db |||||
 4 GGTC 1

RESULT 23

AAZ893241
 ID AAZ893241 standard; DNA; 6 BP.
 XX
 AC AAZ893241;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE PCR primer 6B2-Hgb used to produce a population of hybrid DNA molecules.
 KW Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;
 KW lambda integrase; therapeutic; ss.
 XX
 OS Bacteriophage lambda.
 OS Synthetic.
 XX
 PN WO200142509-A1.
 XX
 PD 14-JUN-2001.
 XX
 PF 11-DEC-2000; 2000WO-US033546.
 XX
 PR 10-DEC-1999; 99US-0169983P.
 PR 09-MAR-2000; 2000US-0188020P.
 XX
 XX (CHEO/) CHEO D.
 PA (BRAS/) BRASCH M A.
 PA (TEMP/) TEMPLE G F.
 PA (HART/) HARTLEY J L.
 PA (BYRD/) BYRD D R N.
 XX
 PI Cheo D, Brasch MA, Temple GF, Hartley JL, Byrd DRN;
 XX
 DR WPI; 2001-356174/37.
 XX
 PT Producing hybrid nucleic acids, useful for expressing novel therapeutic
 PT polypeptides, by mixing the same or different nucleic acids having one or
 PT more recombination sites in the presence of recombination proteins, e.g.
 PT Cre.
 XX
 PS Example 8; Page 213; 357pp; English.
 XX
 CC AAS06174-AAS06322 represent Bacteriophage lambda att recombination site
 CC nucleic acid sequences, and PCR primers of the invention. The att
 CC sequences are recognised by the recombination protein lambda integrase
 CC (Int). The invention is a new method of producing a population of hybrid
 CC nucleic acids comprising mixing at least a first population of nucleic
 CC acids comprising one or more recombination sites with at least one target
 CC nucleic acid comprising one or more recombination sites and causing some
 CC or all of the nucleic acids to recombine with all or some of the target
 CC nucleic acids. The method is useful for producing a population of hybrid
 CC nucleic acids which may be the same or different. The nucleic acids may
 CC be used to express therapeutic proteins or peptides and they may also be
 CC used to create novel fusion proteins by expressing different sequences
 CC linked to each other. The method allows simultaneous cloning of two or
 CC more different nucleic acids
 XX
 SQ Sequence 6 BP; 0 A; 1 C; 3 G; 2 T; 0 U; 0 Other;
 Query Match 66.7%; Score 4; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGT 4
 Db |||||
 3 GGGT 6

RESULT 24
 ABK72534
 ID ABK72534 standard; DNA; 6 BP.
 XX
 AC ABK72534;
 XX

DT 13-AUG-2002 (first entry)
 XX Human OPAL gene, exon/intron junction #1.
 DE
 XX
 XX Human; ophthalmological; OPAL; autosomal dominant optic atrophy; ADOA;
 KW gene; da.
 XX
 XX Homo sapiens.
 OS
 XX WO200227022-A2.
 PN
 XX 04-APR-2002.
 PD
 XX 26-SEP-2001; 2001WO-GB004284.
 XX
 XX 26-SEP-2000; 2000GB-00023555.
 PF
 XX (UNLO) UNIV COLLEGE LONDON.
 PA (UYEY-) UNIV EYE HOSPITAL.
 XX
 XX Bhattacharya S, Wisinger B, Alexander C, Votruba M;
 PI WPI; 2002-416484/44.
 XX
 XX Novel human normal or mutant OPAL (the predominant locus for autosomal
 PT dominant optic atrophy (ADOA)) polypeptides and the OPAL gene, useful in
 PT the diagnosis and treatment of autosomal dominant optic atrophy ADOA.
 XX
 XX Disclosure; Fig 12; 75pp; English.
 PS
 XX The invention relates to an isolated human normal or mutant OPAL (the
 CC predominant locus for autosomal dominant optic atrophy (ADOA))
 CC polypeptide (I), characterised by a molecular weight of about 112 kDa,
 CC and substantially free of other human proteins. Also described is the DNA
 CC (II) encoding (I). (I) and (II) are useful as a medicament, for the
 CC treatment of a medical condition resulting from a defect in the OPAL
 CC gene, which results in autosomal dominant optic atrophy. The nucleic acid
 CC and antibodies to (I) are useful in a variety of hybridisation and
 CC immunological assays to screen for, and to detect the presence of, either
 CC a normal or a defective OPAL gene or gene product. ABK72533-ABK72593
 CC represent the human OPAL gene and intron/exon splice junctions
 XX
 XX Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 66.7%; Score 4; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0;
 QY 3 GTGG 6
 Db |||||
 3 GTGG 6
 RESULT 25
 ABS77550
 ID ABS77550 standard; DNA; 6 BP.
 XX
 XX ABS77550;
 AC
 XX 13-DEC-2002 (first entry)
 DT
 XX Angiogenesis inhibitory oligonucleotide #34.
 DE
 XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
 KW rubecosis; Osler-Webber Syndrome; myocardial angiogenesis;
 KW plaque neovascularisation; telangiectasia; haemophilic joint;
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
 KW scleroderma; hypertrophic scar.
 XX
 XX Synthetic.
 OS
 WO200253141-A2.
 PN
 XX 11-JUL-2002.
 PD
 XX 14-DEC-2001; 2001WO-US048458.
 PF
 XX 14-DEC-2000; 2000US-0255534P.
 PR
 XX (COLE-) COLEY PHARM GROUP INC.
 PA
 XX Bratzler RL;
 XX
 XX WPI; 2002-566690/60.
 DR
 XX Inhibiting angiogenesis in a subject, involves administering at least one
 PT antiangiogenic nucleic acid molecule to the subject.
 PT
 XX Claim 2; Page 20; 276pp; English.
 PS
 XX The invention relates to inhibiting angiogenesis in a subject, comprising
 CC administering at least one antiangiogenic nucleic acid molecule. Also
 CC included is a kit comprising a first container housing the antiangiogenic
 CC nucleic acids, and instructions for administering them to a subject
 CC having a condition characterised by unwanted angiogenesis. The method is
 CC useful for inhibiting angiogenesis associated with solid tumour growth,
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
 CC rubecosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
 CC acid of the invention
 XX
 XX Sequence 6 BP; 0 A; 1 C; 3 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 66.7%; Score 4; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0;
 QY 3 GTGG 6
 Db |||||
 3 GTGG 6
 RESULT 26
 ABS65903/c
 ID ABS65903 standard; DNA; 6 BP.
 XX
 XX ABS65903;
 AC
 XX 15-NOV-2002 (first entry)
 DT
 XX Inhibitory oligonucleotide specific for hepatitis C virus #109.
 DE
 XX Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;
 KW non-B hepatitis; acute hepatitis; chronic hepatitis;
 KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;
 KW gene therapy; ss.
 XX
 XX Synthetic.
 OS
 XX US2002081577-A1.
 PN
 XX 27-JUN-2002.
 PD
 XX 02-JUL-1997; 97US-00887505.
 PF
 XX 06-JUN-1995; 95US-00471968.
 PR 02-JUL-1996; 96US-0021104P.
 XX
 XX (KILK/) KILKUSKIE R L.

PA (FRAN/) FRANK B L.
PA (GOOD/) GOODCHILD J.
PA (WOLF/) WOLFE J L.
PA (ROBE/) ROBERTS P C.
PA (HAML/) HAMLIN H A.
PA (ROBE/) ROBERTS N A.
PA (WALT/) WALTHER D M.
XX
XX Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;
PI Hamlin HA, Roberts NA, Walther DM;
XX
XX WPI; 2002-537132/57.
XX
XX Synthetic oligonucleotides complementary to a portion of the 5'
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and
PT treating HCV infections and hepatocellular carcinoma.
XX
XX Claim 1; Page 6; 74pp; English.
XX
XX The invention describes synthetic oligonucleotides complementary to a
CC portion of the 5' untranslated region of hepatitis C virus. The
CC oligonucleotides may be used in methods for controlling, preventing, and
CC treating hepatitis C virus infection, in antisense technology and gene
CC therapy, and of detecting the presence of hepatitis C virus in a sample.
CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded
CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non
CC -B, acute and chronic hepatitis, and has been associated with
CC hepatocellular carcinoma. The invention describes methods and kits for
CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic
CC acid and protein, and for treating HCV infections. This sequence
CC represents a synthetic oligonucleotide used for inhibiting HCV
CC replication and expression of HCV
XX
XX Sequence 6 BP; 1 A; 3 C; 2 G; 0 T; 0 U; 0 Other;
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Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGT 4
Db ||||
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RESULT 27
ABS65904
ID ABS65904 standard; DNA; 6 BP.
XX
XX ABS65904;
AC
XX 15-NOV-2002 (first entry)
DT
XX Inhibitory oligonucleotide specific for hepatitis C virus #110.
DE
XX Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;
KW non-B hepatitis; acute hepatitis; chronic hepatitis;
KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;
KW gene therapy; ss.
XX
XX Synthetic.
OS
XX US2002081577-A1.
PN
XX 27-JUN-2002.
PD
XX 02-JUL-1997; 97US-00887505.
XX
XX 06-JUN-1995; 95US-00471968.
PR
XX 02-JUL-1996; 96US-0021104P.
XX
XX (KILK/) KILKUSKIE R L.
PA (FRAN/) FRANK B L.
PA (GOOD/) GOODCHILD J.

PA (WOLF/) WOLFE J L.
PA (ROBE/) ROBERTS P C.
PA (HAML/) HAMLIN H A.
PA (ROBE/) ROBERTS N A.
PA (WALT/) WALTHER D M.
XX
XX Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;
PI Hamlin HA, Roberts NA, Walther DM;
XX
XX WPI; 2002-537132/57.
XX
XX Synthetic oligonucleotides complementary to a portion of the 5'
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and
PT treating HCV infections and hepatocellular carcinoma.
XX
XX Claim 1; Page 6; 74pp; English.
XX
XX The invention describes synthetic oligonucleotides complementary to a
CC portion of the 5' untranslated region of hepatitis C virus. The
CC oligonucleotides may be used in methods for controlling, preventing, and
CC treating hepatitis C virus infection, in antisense technology and gene
CC therapy, and of detecting the presence of hepatitis C virus in a sample.
CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded
CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non
CC -B, acute and chronic hepatitis, and has been associated with
CC hepatocellular carcinoma. The invention describes methods and kits for
CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic
CC acid and protein, and for treating HCV infections. This sequence
CC represents a synthetic oligonucleotide used for inhibiting HCV
CC replication and expression of HCV
XX
XX Sequence 6 BP; 2 A; 0 C; 3 G; 1 T; 0 U; 0 Other;
SQ
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Best Local Similarity 100.0%; Pred. No. 9.7e+08;
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QY 1 GGGT 4
Db ||||
2 GGGT 5
RESULT 28
ABK30087/C
ID ABK30087 standard; DNA; 6 BP.
XX
XX ABK30087;
AC
XX 23-APR-2002 (first entry)
DT
XX Beta-lactamase promoter, -35 to -30 region mutant M21.
DE
XX
XX Cyclin D1 promoter; CD40L promoter; hepatitis B virus promoter;
KW HBV promoter; vancomycin-resistant enterococci promoter; VRE promoter;
KW vanH promoter; androgen receptor promoter; AR promoter;
KW human epidermal growth factor receptor 2 promoter; her2 promoter;
KW beta lactamase promoter; Bla promoter; transgene; cancer; breast cancer;
KW colon cancer; immunological disorder; prostate cancer; cytostatic;
KW autoimmune disease; HBV pre-S promoter; HBV-X promoter;
KW Enterococcus infection; immunosuppressive; antibacterial; antiviral;
KW gene expression modulator; multiple sclerosis; MS;
KW chronic hepatic insufficiency; cirrhosis; hepatocellular carcinoma;
KW systematic lupus erythematosus; SLE; graft-vs-host disease; GVHD;
KW familial adenomatous polyposis; rheumatoid arthritis; PCR; primer;
KW mutant; transgenic; ds.
XX
XX Escherichia coli.
OS
XX WO200194600-A2.
PN
XX 13-DEC-2001.
PD
XX 06-JUN-2001; 2001WO-US018343.
PF

XX	06-JUN-2000; 2000US-0209549P.	PD	13-MAR-2003.
PR	(GENE-) GENELABS TECHNOLOGIES INC.	XX	29-MAR-2002; 2002US-00112653.
PA	Kim JP, Starr DB, Tam AW, Laurance ME, Michelotti EF;	PR	29-MAR-2001; 2001US-0279642P.
XX	PI Velligan MD, Latour DR, Thomas RL, Kongpachith A, Sheppard LT;	XX	(KRIE/) KRIEG A M.
PI	Lim MY, Bruce TW;	PA	(BERG/) BERG D J.
XX	WPI; 2002-130595/17.	XX	Krieg AM, Berg DJ;
DR		PI	WPI; 2003-521815/49.
XX	New nucleic acid regulatory sequences, which are able to regulate	XX	Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT	expression of a gene operably linked to a promoter, useful for regulating	XX	allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT	the expression of transgenes and for treating e.g., cancer and	PT	disease by administering an immunostimulatory nucleic acid.
PT	immunological diseases.	PT	
XX	Example 7; Page 57; 95pp; English.	XX	Disclosure; Page 9; 229pp; English.
PS		PS	
CC	The invention describes an isolated nucleic acid regulatory sequence for	CC	The invention describes a method of treating non-allergic inflammatory
CC	a cyclin D1 promoter, a CD40L promoter, vancomycin-resistant enterococci	CC	disease comprising administering to a subject having or at risk of
CC	(VRE) promoter, an HBV promoter, androgen receptor (AR) promoter, Human	CC	developing a non-allergic inflammatory disease an immunostimulatory
CC	epidermal growth factor receptor 2 (HER2) promoter, or a beta lactamase	CC	nucleic acid for prevention or treatment of the disease. The method is
CC	(Bla) promoter. Transcription regulatory sequences may be used to	CC	useful for treating non-allergic inflammatory diseases, such as
CC	regulate expression of the endogenous, autologous or heterologous genes	CC	psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC	operably linked to the promoter, and may be incorporated into	CC	inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC	heterologous nucleic acid constructs for use in regulated expression of	CC	This sequence represents an immunostimulatory nucleic acid
CC	transgenes. Regulated expression of cyclin D1 can be used in cancer	XX	
CC	therapies, such as breast, colon or pancreatic cancers and familial	XX	Sequence 6 BP; 0 A; 1 C; 3 G; 2 T; 0 U; 0 Other;
CC	adenomatous polyposis. Regulation of the activity of CD40L gene promoter	SQ	
CC	may be used in the treatment of immunological disorders, such as	Query Match	66.7%; Score 4; DB 9; Length 6;
CC	autoimmune diseases e.g. multiple sclerosis (MS), systemic lupus	Best Local Similarity	100.0%; Pred. No. 9.7e+08;
CC	erythematosus (SLE), graft-vs-host disease (GVHD) and rheumatoid	Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC	arthritis. Regulated expression of genes under the control of the HBV		
CC	(hepatitis B)-specific core, pre-S and X promoters can be used in the	Qy	3 GTGG 6
CC	therapy of HBV disease, chronic hepatic insufficiency, cirrhosis,	Db	
CC	hepatocellular carcinoma, and in the regulated expression of liver cell-		3 GTGG 6
CC	specific genes. Regulated expression of the vavh gene promoter can be		
CC	used in treatment of Enterococcus infection, while regulated expression		
CC	of the androgen receptor gene can be used in the treatment of prostate		
CC	cancer. This sequence represents a mutated promoter region used in the		
CC	invention to determine the regulatory regions involved in gene		
CC	expression, described in the method of the invention		
XX		RESULT 30	
SQ	Sequence 6 BP; 1 A; 3 C; 2 G; 0 T; 0 U; 0 Other;	ADD71358/c	
		ID	ADD71358 standard; DNA; 6 BP.
		XX	AC ADD71358;
		XX	15-JAN-2004 (first entry)
		DT	Human sclerosteosis (SOST) gene regulatory region downstream E box.
		DE	ds; human; sclerosteosis; SOST; gene regulatory region;
		XX	bone degenerative diseases; bone formation; non-union fracture;
		KW	bone cavity; tumour resection; fresh fracture;
		KW	cranial/facial abnormality; spinal fusion; cancer; arthritis;
		KW	osteoarthritis; osteoporosis; bone/prosthesis in-growth;
		KW	dental implant/bone integration.
		XX	Homo sapiens.
		OS	
		XX	US2003186915-A1.
		PN	02-OCT-2003.
		XX	11-FEB-2003; 2003US-00365737.
		PF	11-FEB-2002; 2002US-0356212P.
		PR	(PANY/) PAN Y.
		XX	(SEVE/) SEVETSON B R.
		PA	(DERR/) DERRY J M J.
		PA	
		XX	Pan Y, Sevetson BR, Derry JMJ;
		PI	WPI; 2003-831265/77.
		XX	
		DR	

XX New nucleic acid from a regulatory region of the SOST gene, useful for
PT identifying agents which affect transcription of an operably linked gene,
PT which are potentially useful for treating bone degenerative diseases such
PT as osteoporosis.
XX
PS Example 3; SEQ ID NO 5; 20pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule comprising a
CC regulatory polynucleotide. The method is useful for screening for agents
CC that affect expression of a gene operably linked to the nucleic acid.
CC Identified agents are potentially useful in treating bone degenerative
CC diseases and in promoting bone formation. The bone degenerative disease
CC or disorder is especially a non-union fracture, bone cavity, tumour
CC resection, fresh fracture, cranial/facial abnormality, spinal fusion,
CC cancer, arthritis, osteoarthritis and osteoporosis. The nucleic acid is
CC useful in the methods. The treatment methods are also useful for
CC promoting or inhibiting bone in-growth into a prosthesis, and for
CC promoting the integration of dental implants into bone. The present
CC sequence represents the human sclerosteosis (SOST) gene regulatory region
CC downstream E box.
XX
SQ Sequence 6 BP; 1 A; 3 C; 1 G; 1 T; 0 U; 0 Other;
Query Match 66.7%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGTG 5
Db ||||
4 GGTG 1
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Job time : 190.4 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 21:47:48 ; Search time 738.2 Seconds
(without alignments)
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Title: US-09-735-363A-25

Perfect score: 6
Sequence: 1 999tgg 6

Scoring table: IDENTITY NUC

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Total number of hits satisfying chosen parameters: 4754

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Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

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1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
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12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	6	100.0	6	6	CQ756501 Sequence
C 3	6	100.0	6	6	CQ757982 Sequence
C 4	6	100.0	6	6	CQ758739 Sequence
C 5	6	100.0	6	6	AX175261 Sequence
C 6	6	100.0	6	6	AX175310 Sequence
C 7	6	100.0	6	6	AX175315 Sequence
C 8	6	100.0	6	6	AX189456 Sequence
C 9	6	100.0	6	6	AX743309 Sequence
C 10	6	100.0	6	6	AX743311 Sequence
C 11	6	100.0	6	6	AX743313 Sequence
C 12	6	100.0	6	6	AX743315 Sequence
C 13	6	100.0	6	6	AX764782 Sequence
C 14	6	100.0	6	6	AX765539 Sequence
C 15	6	100.0	6	6	AX816714 Sequence
C 16	5	83.3	5	6	CQ868990 Sequence
C 17	5	83.3	5	6	CQ869027 Sequence
C 18	5	83.3	5	6	CQ869139 Sequence
C 19	5	83.3	5	6	CQ869176 Sequence

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	27	5	83.3	5	6	CQ755772 Sequence
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	29	5	83.3	5	6	CQ755836 Sequence
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	32	5	83.3	5	6	CQ757964 Sequence
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	35	5	83.3	5	6	CQ758064 Sequence
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	86	4	66.7	6	6	CQ755759 Sequence
	87	4	66.7	6	6	CQ755765 Sequence
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	92	4	66.7	6	6	CQ755817 Sequence

AX175261
LOCUS AX175261 6 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 25 from Patent WO0144465.
ACCESSION AX175261
VERSION AX175261.1 GI:14598629
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 6)
AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 25 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
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Db 1 GGGTGG 6
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AX175310
LOCUS AX175310 6 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 74 from Patent WO0144465.
ACCESSION AX175310
VERSION AX175310.1 GI:14598678
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 6)
AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 74 21-JUN-2001;
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LOCUS AX175315 6 bp DNA linear PAT 03-JUL-2001
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ACCESSION AX175315
VERSION AX175315.1 GI:14598683
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 6)
AUTHORS Phillips,N.C. and Filion,M.C.

AX189456
LOCUS AX189456 6 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from Patent WO0147561.
ACCESSION AX189456
VERSION AX189456.1 GI:15142968
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 6)
AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Hyaluronic acid in the treatment of cancer
JOURNAL Patent: WO 0147561-A 1 05-JUL-2001;
Bioniche Life Sciences Inc. (CA)
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DEFINITION Sequence 1 from Patent WO03028764.
ACCESSION AX743309
VERSION AX743309.1 GI:30577235
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Phillips,N.C., Filion,M.C. and Herrera-Gayol,A.C.
TITLE Therapeutically useful triethyleneglycol cholesteryl
oligonucleotides
JOURNAL Patent: WO 03028764-A 1 10-APR-2003;
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VERSION            AX743311.1 GI:30577237
KEYWORDS            .
SOURCE              synthetic construct
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REFERENCE           1
AUTHORS             Phillips,N.C., Filion,M.C. and Herrera-Gayol,A.C.
TITLE              Therapeutically useful triethyleneglycol cholesteryl
                   oligonucleotides
JOURNAL             Patent: WO 03028764-A 3 10-APR-2003;
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RESULT 11
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DEFINITION         Sequence 5 from Patent WO03028764.
ACCESSION          AX743313
VERSION            AX743313.1 GI:30577239
KEYWORDS            .
SOURCE              synthetic construct
ORGANISM            other sequences; artificial sequences.
REFERENCE           1
AUTHORS             Phillips,N.C., Filion,M.C. and Herrera-Gayol,A.C.
TITLE              Therapeutically useful triethyleneglycol cholesteryl
                   oligonucleotides
JOURNAL             Patent: WO 03028764-A 5 10-APR-2003;
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    |||||
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RESULT 12
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VERSION            AX743315.1 GI:30577241
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ORGANISM            other sequences; artificial sequences.
REFERENCE           1
AUTHORS             Phillips,N.C., Filion,M.C. and Herrera-Gayol,A.C.
TITLE              Therapeutically useful triethyleneglycol cholesteryl
                   oligonucleotides
JOURNAL             Patent: WO 03028764-A 7 10-APR-2003;
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VERSION            AX764782.1 GI:32258990
KEYWORDS            .
SOURCE              synthetic construct
ORGANISM            other sequences; artificial sequences.
REFERENCE           1
AUTHORS             Otte,A.P. and Kruckeberg,A.L.
TITLE              Dna sequences comprising gene transcription regulatory qualities
                   and methods for detecting and using such dna sequences
JOURNAL             Patent: WO 03004704-A 252 16-JAN-2003;
FEATURES            Chromagenics B.V. (NL)
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                    /note="oligonucleotide patterns over-represented in STAR
                    elements"

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Query Match          100.0%; Score 6; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTGG 6
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Db 6 GGGTGG 1

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RESULT 14
AX765539/c
LOCUS AX765539 6 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 1009 from Patent WO03004704.
ACCESSION AX765539
VERSION AX765539.1 GI:32259747
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Otte, A.P. and Kruckeberg, A.L.
TITLE Dna sequences comprising gene transcription regulatory qualities
and methods for detecting and using such dna sequences
JOURNAL Patent: WO 03004704-A 1009 16-JAN-2003;
Chromagenics B.V. (NL)
FEATURES
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/organism="synthetic construct"
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/note="Dyad patterns over-represented in STAR elements"
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Query Match 100.0%; Score 6; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGTGG 6
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Db 6 GGGTGG 1
RESULT 15
AX816714
LOCUS AX816714 6 bp DNA linear PAT 09-DEC-2003
DEFINITION Sequence 2 from Patent WO02085340.
ACCESSION AX816714
VERSION AX816714.1 GI:39647043
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Filion, M.C. and Phillips, N.C.
TITLE Oligonucleotide compositions and their use to induce
differentiation of cells
JOURNAL Patent: WO 02085340-A 2 31-OCT-2002;
Bioniche Life Sciences Inc. (CA)
FEATURES
source
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/db_xref="taxon:32630"
/note="Oligonucleotide"
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Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGTGG 6
|||||
Db 1 GGGTGG 6
RESULT 16
CQ868990
LOCUS CQ868990 5 bp DNA linear PAT 13-SEP-2004
DEFINITION Sequence 144 from Patent WO2004074429.
ACCESSION CQ868990
VERSION CQ868990.1 GI:51998917
KEYWORDS

synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS freskg Rd, P.O., Gouliaev, A.H., Thisted, T. and Olsen, E.K.
TITLE Method for producing second-generation library
JOURNAL Patent: WO 2004074429-A 144 02-SEP-2004;
Nuevolution A/S (DK)
FEATURES
source
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/db_xref="taxon:32630"
/note="synthetic construct"
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 9.7e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGTGG 6
|||||
Db 1 GGTGG 5
RESULT 17
CQ869027
LOCUS CQ869027 5 bp DNA linear PAT 13-SEP-2004
DEFINITION Sequence 181 from Patent WO2004074429.
ACCESSION CQ869027
VERSION CQ869027.1 GI:51998954
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS freskg Rd, P.O., Gouliaev, A.H., Thisted, T. and Olsen, E.K.
TITLE Method for producing second-generation library
JOURNAL Patent: WO 2004074429-A 181 02-SEP-2004;
Nuevolution A/S (DK)
FEATURES
source
1..5
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic construct"
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 9.7e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTGG 5
|||||
Db 1 GGTGG 5
RESULT 18
CQ869139
LOCUS CQ869139 5 bp DNA linear PAT 13-SEP-2004
DEFINITION Sequence 293 from Patent WO2004074429.
ACCESSION CQ869139
VERSION CQ869139.1 GI:51999066
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS freskg Rd, P.O., Gouliaev, A.H., Thisted, T. and Olsen, E.K.
TITLE Method for producing second-generation library
JOURNAL Patent: WO 2004074429-A 293 02-SEP-2004;
Nuevolution A/S (DK)
FEATURES
Location/Qualifiers

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source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic construct"

ORIGIN
Query Match
Best Local Similarity 83.3%; Score 5; DB 6; Length 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGTGG 6
    |||||
Db 1 GGTGG 5

RESULT 19
CQ869176
LOCUS
DEFINITION
Sequence 330 from Patent WO2004074429. PAT 13-SEP-2004
ACCESSION
CQ869176
VERSION
CQ869176.1 GI:51999103
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
freskg Rd,P.O., Goulliaev,A.H., Thisted,T. and Olsen,E.K.
TITLE
Method for producing second-generation library
JOURNAL
Patent: WO 2004074429-A 330 02-SEP-2004;
Nuevolution A/S (DK)
FEATURES
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic construct"

ORIGIN
Query Match
Best Local Similarity 83.3%; Score 5; DB 6; Length 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGG 5
    |||||
Db 1 GGTGG 5

RESULT 20
AX046167/c
LOCUS
DEFINITION
Sequence 46 from Patent WO0066734. PAT 24-NOV-2000
ACCESSION
AX046167
VERSION
AX046167.1 GI:11344250
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 5)
AUTHORS
Lee,M.E. and Yet,S.F.
TITLE
Methods of treating hypertension
JOURNAL
Patent: WO 0066734-A 46 09-NOV-2000;
PRESIDENT AND FELLOWS OF HARVARD COLLEGE (US)
FEATURES
Location/Qualifiers
source
1..5
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="artif. peptide"

ORIGIN
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Best Local Similarity 83.3%; Score 5; DB 6; Length 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGG 5
    |||||
Db 1 GGTGG 5

RESULT 21
AX175296
LOCUS
DEFINITION
Sequence 60 from Patent WO0144465. PAT 03-JUL-2001
ACCESSION
AX175296
VERSION
AX175296.1 GI:14598664
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 5)
AUTHORS
Phillips,N.C. and Filion,M.C.
TITLE
Therapeutically useful synthetic oligonucleotides
JOURNAL
Patent: WO 0144465-A 60 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
Location/Qualifiers
source
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/organism="synthetic construct"
/mol_type="genomic DNA"
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ORIGIN
Query Match
Best Local Similarity 83.3%; Score 5; DB 6; Length 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGTGG 6
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Db 1 GGTGG 5

RESULT 22
AX175297
LOCUS
DEFINITION
Sequence 61 from Patent WO0144465. PAT 03-JUL-2001
ACCESSION
AX175297
VERSION
AX175297.1 GI:14598665
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 5)
AUTHORS
Phillips,N.C. and Filion,M.C.
TITLE
Therapeutically useful synthetic oligonucleotides
JOURNAL
Patent: WO 0144465-A 61 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
Location/Qualifiers
source
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/organism="synthetic construct"
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ORIGIN
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Best Local Similarity 83.3%; Score 5; DB 6; Length 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGG 5
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Db 1 GGTGG 5

RESULT 23
AX805865
LOCUS
DEFINITION
Sequence 11 from Patent WO03060163. PAT 25-NOV-2003

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Otte,A.P., Kruckeberg,A.L. and Satijn,D.P. Means and methods for regulating gene expression Patent: WO 2003106674-A 227 24-DEC-2003; Chromagenics B.V. (NL) Location/Qualifiers 1. .6 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="oligonucleotide patterns over-represented in STAR elements"		Otte,A.P., Kruckeberg,A.L. and Satijn,D.P. Means and methods for regulating gene expression Patent: WO 2003106674-A 227 24-DEC-2003; Chromagenics B.V. (NL) Location/Qualifiers 1. .6 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="oligonucleotide patterns over-represented in STAR elements"	
Otte,A.P., Kruckeberg,A.L. and Satijn,D.P. Means and methods for regulating gene expression Patent: WO 2003106674-A 227 24-DEC-2003; Chromagenics B.V. (NL) Location/Qualifiers 1. .6 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="oligonucleotide patterns over-represented in STAR elements"		Otte,A.P., Kruckeberg,A.L. and Satijn,D.P. Means and methods for regulating gene expression Patent: WO 2003106674-A 227 24-DEC-2003; Chromagenics B.V. (NL) Location/Qualifiers 1. .6 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="oligonucleotide patterns over-represented in STAR elements"	

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/mol_type="unassigned DNA"
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elements"

ORIGIN
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Best Local Similarity 83.3%; Score 5; DB 6; Length 6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGG 5
Db 5 GGTGG 1

RESULT 28
CQ755826/c
LOCUS
DEFINITION
Sequence 327 from Patent WO2003106674.
ACCESSION
CQ755826
VERSION
CQ755826.1 GI:44846631
KEYWORDS
synthetic construct
SOURCE
synthetic construct
other sequences; artificial sequences.
ORGANISM
Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
AUTHORS
Means and methods for regulating gene expression
TITLE
Patent: WO 2003106674-A 327 24-DEC-2003;
JOURNAL
Chromagenics B.V. (NL)
FEATURES
Location/Qualifiers
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/db_xref="taxon:32630"
/note="oligonucleotide patterns over-represented in STAR
elements"

ORIGIN
Query Match
Best Local Similarity 83.3%; Score 5; DB 6; Length 6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGTGG 6
Db 5 GGTGG 1

RESULT 29
CQ755836/c
LOCUS
DEFINITION
Sequence 337 from Patent WO2003106674.
ACCESSION
CQ755836
VERSION
CQ755836.1 GI:44846641
KEYWORDS
synthetic construct
SOURCE
synthetic construct
other sequences; artificial sequences.
ORGANISM
Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
AUTHORS
Means and methods for regulating gene expression
TITLE
Patent: WO 2003106674-A 337 24-DEC-2003;
JOURNAL
Chromagenics B.V. (NL)
FEATURES
Location/Qualifiers
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/organism="synthetic construct"
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elements"

ORIGIN
Query Match
Best Local Similarity 83.3%; Score 5; DB 6; Length 6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGG 5
Db 5 GGTGG 1

RESULT 30
CQ756230/c
LOCUS
DEFINITION
Sequence 731 from Patent WO2003106674.
ACCESSION
CQ756230
VERSION
CQ756230.1 GI:44847035
KEYWORDS
synthetic construct
SOURCE
synthetic construct
other sequences; artificial sequences.
ORGANISM
Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
AUTHORS
Means and methods for regulating gene expression
TITLE
Patent: WO 2003106674-A 731 24-DEC-2003;
JOURNAL
Chromagenics B.V. (NL)
FEATURES
Location/Qualifiers
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/organism="synthetic construct"
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Best Local Similarity 83.3%; Score 5; DB 6; Length 6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGG 5
Db 5 GGTGG 1

Search completed: July 21, 2005, 00:00:38
Job time : 741.2 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:43:13 ; Search time 57 Seconds
(without alignments)
172.240 Million cell updates/sec

Title: US-09-735-363A-25

Perfect score: 6

Sequence: 1 999tgg 6

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2678

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents NA:*

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- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfileseq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	5	83.3	6	1	US-08-234-613-10
3	5	83.3	6	1	US-08-153-051B-53
4	5	83.3	6	1	US-08-060-952C-52
5	5	83.3	6	2	US-08-151-477A-53
6	5	83.3	6	2	US-08-237-973-10
7	5	83.3	6	2	US-08-237-973-26
8	5	83.3	6	3	US-08-819-867-70
9	5	83.3	6	3	US-08-464-011B-52
10	5	83.3	6	3	US-09-196-099-17
11	5	83.3	6	4	US-09-378-535-70
12	5	83.3	6	4	US-09-288-719B-17
13	4.4	73.3	6	1	US-08-234-613-9
14	4.4	73.3	6	2	US-08-237-973-9
15	4.4	73.3	6	3	US-08-920-422-15
16	4.4	73.3	6	3	US-08-920-422-16
17	4.4	73.3	6	3	US-09-593-323-29
18	4.4	73.3	6	3	US-09-594-108-29
19	4.4	73.3	6	3	US-09-344-300-29
20	4.4	73.3	6	4	US-09-924-346-6
21	4.4	73.3	6	4	US-09-483-184A-6
22	4	66.7	5	1	US-08-153-051B-47
23	4	66.7	5	1	US-08-060-952C-20
24	4	66.7	5	2	US-08-151-477A-47
25	4	66.7	5	3	US-08-819-867-44
26	4	66.7	5	3	US-08-973-068-59
27	4	66.7	5	3	US-08-973-068-60

ALIGNMENTS

RESULT 1

US-09-305-839-46/c
; Sequence 46, Application US/09305839
; Patent No. 6514935
; GENERAL INFORMATION:
; APPLICANT: Lee, Mu-En
; APPLICANT: Yet, Shaw-Fang
; TITLE OF INVENTION: Methods of Treating Hypertension
; FILE REFERENCE: 21508-064
; CURRENT APPLICATION NUMBER: US/09/305,839
; CURRENT FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: 08/818,655
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: artif: peptide
US-09-305-839-46

Query Match 83.3%; Score 5; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+08; 0; Indels 0;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 1 GGGTG 5
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Db 5 GGGTG 1

RESULT 2

US-08-234-613-10
; Sequence 10, Application US/08234613
; Patent No. 5582981
; GENERAL INFORMATION:
; APPLICANT: TOOLE, JOHN J.
; APPLICANT: LATHAM, JOHN
; APPLICANT: BOCK, LOUIS C.
; APPLICANT: GRIFFIN, LINDA C.
; TITLE OF INVENTION: APTAMER TARGET ELUTION METHOD
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,613
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/744,870
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: GRACEY, NANCEY J.
; REGISTRATION NUMBER: 28,216
; REFERENCE/DOCKET NUMBER: 24610-20030.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600

; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-234-613-10

Query Match 83.3%; Score 5; DB 1; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTGG 6
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Db 1 GGNTGG 6

RESULT 3

US-08-153-051B-53
; Sequence 53, Application US/08153051B
; Patent No. 5645986
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Jerry W. Shay
; APPLICANT: Woodring E. Wright
; APPLICANT: Elizabeth Blackburn
; APPLICANT: Nam Woo Kim
; APPLICANT: Calvin B. Harley
; APPLICANT: Scott L. Weinrich
; APPLICANT: Catherine Strahl
; APPLICANT: Michael J. McEachern
; APPLICANT: Homayoun Vaziri
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: CONDITIONS RELATED TO TELOMERE
; TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,051B
; FILING DATE: No. 5645986ember 12, 1993
; APPLICATION DATA:
; APPLICATION NUMBER: 08/038,766
; FILING DATE: March 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 204/195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-153-051B-53

Query Match 83.3%; Score 5; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 1 GGGTG 5
| | | | |
Db 2 GGGTG 6

RESULT 4

US-08-060-952C-52
; Sequence 52, Application US/08060952C
; Patent No. 5695932
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Jerry W. Shay
; APPLICANT: Woodring B. Wright
; APPLICANT: Elizabeth Blackburn
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
; TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR
; TITLE OF INVENTION: TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/060,952C
; FILING DATE: May 13, 1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/882,438
; FILING DATE: May 13, 1992
; APPLICATION NUMBER: 08/038,766
; FILING DATE: March 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 202/045
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-060-952C-52

Query Match 83.3%; Score 5; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 1 GGGTG 5
| | | | |
Db 2 GGGTG 6

RESULT 5

US-08-151-477A-53

; Sequence 53, Application US/08151477A
; Patent No. 5830644
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Jerry W. Shay
; APPLICANT: Woodring B. Wright
; APPLICANT: Elizabeth Blackburn
; APPLICANT: Nam Woo Kim
; APPLICANT: Calvin B. Harley
; APPLICANT: Scott L. Weinrich
; APPLICANT: Catherine Strahl
; APPLICANT: Michael J. McEachern
; APPLICANT: Homayoun Vaziri
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: CONDITIONS RELATED TO TELOMERE
; TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,477A
; FILING DATE: No. 5830644ember 12, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/038,766
; FILING DATE: March 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 202/189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-151-477A-53

Query Match 83.3%; Score 5; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 1 GGGTG 5
| | | | |
Db 2 GGGTG 6

RESULT 6

US-08-237-973-10
; Sequence 10, Application US/08237973
; Patent No. 5840867
; GENERAL INFORMATION:
; APPLICANT: TOOLE, JOHN J.
; APPLICANT: LATHAM, JOHN
; APPLICANT: BOCK, LOUIS C.
; APPLICANT: GRIFFIN, LINDA C.
; TITLE OF INVENTION: APTAMER ANALOGS SPECIFIC FOR
; TITLE OF INVENTION: BIOMOLECULES

NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/237,973
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,921
FILING DATE: 06-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: GRACEY, NANCY J.
REGISTRATION NUMBER: 28,216
REFERENCE/DOCKET NUMBER: 24610-20032.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-237-973-10

Query Match 83.3%; Score 5; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTGG 6
|||
Db 1 GGNTGG 6

RESULT 7
US-08-237-973-26
Sequence 26, Application US/08237973
Patent No. 5840867
GENERAL INFORMATION:
APPLICANT: TOOLE, JOHN J.
APPLICANT: LATHAM, JOHN
APPLICANT: BOCK, LOUIS C.
APPLICANT: GRIFFIN, LINDA C.
TITLE OF INVENTION: APTAMER ANALOGS SPECIFIC FOR
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/237,973
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,921
FILING DATE: 06-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: GRACEY, NANCY J.
REGISTRATION NUMBER: 28,216
REFERENCE/DOCKET NUMBER: 24610-20032.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: misc_feature
LOCATION: 3
OTHER INFORMATION: /note= "N is T, A, U, dU (i.e., thymine in
OTHER INFORMATION: deacyl as a substitute base for thymine in
OTHER INFORMATION: deoxyribonucleic acid) or G."
US-08-237-973-26

Query Match 83.3%; Score 5; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTGG 6
|||
Db 1 GGNTGG 6

RESULT 8
US-08-819-867-70
Sequence 70, Application US/08819867
Patent No. 6007989
GENERAL INFORMATION:
APPLICANT: Michael D. West
APPLICANT: Calvin B. Harley
APPLICANT: Scott L. Weinrich
APPLICANT: Catherine M. Strahl
APPLICANT: Michael J. Mceachern
APPLICANT: Jerry Shay
APPLICANT: Woodring E. Wright
APPLICANT: Elizabeth H. Blackburn
APPLICANT: Nam Woo Kim
APPLICANT: Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: CONDITIONS RELATED TO
TITLE OF INVENTION: TELOMERE LENGTH AND/OR
TITLE OF INVENTION: TELOMERE LENGTH AND/OR
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Fast-SEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,867
FILING DATE: March 14, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

```
; APPLICATION NUMBER: 08/153,051
; FILING DATE: No. 6007989 September 12, 1993
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Chambers, Daniel M.
; REGISTRATION NUMBER: 34,561
; REFERENCE/DOCKET NUMBER: 224/232
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-819-867-70

Query Match      83.3%; Score 5; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGTGG 5
DB      2 GGTGG 6
      |||||

RESULT 9
US-08-464-011B-52
; Sequence 52, Application US/08464011B
; Patent No. 6368789
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; Jerry W. Shay
; Woodring E. Wright
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
; RELATED TO TELOMERE LENGTH AND/OR
; TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,011B
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/882,438
; FILING DATE: May 13, 1992
; APPLICATION NUMBER: 08/038,766
; FILING DATE: March 24, 1993
; APPLICATION NUMBER: 08/060,952
; FILING DATE: May 13, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 202/045
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440

; APPLICATION NUMBER: 08/153,051
; FILING DATE: No. 6007989 September 12, 1993
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Chambers, Daniel M.
; REGISTRATION NUMBER: 34,561
; REFERENCE/DOCKET NUMBER: 224/232
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-464-011B-52

Query Match      83.3%; Score 5; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGTGG 5
DB      2 GGTGG 6
      |||||

RESULT 10
US-09-196-099-17/c
; Sequence 17, Application US/09196099
; Patent No. 6465246
; GENERAL INFORMATION:
; APPLICANT: MUELLER, Rolf
; APPLICANT: SEDLACEK, Hans-Harald
; TITLE OF INVENTION: ONCOGENE- OR VIRUS-CONTROLLED EXPRESSION SYSTEM
; FILE REFERENCE: 26083/190
; CURRENT APPLICATION NUMBER: US/09/196,099
; CURRENT FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: DE 19751587.8
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; US-09-196-099-17

Query Match      83.3%; Score 5; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GGTGG 6
DB      6 GGTGG 2
      |||||

RESULT 11
US-09-378-535-70
; Sequence 70, Application US/09378535
; Patent No. 6551774
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; Calvin B. Harley
; Scott L. Weinrich
; Catherine M. Strahl
; Michael J. McEachern
; Jerry Shay
; Woodring E. Wright
; Elizabeth H. Blackburn
; Nam Woo Kim
; Homayoun Vaziri
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
; CONDITIONS RELATED TO
; TELOMERE LENGTH AND/OR
; TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
```

STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/378,535
FILING DATE: 20-Aug-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/819,867
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 224/232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 70:
US-09-378-535-70
Query Match 83.3%; Score 5; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTGG 5
Db |||||
2 GGTGG 6
RESULT 12
US-09-288-719B-17/c
Sequence 17, Application US/09288719B
Patent No. 6759518
GENERAL INFORMATION:
APPLICANT: KONTERMANN, Roland
APPLICANT: SEDLACEK, Hans-Herald
APPLICANT: MUELLER, Rolf
TITLE OF INVENTION: SINGLE-CHAIN MULTIPLE ANTIGEN-BINDING MOLECULE, ITS PREPARATION
FILE REFERENCE: 38005-0121
CURRENT APPLICATION NUMBER: US/09/288,719B
CURRENT FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: DE 198 27 239.1
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: DE 198 16 141.7
PRIOR FILING DATE: 1998-04-09
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
LENGTH: 6
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic nucleotide
US-09-288-719B-17
Query Match 83.3%; Score 5; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+08;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGTGG 6
Db |||||
6 GGTGG 2
RESULT 13
US-08-234-613-9
Sequence 9, Application US/08234613
Patent No. 5582981
GENERAL INFORMATION:
APPLICANT: TOOLE, JOHN J.
APPLICANT: LATHAM, JOHN
APPLICANT: BOCK, LOUIS C.
APPLICANT: GRIFFIN, LINDA C.
TITLE OF INVENTION: APTAMER TARGET ELUTION METHOD
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/234,613
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/744,870
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GRACEY, NANCEY J.
REGISTRATION NUMBER: 28,216
REFERENCE/DOCKET NUMBER: 24610-20030.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-234-613-9
Query Match 73.3%; Score 4.4; DB 1; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGTGG 6
Db |||||
1 GGTGG 6
RESULT 14
US-08-237-973-9
Sequence 9, Application US/08237973
Patent No. 5840867
GENERAL INFORMATION:
APPLICANT: TOOLE, JOHN J.
APPLICANT: LATHAM, JOHN
APPLICANT: BOCK, LOUIS C.
APPLICANT: GRIFFIN, LINDA C.
TITLE OF INVENTION: APTAMER ANALOGS SPECIFIC FOR
OTHER INFORMATION: BIOMOLECULES


```
; APPLICANT: Morgan, Antony R.
; APPLICANT: Severini, Alberto
; TITLE OF INVENTION: Compositions and Methods for Determining the Activity
; TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of
; TITLE OF INVENTION: Transcription
; FILE REFERENCE: DNAB-02921
; CURRENT APPLICATION NUMBER: US/09/594,108
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: 09/344,300
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-594-108-29

Query Match          73.3%; Score 4.4; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGTGG 6
      |||||
Db      1 GGGCGG 6

RESULT 19
US-09-344-300-29
; Sequence 29, Application US/09344300B
; Patent No. 6297013
; GENERAL INFORMATION:
; APPLICANT: Morgan, Antony R.
; APPLICANT: Severini, Alberto
; TITLE OF INVENTION: Compositions and Methods for Determining the Activity
; TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of
; TITLE OF INVENTION: Transcription
; FILE REFERENCE: DNAB-02921
; CURRENT APPLICATION NUMBER: US/09/344,300B
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-344-300-29

Query Match          73.3%; Score 4.4; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGTGG 6
      |||||
Db      1 GGGCGG 6

RESULT 20
US-09-924-346-6
; Sequence 6, Application US/09924346
; Patent No. 655674
; GENERAL INFORMATION:
; APPLICANT: Jens Tornoe
; TITLE OF INVENTION: The Jet Promoter
; FILE REFERENCE: 19313-005
; CURRENT APPLICATION NUMBER: US/09/924,346
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/224,087
; PRIOR FILING DATE: 2000-08-09
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; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Chemically
; OTHER INFORMATION: Synthesized
US-09-924-346-6

Query Match          73.3%; Score 4.4; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGTGG 6
      |||||
Db      1 GGGCGG 6

RESULT 21
US-09-483-184A-6/c
; Sequence 6, Application US/09483184A
; Patent No. 6800750
; GENERAL INFORMATION:
; APPLICANT: DARTMOUTH COLLEGE
; APPLICANT: CRAIG, Ruth W.
; APPLICANT: BINGLE, Colin D.
; APPLICANT: WHYTE, Moira
; TITLE OF INVENTION: Mcl-1 GENE REGULATORY ELEMENTS AND A PRO-APOPTOTIC Mcl-1 VARIANT
; FILE REFERENCE: DART1110-1
; CURRENT APPLICATION NUMBER: US/09/483,184A
; CURRENT FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/166,113
; PRIOR FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide for PCR
US-09-483-184A-6

Query Match          73.3%; Score 4.4; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.5e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGTGG 6
      |||||
Db      6 GGGCGG 1

RESULT 22
US-08-153-051B-47
; Sequence 47, Application US/08153051B
; Patent No. 5645986
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Jerry W. Shay
; APPLICANT: Woodring E. Wright
; APPLICANT: Elizabeth Blackburn
; APPLICANT: Nam Woo Kim
; APPLICANT: Calvin B. Harley
; APPLICANT: Scott L. Weinrich
; APPLICANT: Catherine Strahl
; APPLICANT: Michael J. McEachern
; APPLICANT: Homayoun Vaziri
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: CONDITIONS RELATED TO TELOMERE
; TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 58
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/038,766
; FILING DATE: March 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 204/195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-153-051B-47

Query Match 66.7%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGTC 5
Db 2 GGTC 5

RESULT 23
US-08-060-952C-20
; Sequence 20, Application US/08060952C
; Patent No. 5695932
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Jerry W. Shay
; APPLICANT: Woodring B. Wright
; APPLICANT: Elizabeth Blackburn
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
; TITLE OF INVENTION: RELATED TO TELOMERASE LENGTH AND/OR
; TITLE OF INVENTION: TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/038,766
; FILING DATE: March 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 202/045
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-060-952C-20

Query Match 66.7%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGTC 5
Db 2 GGTC 5

RESULT 24
US-08-151-477A-47
; Sequence 47, Application US/08151477A
; Patent No. 5830644
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Jerry W. Shay
; APPLICANT: Woodring B. Wright
; APPLICANT: Elizabeth Blackburn
; APPLICANT: Nam Woo Kim
; APPLICANT: Calvin B. Harley
; APPLICANT: Scott L. Weinrich
; APPLICANT: Catherine Strahl
; APPLICANT: Michael J. McEachern
; APPLICANT: Homayoun Vaziri
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: CONDITIONS RELATED TO TELOMERASE
; TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,477A
; FILING DATE: No. 5830644ember 12, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/038,766
; FILING DATE: March 24, 1993
; ATTORNEY/AGENT INFORMATION:
```

NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-151-477A-47

Query Match 66.7%; Score 4; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGTG 5
Db 2 GGTG 5

RESULT 25
US-08-819-867-44
Sequence 44, Application US/08819867
Patent No. 6007989
GENERAL INFORMATION:
APPLICANT: Michael D. West
APPLICANT: Calvin B. Harley
APPLICANT: Scott L. Weinrich
APPLICANT: Catherine M. Strahl
APPLICANT: Michael J. McEachern
APPLICANT: Jerry Shay
APPLICANT: Woodring E. Wright
APPLICANT: Elizabeth H. Blackburn
APPLICANT: Nam Woo Kim
APPLICANT: Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: CONDITIONS RELATED TO
TITLE OF INVENTION: TEOLOMERE LENGTH AND/OR
TITLE OF INVENTION: TEOLOMERASE ACTIVITY
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,867
FILING DATE: March 14, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/153,051
FILING DATE: No. 6007989eember 12, 1993
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 224/232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-819-867-44

Query Match 66.7%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGTG 5
Db 2 GGTG 5

RESULT 26
US-08-973-068-59/c
Sequence 59, Application US/08973068
Patent No. 6127604
GENERAL INFORMATION:
APPLICANT: Dale, James Langham
APPLICANT: Harding, Robert Maxwell
APPLICANT: Dugdale, Benjamin
APPLICANT: Beetham, Peter Ronald
APPLICANT: Hainer, Gregory John
APPLICANT: Becker, Douglas Kenneth
TITLE OF INVENTION: INTERGENIC REGIONS OF BANANA BUNCHY TOP VIRUS
FILE REFERENCE: 09657/002001
CURRENT APPLICATION NUMBER: US/08/973,068
CURRENT FILING DATE: 1998-03-12
EARLIER APPLICATION NUMBER: PCT/AU96/00335
EARLIER FILING DATE: 1996-05-31
NUMBER OF SEQ ID NOS: 61
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 59
LENGTH: 5
TYPE: DNA
ORGANISM: Banana Bunchy Top Virus (BBTV)
US-08-973-068-59

Query Match 66.7%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GTGG 6
Db 4 GTGG 1

RESULT 27
US-08-973-068-60
Sequence 60, Application US/08973068
Patent No. 6127604
GENERAL INFORMATION:
APPLICANT: Dale, James Langham
APPLICANT: Harding, Robert Maxwell
APPLICANT: Dugdale, Benjamin
APPLICANT: Beetham, Peter Ronald
APPLICANT: Hainer, Gregory John
APPLICANT: Becker, Douglas Kenneth
TITLE OF INVENTION: INTERGENIC REGIONS OF BANANA BUNCHY TOP VIRUS
FILE REFERENCE: 09657/002001
CURRENT APPLICATION NUMBER: US/08/973,068
CURRENT FILING DATE: 1998-03-12
EARLIER APPLICATION NUMBER: PCT/AU96/00335
EARLIER FILING DATE: 1996-05-31
NUMBER OF SEQ ID NOS: 61
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 60

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; LENGTH: 5
; TYPE: DNA
; ORGANISM: Banana Bunchy Top Virus (BBTV)
US-08-973-068-60

Query Match 66.7%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+08; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 3 GTGG 6
Db 2 GTGG 5

RESULT 28
US-08-464-011B-20
; Sequence 20, Application US/08464011B
; Patent No. 6368789
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; Jerry W. Shay
; Woodring E. Wright
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
; RELATED TO TELOMERE LENGTH AND/OR
; TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,011B
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/882,438
; FILING DATE: May 13, 1992
; APPLICATION NUMBER: 08/038,766
; FILING DATE: March 24, 1993
; APPLICATION NUMBER: 08/060,952
; FILING DATE: May 13, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 202/045
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-08-464-011B-20

Query Match 66.7%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GTGG 5

; LENGTH: 5
; TYPE: DNA
; ORGANISM: Banana Bunchy Top Virus (BBTV)
US-09-735-363a-25.szlm6.rni

Query Match 66.7%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+08; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 3 GTGG 6
Db 2 GTGG 5

RESULT 29
US-09-638-509C-22/c
; Sequence 22, Application US/09638509C
; Patent No. 6372435
; GENERAL INFORMATION:
; APPLICANT: Tang, Jianming
; APPLICANT: Kaslow, Richard A.
; TITLE OF INVENTION: Methods of Surveying For CC (Beta) Chemokine
; TITLE OF INVENTION: Receptor Variants and Their Association With HIV-1
; TITLE OF INVENTION: Transmission and/or Disease Progression
; FILE REFERENCE: D6217
; CURRENT APPLICATION NUMBER: US/09/638,509C
; CURRENT FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/148,530
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 22
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: allele
; OTHER INFORMATION: CCR5 promoter allele P*0201
US-09-638-509C-22

Query Match 66.7%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+08; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 3 GTGG 6
Db 5 GTGG 2

RESULT 30
US-09-378-535-44
; Sequence 44, Application US/09378535
; Patent No. 6551774
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; Calvin B. Harley
; Scott L. Weinrich
; Catherine M. Strahl
; Michael J. McEachern
; Jerry Shay
; Woodring E. Wright
; Elizabeth H. Blackburn
; Nam Woo Kim
; Homayoun Vaziri
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
; CONDITIONS RELATED TO
; TELOMERE LENGTH AND/OR
; TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/378,535
; FILING DATE: 20-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/819,867
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Chambers, Daniel M.
; REGISTRATION NUMBER: 34,561
; REFERENCE/DOCKET NUMBER: 224/232
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-378-535-44

Query Match      66.7%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GGTG 5
        ||||
Db      2 GGTG 5

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Search completed: July 21, 2005, 04:29:19
Job time : 60 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:25:43 ; Search time 1348.8 Seconds

(without alignments)
169.325 Million cell updates/sec

Title: US-09-735-363A-25

Perfect score: 6

Sequence: 1 999tgg 6

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 1216

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	5	83.3	6	7	CF312755 ABP--08-K
2	3.4	56.7	5	7	CF327761 NACL--02
3	3.4	56.7	5	7	CF339974 RCL1--06
4	3.4	56.7	5	7	CF340386 RCL1--07
5	3.4	56.7	5	7	CF340514 RCL1--08
6	3.4	56.7	5	7	CF920850 gmrhRw3-
7	3.4	56.7	5	9	CL423849 OIS0750-0
8	3.4	56.7	5	9	CL64862 PR10148a
9	3.4	56.7	5	9	CL685110 PR10140b
10	3.4	56.7	6	6	CA851633 D15H03 OI
11	3.4	56.7	6	6	CA851767 D17C12 E2
12	3.4	56.7	6	7	CF339116 RCL1--03
13	3.4	56.7	6	7	CF340012 RCL1--06
14	3.4	56.7	6	7	CF340239 RCL1--07
15	3.4	56.7	6	9	CL689395 PR10151a
16	3	50.0	3	6	CA850938 D08D06 H1
17	3	50.0	3	6	CA851961 D19E06 I1
18	3	50.0	3	7	CF315089 HD--03-N2
19	3	50.0	3	7	CF338538 RCL1--01
20	3	50.0	3	7	CF339357 RCL1--04
21	3	50.0	3	7	CF339421 RCL1--04
22	3	50.0	3	7	CF339646 RCL1--05
23	3	50.0	3	7	CF339761 RCL1--05
24	3	50.0	3	9	CL423861 OIS0750-0

CL655746	PRI0127b-	3	50.0	3	9	CL655746
CL668376	PRI0157c-	3	50.0	3	9	CL668376
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CA853352	B07C08.se	4	50.0	4	6	CA853352
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CF306914	HDA1--05	4	50.0	4	7	CF306914
CF324158	HDA1--05-M	4	50.0	4	7	CF324158
CF324308	HDA1--06-D	4	50.0	4	7	CF324308
CF336880	JMT--07-B	4	50.0	4	7	CF336880
CF338536	RCL1--01	4	50.0	4	7	CF338536
CF340391	RCL1--07	4	50.0	4	7	CF340391
CF340642	RCL1--08	4	50.0	4	7	CF340642
CF340653	RCL1--08	4	50.0	4	7	CF340653
CF323326	HDA1--03-I	4	50.0	4	7	CF323326
CF930992	CF--05-R	5	50.0	5	7	CF930992
CL661701	PRI013c-C	5	50.0	5	9	CL661701
CL686637	PRI014a-B	5	50.0	5	9	CL686637
CA850792	D06E12 E1	6	50.0	6	6	CA850792
CA850905	D07H12 O2	6	50.0	6	6	CA850905
CF302557	7LEAF--08	6	50.0	6	7	CF302557
CF307125	HDA1--05	6	50.0	6	7	CF307125
CF310635	ABP--05-G	6	50.0	6	7	CF310635
CF323984	HDA1--05-E	6	50.0	6	7	CF323984
CF921483	gmrhRw3-	6	50.0	6	7	CF921483
CF787556	DFZp469C	6	50.0	6	7	CF787556
CF333346	JMT--04-P	4	40.0	4	7	CF333346
CKS82549	IST W15 4	4	40.0	4	7	CKS82549
CL655267	PRI0122d	4	40.0	4	7	CL655267
CA853329	B07A01.se	5	40.0	5	6	CA853329
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CF297897	7LEAF--01	5	40.0	5	7	CF297897
CF300956	7LEAF--05	5	40.0	5	7	CF300956
CF302927	7LEAF--08	5	40.0	5	7	CF302927
CF307095	HDA1--05	5	40.0	5	7	CF307095
CF307842	ABP--01-G	5	40.0	5	7	CF307842
CF318944	HD--09-E0	5	40.0	5	7	CF318944
CF320271	HD--11-B1	5	40.0	5	7	CF320271
CF327578	NACL--02	5	40.0	5	7	CF327578
CL423373	OIS0554-0	5	40.0	5	9	CL423373
AL043164	DFZp434F	6	40.0	6	1	AL043164
CF314367	HD--02-N2	6	40.0	6	1	CF314367
CF329138	NACL--04	6	40.0	6	7	CF329138
CF338772	RCL1--02	6	40.0	6	7	CF338772
CL665420	PRI0149C	6	40.0	6	9	CL665420
CL680271	PRI0149C	6	40.0	6	9	CL680271
CL682618	PRI0134C	6	40.0	6	9	CL682618
BX266185	BX266185	2	33.3	2	5	BX266185
BX266563	BX266563	2	33.3	2	5	BX266563
BX267118	BX267118	2	33.3	2	5	BX267118
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CF291112	14ROOF--0	2	33.3	2	7	CF291112
CF299820	7LEAF--03	2	33.3	2	7	CF299820
CF301411	7LEAF--06	2	33.3	2	7	CF301411
CF306288	HDA1--03	2	33.3	2	7	CF306288
CF307123	HDA1--05	2	33.3	2	7	CF307123
CF311851	ABP--07-E	2	33.3	2	7	CF311851
CF315237	HD--04-B0	2	33.3	2	7	CF315237
CF331310	NACL--07	2	33.3	2	7	CF331310
CF333014	JMT--01-L	2	33.3	2	7	CF333014
CN411958	170005322	2	33.3	2	7	CN411958
CR792627	NT015C D1	2	33.3	2	7	CR792627
CR774574	DFZp469G	2	33.3	2	7	CR774574
CR787484	DFZp469H	2	33.3	2	7	CR787484
CL661289	PRI0139b-	2	33.3	2	9	CL661289
CL670560	PRI0162b-	2	33.3	2	9	CL670560
CL682684	PRI0134C	2	33.3	2	9	CL682684
CL688205	PRI0148d	2	33.3	2	9	CL688205
CL688890	PRI014d A	2	33.3	2	9	CL688890
CL688912	PRI014d C	2	33.3	2	9	CL688912
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CL694963	PRI0165C	2	33.3	2	9	CL694963
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99      2 33.3 2 9 CL876415 CL876415 abf13c11.
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ALIGNMENTS

RESULT 1
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LOCUS ABP--08-K07.b1 ABP3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABP--08-K07, mRNA sequence.
ACCESSION CF312755
VERSION 1
KEYWORDS GI:33684516
SOURCE EST.
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
1 (bases 1 to 6)
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..6
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABP--08-K07"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABP3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

ORIGIN
Query Match 83.3%; Score 5; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.3e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
DB 2 GGGTG 6

RESULT 2
CF327761/c 5 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--02-G02.g1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--02-G02, mRNA
sequence.
ACCESSION CF327761
VERSION 1
KEYWORDS GI:33803773
SOURCE EST.
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
1 (bases 1 to 5)
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
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/mol_type="mRNA"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN
Query Match 56.7%; Score 3.4; DB 7; Length 5;
Best Local Similarity 80.0%; Pred. No. 7.6e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTG 5
DB 5 GGGCG 1

RESULT 3
CF339974 5 bp mRNA linear EST 18-AUG-2003
LOCUS RCL1--06-118.g1 Regenerated callus lambda phage cDNA library (RCL1)
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone RCL1--06-118,
mRNA sequence.
ACCESSION CF339974
VERSION 1
KEYWORDS GI:33828316
SOURCE EST.
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
1 (bases 1 to 5)
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
1 (bases 1 to 5)
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN
Query Match 56.7%; Score 3.4; DB 7; Length 5;
Best Local Similarity 80.0%; Pred. No. 7.6e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTG 5
DB 5 GGGCG 1

RESULT 3
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LOCUS RCL1--06-118.g1 Regenerated callus lambda phage cDNA library (RCL1)
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone RCL1--06-118,
mRNA sequence.
ACCESSION CF339974
VERSION 1
KEYWORDS GI:33828316
SOURCE EST.
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
1 (bases 1 to 5)
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

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/clone="RCL1--06-118"


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 (RCL1)"
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 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
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 induced on 2N6 media for 30 days and cultured for 36hrs on
 regenerated media"

ORIGIN

Query Match 56.7%; Score 3.4; DB 7; Length 5;
 Best Local Similarity 80.0%; Pred. NO. 7.6e+09;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGTGG 6
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 Db 1 GCTGG 5

RESULT 4

CF340386 5 bp mRNA linear EST 18-AUG-2003
 LOCUS RCL1--07-N21.g1 Regenerated callus lambda phage cDNA library (RCL1)
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone RCL1--07-N21,
 mRNA sequence.

ACCESSION CF340386

VERSION CF340386.1 GI:33829128

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 5)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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 /mol_type="mRNA"
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 /clone_lib="Regenerated callus lambda phage cDNA library
 (RCL1)"

/notes="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
 end with SstI and 3' end with XhoI site. Callus was
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 regenerated media"

ORIGIN

Query Match 56.7%; Score 3.4; DB 7; Length 5;
 Best Local Similarity 80.0%; Pred. NO. 7.6e+09;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGTGG 6
 | | |
 Db 1 GCTGG 5

RESULT 5

CF340514

LOCUS

DEFINITION

CF340514 5 bp mRNA linear EST 18-AUG-2003
 RCL1--08-E10.g1 Regenerated callus lambda phage cDNA library (RCL1)

Oryza sativa (japonica cultivar-group) cDNA clone RCL1--08-E10,
 mRNA sequence.

ACCESSION CF340514

VERSION CF340514.1 GI:33829381

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 5)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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 (RCL1)"
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 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
 end with SstI and 3' end with XhoI site. Callus was
 induced on 2N6 media for 30 days and cultured for 36hrs on
 regenerated media"

ORIGIN

Query Match 56.7%; Score 3.4; DB 7; Length 5;
 Best Local Similarity 80.0%; Pred. NO. 7.6e+09;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGTGG 6
 | | |
 Db 1 GCTGG 5

RESULT 6

CF920850/c

LOCUS

DEFINITION

CF920850 5 bp mRNA linear EST 05-NOV-2003
 smrhrw3-02_E07_1_055 Soybean root hair subtracted cDNA library

smrhrw3 Glycine max cDNA, mRNA sequence.

ACCESSION CF920850

VERSION CF920850.1 GI:38191644

KEYWORDS EST.

SOURCE Glycine max (soybean)

ORGANISM

Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.

REFERENCE 1 (bases 1 to 5)

AUTHORS Scheffler, B.E., Huang, S., Liu, X., Nguyen, H., Duke, M. and Stacey, G.
 TITLE Expressed sequence tags from soybean root hair subtractive cDNA


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ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 5)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppADB: an AcedB database for the nematode satellite organism
JOURNAL Pristionchus pacificus
COMMENT Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
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Best Local Similarity 80.0%; Pred. No. 7.6e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCGTG 5
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Db 1 GCGTG 5

RESULT 10
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LOCUS D15H03.015_16.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
DEFINITION cDNA clone D15H03 5', mRNA sequence.
ACCESSION CA851633
VERSION CA851633.1 GI:33388426
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 6)
Alkharouf,N.W., Khan,R. and Matthews,B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.
FEATURES             source
    1..6
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            /dev_stage="Seedlings"
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            /note="Vector: pBluescript SK-; cDNA clones from mRNA
            extracted from Peking roots 2 and 4 days past invasion."
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Query Match      56.7%; Score 3.4; DB 6; Length 6;
Best Local Similarity 80.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCGTG 5
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Db 6 GTGTG 2

RESULT 12
CF339116
LOCUS CF339116
DEFINITION RCL1--03-N11.g1 Regenerated callus lambda phage cDNA library (RCL1)
Oryza sativa [japonica cultivar-group] cDNA clone RCL1--03-N11,
mRNA sequence.
CF339116
ACCESSION CF339116
    6 bp mRNA linear EST 18-AUG-2003
RCL1--03-N11.g1 Regenerated callus lambda phage cDNA library (RCL1)
Oryza sativa [japonica cultivar-group] cDNA clone RCL1--03-N11,
mRNA sequence.
CF339116

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ORIGIN
Query Match      56.7%; Score 3.4; DB 6; Length 6;
Best Local Similarity 80.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGTGG 6
    |||
Db 5 GTTGG 1

RESULT 11
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LOCUS CA851767
DEFINITION D17C12.E24_06.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
cDNA clone D17C12 5', mRNA sequence.
ACCESSION CA851767
VERSION CA851767.1 GI:33388560
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 6)
Alkharouf,N.W., Khan,R. and Matthews,B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.
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            /tissue_type="Roots"
            /dev_stage="Seedlings"
            /clone_lib="cDNA Peking library 2, 4 day SCN3"
            /note="Vector: pBluescript SK-; cDNA clones from mRNA
            extracted from Peking roots 2 and 4 days past invasion."
ORIGIN
Query Match      56.7%; Score 3.4; DB 6; Length 6;
Best Local Similarity 80.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCGTG 5
    |||
Db 6 GTGTG 2

RESULT 12
CF339116
LOCUS CF339116
DEFINITION RCL1--03-N11.g1 Regenerated callus lambda phage cDNA library (RCL1)
Oryza sativa [japonica cultivar-group] cDNA clone RCL1--03-N11,
mRNA sequence.
CF339116
ACCESSION CF339116
    6 bp mRNA linear EST 18-AUG-2003
RCL1--03-N11.g1 Regenerated callus lambda phage cDNA library (RCL1)
Oryza sativa [japonica cultivar-group] cDNA clone RCL1--03-N11,
mRNA sequence.
CF339116

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VERSION      CF339116.1  GI:33826619
KEYWORDS
SOURCE       Oryza sativa (japonica cultivar-group)
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 6)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

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        /note="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

ORIGIN
    Query Match      56.7%; Score 3.4; DB 7; Length 6;
    Best Local Similarity 80.0%; Pred. No. 6.3e+09;
    Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GCTGG 6
        ||||
DB      2 GCTGG 6

RESULT 13
CF340012
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone RCL1--06-K19,
mRNA sequence.
ACCESSION
CF340012.1  GI:33828387
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 6)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

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        /clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
        /note="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

ORIGIN
    Query Match      56.7%; Score 3.4; DB 7; Length 6;
    Best Local Similarity 80.0%; Pred. No. 6.3e+09;
    Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GCTGG 6
        ||||
DB      2 GCTGG 6

RESULT 13
CF340012
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone RCL1--07-G09,
mRNA sequence.
ACCESSION
CF340239.1  GI:33828836
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 6)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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        /clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
        /note="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

ORIGIN

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Query Match      56.7%; Score 3.4; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GGTGG 6
      ||||
Db      2 GCTGG 6

RESULT 15
CL689395/c
LOCUS
DEFINITION
Pristionchus var. California Pristionchus pacificus genomic, genomic
survey sequence.
CL689395
CL689395.1 GI:50211303
VERSION
KEYWORDS
SOURCE
ORGANISM
Pristionchus pacificus
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE
1 (bases 1 to 6)
AUTHORS
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
APPABD: an AcedB database for the nematode satellite organism
TITLE
Pristionchus pacificus
JOURNAL
Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
FEATURES
source
Location/Qualifiers
1..6
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/db_strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"

ORIGIN

Query Match      56.7%; Score 3.4; DB 9; Length 6;
Best Local Similarity 80.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GGTGG 6
      ||||
Db      6 GATGG 2

RESULT 16
CA850938
LOCUS
DEFINITION
D08D06.H18.07.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
cDNA clone D08D06 5', mRNA sequence.
CA850938
CA850938.1 GI:33387731
VERSION
KEYWORDS
SOURCE
ORGANISM
Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 3)

Query Match      56.7%; Score 3.4; DB 9; Length 6;
Best Local Similarity 80.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GGTGG 6
      ||||
Db      6 GATGG 2

RESULT 16
CA850938
LOCUS
DEFINITION
D08D06.H18.07.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
cDNA clone D08D06 5', mRNA sequence.
CA850938
CA850938.1 GI:33387731
VERSION
KEYWORDS
SOURCE
ORGANISM
Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 3)

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AUTHORS
Alkharouf,N.W., Khan,R. and Matthews,B.F.
TITLE
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
JOURNAL
Unpublished (2002)
COMMENT
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.
FEATURES
source
Location/Qualifiers
1..3
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D08D06"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."

ORIGIN

Query Match      50.0%; Score 3; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 TGG 6
      |||
Db      1 TGG 3

RESULT 17
CA851961
LOCUS
DEFINITION
D19E06.H18.09.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
cDNA clone D19E06 5', mRNA sequence.
CA851961
CA851961.1 GI:33388754
VERSION
KEYWORDS
SOURCE
ORGANISM
Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 3)

REFERENCE
1 (bases 1 to 3)
AUTHORS
Alkharouf,N.W., Khan,R. and Matthews,B.F.
TITLE
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
JOURNAL
Unpublished (2002)
COMMENT
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.
FEATURES
source
Location/Qualifiers
1..3
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D19E06"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA

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extracted from Peking roots 2 and 4 days past invasion."

ORIGIN	CF338538.1	GI:33825464	EST.	Oryza sativa (japonica cultivar-group)
Query Match	50.0%;	Score 3;	DB 6;	Length 3;
Best Local Similarity	100.0%;	Pred. No. 1.3e+10;		
Matches	3;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	2 GGT 4			
Db	1 GGT 3			
RESULT 18	CF315089	3 bp	mRNA	linear
LOCUS	HD--03-N24.g1	OSHDAC1-overexpressing transgenic rice plasmid cDNA		EST 15-AUG-2003
DEFINITION	library (HD) Oryza sativa (japonica cultivar-group) cDNA clone			
ACCESSION	CF315089	HD--03-N24, mRNA sequence.		
VERSION	CF315089.1	GI:33686850		
KEYWORDS	EST.			
SOURCE	Oryza sativa (japonica cultivar-group)			
ORGANISM	Oryza sativa (japonica cultivar-group)			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.			
REFERENCE	1 (bases 1 to 3)			
AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.			
TITLE	Large-scale Sequencing Analysis of Rice ESTs			
JOURNAL	Unpublished (2003)			
COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@bio.myongji.ac.kr.			
FEATURES	source			
	1..3			
	/organism="Oryza sativa (japonica cultivar-group)"			
	/mol_type="mRNA"			
	/cultivar="Nackdong"			
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	/clone="RCL1-01-P24"			
	/tissue_type="callus"			
	/dev_stage="proliferated callus on 2N6 media for 30 days"			
	/lab_host="E.coli SOLR"			
	/clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"			
	/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector"at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"			
ORIGIN				
Query Match	50.0%;	Score 3;	DB 7;	Length 3;
Best Local Similarity	100.0%;	Pred. No. 1.3e+10;		
Matches	3;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	4 TGG 6			
Db	1 TGG 3			
RESULT 20	CF339357	3 bp	mRNA	linear
LOCUS	RCL1--04-K02.g1	Regenerated callus lambda phage cDNA library (RCL1)		EST 18-AUG-2003
DEFINITION	Oryza sativa (japonica cultivar-group) cDNA clone RCL1--04-K02, mRNA sequence.			
ACCESSION	CF339357			
VERSION	CF339357.1	GI:33827102		
KEYWORDS	EST.			
SOURCE	Oryza sativa (japonica cultivar-group)			
ORGANISM	Oryza sativa (japonica cultivar-group)			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.			
REFERENCE	1 (bases 1 to 3)			
AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.			
TITLE	Large-scale Sequencing Analysis of Rice ESTs			
JOURNAL	Unpublished (2003)			
COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@bio.myongji.ac.kr.			
FEATURES	source			
	1..3			
	/organism="Oryza sativa (japonica cultivar-group)"			
	/mol_type="mRNA"			
	/cultivar="Nackdong"			
	/db_xref="taxon:39947"			
	/clone="HD--03-N24"			
	/tissue_type="callus"			
	/dev_stage="proliferated callus on 2N6 media for 2 weeks"			
	/lab_host="E.coli DH10B"			
	/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"			
	/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."			
ORIGIN				
Query Match	50.0%;	Score 3;	DB 7;	Length 3;
Best Local Similarity	100.0%;	Pred. No. 1.3e+10;		
Matches	3;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1 GGG 3			
Db	1 GGG 3			
RESULT 19	CF338538	3 bp	mRNA	linear
LOCUS	RCL1--01-P24.g1	Regenerated callus lambda phage cDNA library (RCL1)		EST 18-AUG-2003
DEFINITION	Oryza sativa (japonica cultivar-group) cDNA clone RCL1--01-P24, mRNA sequence.			
ACCESSION	CF338538			

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FEATURES
source
1. .3
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="RCL1--04-K02"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
/notes="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGG 6
Db |||
1 TGG 3

RESULT 21
LOCUS CF339421 3 bp mRNA linear EST 18-AUG-2003
DEFINITION RCL1--04-N02.g1 Regenerated callus lambda phage cDNA library (RCL1)
Oryza sativa (japonica cultivar-group) cDNA clone RCL1--04-N02, mRNA sequence.
ACCESSION CF339421
VERSION CF339421.1 GI:33827229
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .3
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="RCL1--05-I07"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
/notes="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TGG 6
Db |||
1 TGG 3

RESULT 23
LOCUS CF339761 3 bp mRNA linear EST 18-AUG-2003
DEFINITION RCL1--03-N20.g1 Regenerated callus lambda phage cDNA library (RCL1)
Oryza sativa (japonica cultivar-group) cDNA clone RCL1--03-N20, mRNA sequence.
ACCESSION CF339761
VERSION CF339761.1 GI:33827892
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)

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ORGANISM      Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .3
   /organism="Oryza sativa (japonica cultivar-group)"
   /mol_type="mRNA"
   /cultivar="Nackdong"
   /db_xref="taxon:39947"
   /clone="RCL1-05-N20"
   /tissue_type="callus"
   /dev_stage="proliferated callus on 2N6 media for 30 days"
   /lab_host="E.coli SOLR"
   /clone_lib="Regenerated callus lambda phage cDNA library
   (RCL1)"
   /note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
   XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
   end with SstI and 3' end with XhoI site. Callus was
   induced on 2N6 media for 30 days and cultured for 36hrs on
   regenerated media"

ORIGIN
Query Match      50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGG 3
      |||
Db      1 GGG 3

RESULT 24
CL423861/c
LOCUS      CL423861
DEFINITION      CL423861 3 bp DNA linear GSS 16-MAR-2004
O1S0750-04C1-C02 UniformMu MUTAIL Library Zea mays genomic clone
O1S0750-04C1-C02, genomic survey sequence.
ACCESSION      CL423861
VERSION        CL423861.1 GI:45501905
KEYWORDS      GSS.
SOURCE        Zea mays
              Zea mays
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
              clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS      Lathaw,S., Tan,B.-C., Settles,A.M. and McCarty,D.R.
TITLE        Sequence tagged transposon insertions from the UniformMu maize
              population
JOURNAL      Unpublished (2003)
COMMENT      Contact: Donald R. McCarty
              Plant Molecular and Cellular Biology Program
              University of Florida
              PO 110690 Gainesville, FL 32611-0690, USA
              Tel: 352-392-1928 x322
              Email: drm@ufl.edu
              Sequence flanking probable Mu insertion site in UniformMu
              line: O1S0750-04, Primer set: C
              Class: transposon insertion site.
              Location/Qualifiers
              1. .3

ORGANISM      Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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1. .3
   /organism="Oryza sativa (japonica cultivar-group)"
   /mol_type="mRNA"
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   /db_xref="taxon:39947"
   /clone="RCL1-05-N20"
   /tissue_type="callus"
   /dev_stage="proliferated callus on 2N6 media for 30 days"
   /lab_host="E.coli SOLR"
   /clone_lib="Regenerated callus lambda phage cDNA library
   (RCL1)"
   /note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
   XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
   end with SstI and 3' end with XhoI site. Callus was
   induced on 2N6 media for 30 days and cultured for 36hrs on
   regenerated media"

ORIGIN
Query Match      50.0%; Score 3; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GTG 5
      |||
Db      3 GTG 1

RESULT 25
CL656746
LOCUS      CL656746
DEFINITION      CL656746 3 bp DNA linear GSS 09-JUL-2004
PRI0127b_H01 - PRI0127b.B21 (3) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION      CL656746
VERSION        CL656746.1 GI:50137492
KEYWORDS      GSS.
SOURCE        Pristionchus pacificus
              Pristionchus pacificus
              Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
              Neodiplogasteridae; Pristionchus.
REFERENCE
AUTHORS      Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE        AppADB: an AcedB database for the nematode satellite organism
              Pristionchus pacificus
JOURNAL      Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT      Contact: Sommer RJ
              Evolutionary Biology
              Max-Planck-Institute for Developmental Biology
              Spemannstr. 37-39, Tuebingen D-72076, Germany
              Tel: 00497071601371
              Fax: 00497071601498
              Email: ralf.sommer@tuebingen.mpg.de
              This library was generated at Caltech, Pasadena, USA and end
              sequenced at Vancouver, Canada.
              Seq primer: 77
              Class: fosmid ends.
              Location/Qualifiers
              1. .3
               /organism="Pristionchus pacificus"
               /mol_type="genomic DNA"
               /strain="California"
               /db_xref="taxon:54126"
               /clone_lib="Mixed stage fosmid library of P. pacificus
               var. California"
               /note="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Query Match      50.0%; Score 3; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 TGG 6
      |||
Db      1 TGG 3

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RESULT 26
CL668376/c
LOCUS
DEFINITION
    CL668376 3 bp DNA linear GSS 09-JUL-2004
    PRI0157c.D10 - PRI0157c.B21 (3) Note: Recurring String Mixed stage
    fosmid library of P. pacificus var. California Pristionchus
    pacificus genomic, genomic survey sequence.
ACCESSION
CL668376
VERSION
GI:50163606
KEYWORDS
GSS.
SOURCE
Pristionchus pacificus
ORGANISM
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE
1 (bases 1 to 3)
AUTHORS
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE
AppADB: an AcceDB database for the nematode satellite organism
Pristionchus pacificus
JOURNAL
Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
FEATURES
    source
        Location/Qualifiers
            1..3
                /organism="Pristionchus pacificus"
                /mol_type="genomic DNA"
                /strain="California"
                /db_xref="taxon:54126"
                /clone_lib="Mixed stage fosmid library of P. pacificus
                var. California"
                /note="Vector: pEpifos-5 Fosmid vector"
ORIGIN
    Query Match 50.0%; Score 3; DB 9; Length 3;
    Best Local Similarity 100.0%; Pred. No. 1.3e+10;
    Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 TGG 6
    |||
Db 3 TGG 1

RESULT 27
CA853244
LOCUS
DEFINITION
    CA853244 seq cDNA Peking library 12hr SCN3 Glycine max cDNA clone
    B06A04 5', mRNA sequence.
ACCESSION
CA853244
VERSION
GI:33390037
KEYWORDS
EST.
SOURCE
Glycine max (soybean)
ORGANISM
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 4)
AUTHORS
Alkharouf,N.W., Khan,R. and Matthews,B.F.
TITLE
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
JOURNAL
Unpublished (2002)
COMMENT
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
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Db 1 GGG 3

RESULT 28
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    B07C08 5', mRNA sequence.
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CA853352
VERSION
GI:33390145
KEYWORDS
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SOURCE
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ORGANISM
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 4)
AUTHORS
Alkharouf,N.W., Khan,R. and Matthews,B.F.
TITLE
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
JOURNAL
Unpublished (2002)
COMMENT
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
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USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.
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ACCESSION
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GI:33390145
KEYWORDS
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Glycine max (soybean)
ORGANISM
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 4)
AUTHORS
Alkharouf,N.W., Khan,R. and Matthews,B.F.
TITLE
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
JOURNAL
Unpublished (2002)
COMMENT
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
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VERSION
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Oryza sativa (japonica cultivar-group)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 4)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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REFERENCE
1 (bases 1 to 4)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
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VERSION
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

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OM nucleic - nucleic search, using sw model

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53.568 Million cell updates/sec

Title: US-09-735-363A-45

Perfect score: 6

Sequence: 1 gggagg 6

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Searched: 7173243 seqs, 3172129809 residues

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Post-processing: Minimum Match 0%

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Listing first 100 summaries

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Sequence 2, Appl					
Sequence 6, Appl					
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6	16	US-10-190-312A-636	83.3	6	Sequence 636, Appl
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ALIGNMENTS

RESULT 1
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; APPLICANT: Fillion, Mario
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
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; Patent No. US20020091095A1
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; APPLICANT: Fillion, Mario C.
; TITLE OF INVENTION: Modulation of Fas and FasL Expression
; FILE REFERENCE: 02811-0241 42368-256931
; CURRENT APPLICATION NUMBER: US/09/879,668
; CURRENT FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: PCT/CA00/01467
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/228,925

; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: US 60/266,229
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 09/735,363
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/170,325
; PRIOR FILING DATE: 1999-12-13
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; Publication No. US20030045493A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario C.
; TITLE OF INVENTION: Oligonucleotide Compositions and Their Use to Induce Differentiation
; FILE REFERENCE: 02811-0261 (42368-273010)
; CURRENT APPLICATION NUMBER: US/10/127,645
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US 60/286,158
; PRIOR FILING DATE: 2001-04-24
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-127-645-3

Query Match 100.0%; Score 6; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAGG 6
|||||
Db 1 GGGAGG 6

RESULT 4
US-10-280-274-17
; Sequence 17, Application US/10280274
; Publication No. US20030119776A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario C.
; TITLE OF INVENTION: Modulation of Fas and FasL Expression
; FILE REFERENCE: 02811-0242 42368-279803
; CURRENT APPLICATION NUMBER: US/10/280,274
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: PCT/CA00/01467
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 09/879,668
; PRIOR FILING DATE: 2001-06-12

; PRIOR APPLICATION NUMBER: US 60/228,925
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: US 60/266,229
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 09/735,363
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/170,325
; PRIOR FILING DATE: 1999-12-13
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide
US-10-280-274-17

Query Match 100.0%; Score 6; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAGG 6
|||
Db 1 GGGAGG 6

RESULT 5
US-10-264-280-2
; Sequence 2, Application US/10264280
; Publication No. US20030125290A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario C.
; APPLICANT: Phillips, Nigel C.
; TITLE OF INVENTION: Therapeutically Useful Triethyleneglycol Cholesteryl Oligonucleob
; FILE REFERENCE: 02811-0271 42368-277492
; CURRENT APPLICATION NUMBER: US/10/264,280
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 60/326,884
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-264-280-2

Query Match 100.0%; Score 6; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAGG 6
|||
Db 1 GGGAGG 6

RESULT 6
US-10-264-280-6
; Sequence 6, Application US/10264280
; Publication No. US20030125290A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario C.
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Herrera-Gayol, Andrea C.
; TITLE OF INVENTION: Therapeutically Useful Triethyleneglycol Cholesteryl Oligonucleob
; FILE REFERENCE: 02811-0271 42368-277492
; CURRENT APPLICATION NUMBER: US/10/264,280
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 60/326,884

; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
; NAME/KEY: misc feature
; OTHER INFORMATION: 3'-Triethyleneglycol (TEG) Cholesteryl Synthetic Oligonucleotide
US-10-264-280-6

Query Match 100.0%; Score 6; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAGG 6
|||
Db 1 GGGAGG 6

RESULT 7
US-10-420-513A-6
; Sequence 6, Application US/10420513A
; Publication No. US20040058883A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Nigel C.
; APPLICANT: Phillips, Mario C.
; TITLE OF INVENTION: Oligonucleotide Compositions and Their Use for the Modulation of
; FILE REFERENCE: 02811-0301 (42368-283135)
; CURRENT APPLICATION NUMBER: US/10/420,513A
; CURRENT FILING DATE: 2003-04-22
; PRIOR APPLICATION NUMBER: US 60/374,540
; PRIOR FILING DATE: 2002-04-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-420-513A-6

Query Match 100.0%; Score 6; DB 18; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAGG 6
|||
Db 1 GGGAGG 6

RESULT 8
US-10-055-732-14
; Sequence 14, Application US/10055732
; Publication No. US20030135040A1
; GENERAL INFORMATION:
; APPLICANT: Eritja, Ramon
; APPLICANT: Garcia, Ramon Guimil
; APPLICANT: Oste, Christian C.
; TITLE OF INVENTION: Compositions and Methods for Synthesis and Use of No. US2003013504
; FILE REFERENCE: 03038-0202 42892-265833
; CURRENT APPLICATION NUMBER: US/10/055,732
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/162,627
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/702,066
; PRIOR FILING DATE: 2000-10-30

; PRIOR APPLICATION NUMBER: US 60/197,559
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-055-732-14

Query Match 83.3%; Score 5; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6
|||
Db 1 GGAGG 5

RESULT 9
US-10-658-093-55/c
; Sequence 55, Application US/10658093
; Publication No. US20040115704A1
; GENERAL INFORMATION:
; APPLICANT: Daly, John Michael
; TITLE OF INVENTION: Constructs for Gene Expression Analysis
; FILE REFERENCE: 12177722
; CURRENT APPLICATION NUMBER: US/10/658,093
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: USSN 60/274770
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: PCT/AU02/00351
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
; LENGTH: 5
; TYPE: DNA
; ORGANISM: mammalian
US-10-658-093-55

Query Match 83.3%; Score 5; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6
|||
Db 5 GGAGG 1

RESULT 10
US-10-658-093-55/c
; Sequence 55, Application US/10658093
; Publication No. US20040209274A2
; GENERAL INFORMATION:
; APPLICANT: Daly, John Michael
; TITLE OF INVENTION: Constructs for Gene Expression Analysis
; FILE REFERENCE: 12177722
; CURRENT APPLICATION NUMBER: US/10/658,093
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: USSN 60/274770
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: PCT/AU02/00351
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
; LENGTH: 5
; TYPE: DNA
; ORGANISM: mammalian
US-10-658-093-55

Query Match 83.3%; Score 5; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6
|||
Db 5 GGAGG 1

RESULT 11
US-10-664-835-97/c
; Sequence 97, Application US/10664835
; Publication No. US20050042620A1
; GENERAL INFORMATION:
; APPLICANT: Hampel, Arnold
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RNA CATALYST FOR CLEAVING SPECIFIC RNA SEQUENCES
; FILE REFERENCE: 43863-C1YA
; CURRENT APPLICATION NUMBER: US/10/664,835
; CURRENT FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 97
; LENGTH: 5
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ribozyme, portion of ribozyme or ribozyme target substrate
US-10-664-835-97

Query Match 83.3%; Score 5; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6
|||
Db 5 GGAGG 1

RESULT 12
US-09-735-363A-47
; Sequence 47, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Filion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-47

Query Match 83.3%; Score 5; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6
|||
Db 1 GGAGG 5

RESULT 13

US-09-942-487-1
; Sequence 1, Application US/09942487
; Publication No. US20020086310A1
; GENERAL INFORMATION:
; APPLICANT: FAN, FRANK
; APPLICANT: HE, YIPING
; APPLICANT: HUANG, JIANZHONG
; APPLICANT: JIANG, XINHE
; APPLICANT: MCDEVITT, DAMIEN
; APPLICANT: ROSENBERG, MARTIN
; APPLICANT: ST. JOHN, ANNEMARIE
; TITLE OF INVENTION: IDENTIFICATION OF TARGETS OF
; TITLE OF INVENTION: ANTIMICROBIAL COMPOUNDS
; FILE REFERENCE: P51167
; CURRENT APPLICATION NUMBER: US/09/942,487
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/229,965
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-942-487-1

Query Match 83.3%; Score 5; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6
Db 2 GGAGG 6

RESULT 14

US-09-888-049-1
; Sequence 1, Application US/09888049
; Patent No. US20020137215A1
; GENERAL INFORMATION:
; APPLICANT: Francis, Kevin P.
; APPLICANT: Purchio, Anthony F.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE THEREOF IN MODIFYING
; TITLE OF INVENTION: THE GENOMES OF MICROORGANISMS
; FILE REFERENCE: PXE-013 USP / 9400-0013
; CURRENT APPLICATION NUMBER: US/09/888,049
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/216,257
; PRIOR FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 60/274,105
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gram-positive
; OTHER INFORMATION: ribosome binding site
US-09-888-049-1

Query Match 83.3%; Score 5; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6
Db 2 GGAGG 6

RESULT 15

US-10-041-860-191/c
; Sequence 191, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 191
; LENGTH: 6
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-041-860-191

Query Match 83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6
Db 6 GGAGG 2

RESULT 16

US-10-190-312A-212/c
; Sequence 212, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; TITLE OF INVENTION: methods for detecting and using such DNA sequences
; FILE REFERENCE: 2183-4993.1
; CURRENT APPLICATION NUMBER: US/10/190,312A
; CURRENT FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/303,199
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 212
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements
US-10-190-312A-212

Query Match 83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6
Db 6 GGAGG 2

RESULT 17

US-10-190-312A-274/c
; Sequence 274, Application US/10190312A
; Publication No. US20030199468A1

```
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; FILE REFERENCE: 2183-4993.1
; CURRENT APPLICATION NUMBER: US/10/190,312A
; CURRENT FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/303,199
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 274
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements
US-10-190-312A-274

Query Match      83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred.No. 1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
DB      5 GGGAG 1

RESULT 18
US-10-190-312A-321/c
; Sequence 321, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; FILE REFERENCE: 2183-4993.1
; CURRENT APPLICATION NUMBER: US/10/190,312A
; CURRENT FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/303,199
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 321
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements
US-10-190-312A-321

Query Match      83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred.No. 1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GGGAG 6
DB      5 GGGAG 1

RESULT 19
US-10-190-312A-326/c
; Sequence 326, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
```

```
; TITLE OF INVENTION: methods for detecting and using such DNA sequences
; FILE REFERENCE: 2183-4993.1
; CURRENT APPLICATION NUMBER: US/10/190,312A
; CURRENT FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/303,199
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 326
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements
US-10-190-312A-326

Query Match      83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred.No. 1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
DB      6 GGGAG 2

RESULT 20
US-10-190-312A-636/c
; Sequence 636, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; FILE REFERENCE: 2183-4993.1
; CURRENT APPLICATION NUMBER: US/10/190,312A
; CURRENT FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/303,199
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 636
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Dyad patterns over-represented in STAR elements
US-10-190-312A-636

Query Match      83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred.No. 1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GGGAG 6
DB      6 GGGAG 2

RESULT 21
US-10-420-513A-9
; Sequence 9, Application US/10420513A
; Publication No. US2004005883A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Filion, Mario C.
; TITLE OF INVENTION: Oligonucleotide Compositions and Their Use for the Modulation of
; FILE REFERENCE: 02811-0301 (42368-283135)
; CURRENT APPLICATION NUMBER: US/10/420,513A
; CURRENT FILING DATE: 2003-04-22
; PRIOR APPLICATION NUMBER: US 60/374,540
; PRIOR FILING DATE: 2002-04-22
```

; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: "n" = G, C, A or T
US-10-420-513A-9

Query Match 83.3%; Score 5; DB 18; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGG 6
|||
Db 1 GGGNGG 6

RESULT 22
US-10-645-187-12
; Sequence 12, Application US/10645187
; Publication No. US20040191222A1
; GENERAL INFORMATION:
; APPLICANT: Emimi, Emilio A.
; APPLICANT: Shiver, John W.
; APPLICANT: Bett, Andrew J.
; APPLICANT: Casimiro, Danilo R.
; APPLICANT: Kaslow, David C.
; APPLICANT: Chastain, Michael
; TITLE OF INVENTION: ADENOVIRUS SEROTYPE 34 VECTORS, NUCLEIC
; FILE REFERENCE: 21390
; CURRENT APPLICATION NUMBER: US/10/645,187
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: 60/458,825
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: adenovirus serotype 34
US-10-645-187-12

Query Match 83.3%; Score 5; DB 19; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGAG 6
|||
Db 1 GGGAG 5

RESULT 23
US-10-656-450-12/c
; Sequence 12, Application US/10656450
; Publication No. US20050059620A1
; GENERAL INFORMATION:
; APPLICANT: Brunicaudi, F. C.
; TITLE OF INVENTION: Promoter Driven Tissue Specific Cytotoxic Agents
; FILE REFERENCE: A146.0136
; CURRENT APPLICATION NUMBER: US/10/656,450
; CURRENT FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: US/09/686,631
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: 60/161,109

; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-656-450-12

Query Match 83.3%; Score 5; DB 21; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5
|||
Db 5 GGGAG 1

RESULT 24
US-10-948-872-12/c
; Sequence 12, Application US/10948872
; Publication No. US20050137157A1
; GENERAL INFORMATION:
; APPLICANT: Brunicaudi, F. Charles
; TITLE OF INVENTION: Promoter Driven Tissue Specific Cytotoxic Agents and Method of
; FILE REFERENCE: 607110-00002USC2
; CURRENT APPLICATION NUMBER: US/10/948,872
; CURRENT FILING DATE: 2004-09-24
; PRIOR APPLICATION NUMBER: US 10/656,450
; PRIOR FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: US 09/686,631
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: US 60/161,109
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: US 60/224,382
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-948-872-12

Query Match 83.3%; Score 5; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5
|||
Db 5 GGGAG 1

RESULT 25
US-09-735-363A-25
; Sequence 25, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Filion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13

```
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-25

Query Match          73.3%; Score 4.4; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGAGG 6
Db      1 GGGTGG 6

RESULT 26
US-09-735-363A-42
; Sequence 42, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-42

Query Match          73.3%; Score 4.4; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGAGG 6
Db      1 GGAAGG 6

RESULT 27
US-09-735-363A-44
; Sequence 44, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide

; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-44

Query Match          73.3%; Score 4.4; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGAGG 6
Db      1 GGGCGG 6

RESULT 28
US-09-735-363A-46
; Sequence 46, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-46

Query Match          73.3%; Score 4.4; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGAGG 6
Db      1 GGGCGG 6

RESULT 29
US-09-735-363A-74
; Sequence 74, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 74
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
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US-09-735-363A-74

Query Match 73.3%; Score 4.4; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. NO. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGG 6
|||
Db 1 GGGTGG 6

RESULT 30

US-09-735-363A-79/c
; Sequence 79, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 79
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-79

Query Match 73.3%; Score 4.4; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. NO. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGG 6
|||
Db 6 GGGTGG 1

Search completed: July 21, 2005, 07:13:23
Job time : 712.6 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:43:13 ; Search time 57 Seconds
(without alignments)
172.240 Million cell updates/sec

Title: US-09-735-363A-45

Perfect score: 6

Sequence: 1 gggagg 6

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2678

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

- 1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	5	83.3	5	4	US-09-153-242-31
C 2	5	83.3	5	4	US-09-491-795-6
C 3	5	83.3	5	4	US-10-055-732-14
C 4	5	83.3	6	1	US-08-533-912-6
C 5	5	83.3	6	1	US-08-465-590-140
C 6	5	83.3	6	3	US-08-711-417C-140
C 7	5	83.3	6	4	US-09-723-909-140
C 8	5	83.3	6	4	US-09-686-631-12
C 9	5	83.3	6	4	US-09-557-289A-1
C 10	5	83.3	6	4	US-08-453-485B-17
C 11	5	83.3	6	5	PCT-US93-08743-140
C 12	4.4	73.3	6	3	US-08-920-422-15
C 13	4.4	73.3	6	3	US-08-920-422-16
C 14	4.4	73.3	6	3	US-09-593-323-29
C 15	4.4	73.3	6	3	US-09-594-108-29
C 16	4.4	73.3	6	3	US-09-344-300-29
C 17	4.4	73.3	6	4	US-09-924-346-6
C 18	4.4	73.3	6	4	US-09-483-184A-6
C 19	4.4	66.7	4	5	PCT-US94-06456-9
C 20	4	66.7	4	5	PCT-US94-06456-38
C 21	4	66.7	5	1	US-08-247-809A-15
C 22	4	66.7	5	1	US-08-381-097A-14
C 23	4	66.7	5	2	US-08-597-948A-6
C 24	4	66.7	5	2	US-08-711-728-15
C 25	4	66.7	5	3	US-08-873-709-8
C 26	4	66.7	5	4	US-08-921-497-12
C 27	4	66.7	5	4	US-08-921-497-14

5	5	66.7	4	28	PCT-US93-03027-7	Sequence 7, Appli
6	1	66.7	4	29	US-08-242-402-20	Sequence 20, Appl
6	1	66.7	4	30	US-08-270-180-19	Sequence 19, Appl
6	1	66.7	4	31	US-07-724-500B-13	Sequence 13, Appl
6	1	66.7	4	32	US-08-611-510-15	Sequence 15, Appl
6	2	66.7	4	33	US-08-442-809A-1	Sequence 1, Appli
6	2	66.7	4	34	US-08-442-809A-6	Sequence 6, Appli
6	3	66.7	4	35	US-08-682-423-19	Sequence 19, Appl
6	3	66.7	4	36	US-09-056-868B-14	Sequence 14, Appl
6	3	66.7	4	37	US-09-632-538C-10	Sequence 10, Appl
6	4	66.7	4	38	US-09-608-958-50	Sequence 50, Appl
6	4	66.7	4	39	US-09-608-958-51	Sequence 51, Appl
6	4	66.7	4	40	US-09-435-327A-1	Sequence 1, Appli
6	4	66.7	4	41	US-09-975-413A-1	Sequence 2, Appli
6	4	66.7	4	42	US-09-375-413A-2	Sequence 14, Appl
6	4	66.7	4	43	US-09-851-271A-14	Sequence 13, Appl
6	4	66.7	4	44	US-10-134-188-13	Sequence 13, Appl
6	5	66.7	4	45	PCT-US92-08094-63	Sequence 63, Appl
6	5	66.7	4	46	PCT-US95-05141-19	Sequence 19, Appl
5	5	63.3	4	47	PCT-US91-03680-78	Sequence 78, Appl
5	1	56.7	3.8	48	US-07-862-831A-1	Sequence 1, Appli
5	1	56.7	3.4	49	US-07-862-831A-2	Sequence 2, Appli
5	1	56.7	3.4	50	US-08-126-564A-1	Sequence 1, Appli
5	1	56.7	3.4	51	US-08-126-564A-2	Sequence 2, Appli
5	1	56.7	3.4	52	US-08-717-526-53	Sequence 53, Appl
5	2	56.7	3.4	53	US-08-950-709-1	Sequence 1, Appli
5	3	56.7	3.4	54	US-09-107-708-1	Sequence 1, Appli
5	3	56.7	3.4	55	US-09-449-581-1	Sequence 1, Appli
5	4	56.7	3.4	56	US-09-305-839-46	Sequence 46, Appl
5	5	56.7	3.4	57	PCT-US91-03680-76	Sequence 76, Appl
5	5	56.7	3.4	58	PCT-US94-09143-1	Sequence 1, Appli
5	5	56.7	3.4	59	PCT-US94-09143-2	Sequence 2, Appli
6	1	56.7	3.4	60	US-07-791-2130-45	Sequence 45, Appl
6	1	56.7	3.4	61	US-08-234-613-10	Sequence 10, Appl
6	1	56.7	3.4	62	US-08-488-672-1	Sequence 1, Appli
6	1	56.7	3.4	63	US-08-381-097A-12	Sequence 12, Appl
6	1	56.7	3.4	64	US-08-153-051B-53	Sequence 53, Appl
6	1	56.7	3.4	65	US-08-060-952C-52	Sequence 52, Appl
6	1	56.7	3.4	66	US-08-533-912-7	Sequence 7, Appli
6	1	56.7	3.4	67	US-08-533-912-8	Sequence 8, Appli
6	1	56.7	3.4	68	US-08-293-150A-45	Sequence 45, Appl
6	2	56.7	3.4	69	US-08-151-477A-53	Sequence 53, Appl
6	2	56.7	3.4	70	US-08-237-973-10	Sequence 10, Appl
6	2	56.7	3.4	71	US-08-237-973-26	Sequence 26, Appl
6	3	56.7	3.4	72	US-08-819-867-70	Sequence 70, Appl
6	3	56.7	3.4	73	US-08-464-011B-52	Sequence 52, Appl
6	3	56.7	3.4	74	US-09-196-099-17	Sequence 17, Appl
6	4	56.7	3.4	75	US-09-378-535-70	Sequence 70, Appl
6	4	56.7	3.4	76	US-09-220-794-10	Sequence 10, Appl
6	4	56.7	3.4	77	US-08-708-354-1	Sequence 1, Appli
6	4	56.7	3.4	78	US-09-288-719B-17	Sequence 17, Appl
6	4	56.7	3.4	79	US-09-288-719B-18	Sequence 18, Appl
6	4	56.7	3.4	80	US-10-071-411A-61	Sequence 61, Appl
6	5	56.7	3.4	81	PCT-US93-05331-1	Sequence 1, Appli
6	5	53.3	3.2	82	US-08-646-301A-13	Sequence 13, Appl
3	3	50.0	3	83	US-08-268-679B-7	Sequence 7, Appli
3	3	50.0	3	84	US-08-873-709-9	Sequence 9, Appli
3	3	50.0	3	85	US-09-032-365A-36	Sequence 36, Appl
4	1	50.0	3	86	US-07-630-288A-13	Sequence 13, Appl
4	1	50.0	3	87	US-08-393-219-11	Sequence 11, Appl
4	1	50.0	3	88	US-08-468-049-13	Sequence 13, Appl
4	1	50.0	3	89	US-08-463-288A-62	Sequence 62, Appl
4	1	50.0	3	90	US-08-463-288A-63	Sequence 63, Appl
4	2	50.0	3	91	US-08-470-445A-62	Sequence 62, Appl
4	2	50.0	3	92	US-08-470-445A-63	Sequence 63, Appl
4	2	50.0	3	93	US-08-462-679-62	Sequence 62, Appl
4	2	50.0	3	94	US-08-462-679-63	Sequence 63, Appl
4	2	50.0	3	95	US-08-466-210A-62	Sequence 62, Appl
4	2	50.0	3	96	US-08-466-210A-63	Sequence 63, Appl
4	2	50.0	3	97	US-08-467-147A-62	Sequence 62, Appl
4	2	50.0	3	98	US-08-467-147A-63	Sequence 63, Appl
4	2	50.0	3	99	US-08-469-014-62	Sequence 62, Appl
4	2	50.0	3	100	US-08-469-014-63	Sequence 63, Appl

ALIGNMENTS

RESULT 1

US-09-153-242-31/c
; Sequence 31, Application US/09153242
; Patent No. 6482592
; GENERAL INFORMATION:
; APPLICANT: Lundberg, Joakim
; APPLICANT: Uhlen, Mathias
; TITLE OF INVENTION: MODULAR PROBES II
; FILE REFERENCE: 1181-242
; CURRENT APPLICATION NUMBER: US/09/153,242
; CURRENT FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: PCT/GB97/02629
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: H2
US-09-153-242-31

Query Match 83.3%; Score 5; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.1e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6
|||
Db 5 GGAGG 1

RESULT 2

US-09-491-795-6
; Sequence 6, Application US/09491795
; Patent No. 6596281
; GENERAL INFORMATION:
; APPLICANT: Gennaro, Maria L.
; APPLICANT: Lyashchenko, Konstantin P.
; APPLICANT: Manca, Claudia M.A.
; TITLE OF INVENTION: MIXTURES OF ANTIGENS AND GENES,
; FILE REFERENCE: 07763/028002
; CURRENT APPLICATION NUMBER: US/09/491,795
; CURRENT FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: US 08/796,792
; PRIOR FILING DATE: 1997-02-06
; PRIOR APPLICATION NUMBER: US 60/011,364
; PRIOR FILING DATE: 1996-02-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-491-795-6

Query Match 83.3%; Score 5; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.1e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6
|||
Db 1 GGAGG 5

RESULT 3

US-10-055-732-14

; Sequence 14, Application US/10055732
; Patent No. 6831072
; GENERAL INFORMATION:
; APPLICANT: Eritja, Ramon
; APPLICANT: Garcia, Ramon Guimil
; APPLICANT: Oste, Christian C.
; TITLE OF INVENTION: Compositions and Methods for Synthesis and Use of No. 6831072el N
; TITLE OF INVENTION: Structures
; FILE REFERENCE: 03038-0202 42892-265833
; CURRENT APPLICATION NUMBER: US/10/055,732
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/162,627
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/702,066
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 60/197,559
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-055-732-14

Query Match 83.3%; Score 5; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.1e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6
|||
Db 1 GGAGG 5

RESULT 4

US-08-533-912-6
; Sequence 6, Application US/08533912
; Patent No. 5744308
; GENERAL INFORMATION:
; APPLICANT: GUILLOU-BONNICI, Francoise
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: MALLET, Francois
; APPLICANT: LEVASSEUR, Pierre
; APPLICANT: MCALLISTER, William
; TITLE OF INVENTION: CHIMERA OLIGONUCLEOTIDE AND ITS
; TITLE OF INVENTION: UTILIZATION FOR OBTAINING TRANSCRIPTS OF A NUCLEIC ACID
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/533,912
; FILING DATE: 26-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94011455
; FILING DATE: 26-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 36613
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6400
TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-08-533-912-6

Query Match 83.3%; Score 5; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.6e+08; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5
Db 1 GGGAG 5

RESULT 5
US-08-465-590-140
Sequence 140, Application US/08465590
Patent No. 5824770
GENERAL INFORMATION:
APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 164
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,590
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238,212
FILING DATE: 02-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-SEP-1993

ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,695
REFERENCE/DOCKET NUMBER: MPF-006C2DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-465-590-140

Query Match 83.3%; Score 5; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.6e+08; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5
Db 2 GGGAG 6

RESULT 6
US-08-711-417C-140
Sequence 140, Application US/08711417C
Patent No. 6228611
GENERAL INFORMATION:
APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 202
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/711,417C
FILING DATE: 05-SEP-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/238,212
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 08/121,438
FILING DATE: 14-SEP-1993
APPLICATION NUMBER: 07/946,233
FILING DATE: 14-SEP-1992

ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis P.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10287/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
SEQUENCE DESCRIPTION: SEQ ID NO: 140:
US-08-711-417C-140

Query Match 83.3%; Score 5; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.6e+08; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5
Db 2 GGGAG 6

RESULT 7
US-09-723-909-140
Sequence 140, Application US/09723909
Patent No. 6630141
GENERAL INFORMATION:
APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 202
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street

Query Match 83.3%; Score 5; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.6e+08; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5
Db 2 GGGAG 6

RESULT 7
US-09-723-909-140
Sequence 140, Application US/09723909
Patent No. 6630141
GENERAL INFORMATION:
APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 202
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street

/ CITY: Boston
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: Windows 95
/ SOFTWARE: FastSeq for Windows Version 2.0b
/ CURRENT APPLICATION DATA: US/09/723,909
/ FILING DATE: 28-NO. 6630141-2000
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/711,417
/ FILING DATE: 05-Sep-1996
/ APPLICATION NUMBER: 08/238,212
/ FILING DATE: 02-MAY-1994
/ APPLICATION NUMBER: 08/121,438
/ FILING DATE: 14-SEP-1993
/ APPLICATION NUMBER: 07/946,233
/ FILING DATE: 14-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Myers, Louis P.
/ REGISTRATION NUMBER: 35,965
/ REFERENCE/DOCKET NUMBER: 10287/007001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617/542-5070
/ TELEFAX: 617/542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 140:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ SEQUENCE DESCRIPTION: SEQ ID NO: 140:
US-09-723-909-140

Query Match 83.3%; Score 5; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.6e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5
| | | | |
DB 2 GGGAG 6

RESULT 8
US-09-686-631-12/c
/ Sequence 12, Application US/09686631
/ Patent No. 6716824
/ GENERAL INFORMATION:
/ APPLICANT: Bruniardi, F. C.
/ TITLE OF INVENTION: Promoter Driven Tissue Specific Cytotoxic Agents
/ FILE REFERENCE: A146.0136
/ CURRENT APPLICATION NUMBER: US/09/686,631
/ CURRENT FILING DATE: 2000-10-11
/ PRIOR APPLICATION NUMBER: 60/161,109
/ PRIOR FILING DATE: 1999-10-22
/ PRIOR APPLICATION NUMBER: UNKNOWN
/ PRIOR FILING DATE: 2000-08-09
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 12
/ LENGTH: 6
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-686-631-12

Query Match 83.3%; Score 5; DB 4; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.6e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGAG 5
| | | | |
DB 5 GGGAG 1

RESULT 9
US-09-657-289A-1
/ Sequence 1, Application US/09657289A
/ Patent No. 6737245
/ GENERAL INFORMATION:
/ APPLICANT: Francis, Kevin P.
/ APPLICANT: Contag, Pamela R.
/ APPLICANT: Joh, Danny J.
/ TITLE OF INVENTION: LUCIFERASE EXPRESSION CASSETTES AND METHODS OF USE
/ FILE REFERENCE: 9400-0006
/ CURRENT APPLICATION NUMBER: US/09/657,289A
/ CURRENT FILING DATE: 2000-09-07
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 6
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Gram-positive
/ OTHER INFORMATION: ribosome binding site
US-09-657-289A-1

Query Match 83.3%; Score 5; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.6e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGAG 6
| | | | |
DB 2 GGGAG 6

RESULT 10
US-08-453-485E-17
/ Sequence 17, Application US/08453485E
/ Patent No. 6828125
/ GENERAL INFORMATION:
/ APPLICANT: Baxter Biotech Technology Sarl
/ TITLE OF INVENTION: DNA ENCODING FUSED DI-ALPHA GLOBINS AND USE THEREOF
/ FILE REFERENCE: BXTB 1885
/ CURRENT APPLICATION NUMBER: US/08/453,485E
/ CURRENT FILING DATE: 1995-05-30
/ PRIOR APPLICATION NUMBER: 07/789,179
/ PRIOR FILING DATE: 1991-11-08
/ PRIOR APPLICATION NUMBER: 07/671,707
/ PRIOR FILING DATE: 1991-04-01
/ NUMBER OF SEQ ID NOS: 114
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 17
/ LENGTH: 6
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: spacer region
US-08-453-485E-17

Query Match 83.3%; Score 5; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.6e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGAG 6
| | | | |
DB 2 GGGAG 6

RESULT 11
PCT-US93-08743-140
; Sequence 140, Application PC/TUS9308743
; GENERAL INFORMATION:
; APPLICANT: IKAROS: A T CELL PATHWAY REGULATORY GENE
; TITLE OF INVENTION: 152
; NUMBER OF SEQUENCES: 152
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08743
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 946,233
; FILING DATE: 14-SEP-1992
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US93-08743-140

Query Match 83.3%; Score 5; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.6e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5
Db 2 GGGAG 6

RESULT 12
US-08-920-422-15
; Sequence 15, Application US/08920422A
; Patent No. 6255473
; GENERAL INFORMATION:
; APPLICANT: Vitek, Michael P.
; APPLICANT: Mitsuda, No. 6255473iaki
; APPLICANT: Roses, Allen D.
; TITLE OF INVENTION: Presenilin-1 Gene Promoter
; FILE REFERENCE: VITEKPRESENTILIN
; CURRENT APPLICATION NUMBER: US/08/920,422A
; CURRENT FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-920-422-15

Query Match 73.3%; Score 4.4; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.6e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGG 6
Db 1 GGGCGG 6

RESULT 13
US-08-920-422-16/c
; Sequence 16, Application US/08920422A
; Patent No. 6255473

; GENERAL INFORMATION:
; APPLICANT: Vitek, Michael P.
; APPLICANT: Mitsuda, No. 6255473iaki
; APPLICANT: Roses, Allen D.
; TITLE OF INVENTION: Presenilin-1 Gene Promoter
; FILE REFERENCE: VITEKPRESENTILIN
; CURRENT APPLICATION NUMBER: US/08/920,422A
; CURRENT FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-920-422-16

Query Match 73.3%; Score 4.4; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.6e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGG 6
Db 6 GGGCGG 1

RESULT 14
US-09-593-323-29
; Sequence 29, Application US/09593323
; Patent No. 6265213
; GENERAL INFORMATION:
; APPLICANT: Morgan, Antony R.
; APPLICANT: Severini, Alberto
; TITLE OF INVENTION: Compositions and Methods for Determining the Activity
; TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of
; TITLE OF INVENTION: Transcription
; FILE REFERENCE: DNAB-02921
; CURRENT APPLICATION NUMBER: US/09/593,323
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: 09/344,300
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-593-323-29

Query Match 73.3%; Score 4.4; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.6e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGG 6
Db 1 GGGCGG 6

RESULT 15
US-09-594-108-29
; Sequence 29, Application US/09594108
; Patent No. 6284468
; GENERAL INFORMATION:
; APPLICANT: Morgan, Antony R.
; APPLICANT: Severini, Alberto
; TITLE OF INVENTION: Compositions and Methods for Determining the Activity
; TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of
; TITLE OF INVENTION: Transcription
; FILE REFERENCE: DNAB-02921
; CURRENT APPLICATION NUMBER: US/09/594,108

; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: 09/344,300
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-594-108-29

Query Match 73.3%; Score 4.4; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.6e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGG 6
|||
Db 1 GGGCGG 6

RESULT 16

US-09-344-300-29
; Sequence 29, Application US/09344300B
; Patent No. 6297013
; GENERAL INFORMATION:
; APPLICANT: Morgan, Antony R.
; APPLICANT: Severini, Alberto
; TITLE OF INVENTION: Compositions and Methods for Determining the Activity
; TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of
; TITLE OF INVENTION: Transcription
; FILE REFERENCE: DNAB-02921
; CURRENT APPLICATION NUMBER: US/09/344,300B
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-344-300-29

Query Match 73.3%; Score 4.4; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.6e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGG 6
|||
Db 1 GGGCGG 6

RESULT 17

US-09-924-346-6
; Sequence 6, Application US/09924346
; Patent No. 655674
; GENERAL INFORMATION:
; APPLICANT: Jens Tornoe
; TITLE OF INVENTION: The Jet Promoter
; FILE REFERENCE: 19313-005
; CURRENT APPLICATION NUMBER: US/09/924,346
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/224,087
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Chemically
; OTHER INFORMATION: Synthesized
US-09-924-346-6

Query Match 73.3%; Score 4.4; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.6e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGG 6
|||
Db 1 GGGCGG 6

RESULT 18

US-09-483-184A-6/c
; Sequence 6, Application US/09483184A
; Patent No. 6800750
; GENERAL INFORMATION:
; APPLICANT: DARTMOUTH COLLEGE
; APPLICANT: CRAIG, Ruth W.
; APPLICANT: BINGLE, Colin D.
; APPLICANT: WHYTE, Moira
; TITLE OF INVENTION: Mcl-1 GENE REGULATORY ELEMENTS AND A PRO-APOPTOTIC Mcl-1 VARIANT
; FILE REFERENCE: DART1110-1
; CURRENT APPLICATION NUMBER: US/09/483,184A
; CURRENT FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/166,113
; PRIOR FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide for PCR
US-09-483-184A-6

Query Match 73.3%; Score 4.4; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.6e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGG 6
|||
Db 6 GGGCGG 1

RESULT 19

PCT-US94-06456-9/c
; Sequence 9, Application PC/TUS9406456
; GENERAL INFORMATION:
; APPLICANT: Beutel, Bruce A.
; APPLICANT: Coppola, George R.
; APPLICANT: Sherman, Michael I.
; TITLE OF INVENTION: Oligonucleotides Which Inhibit HIV Protease Function
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carelia, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC - DOS
; SOFTWARE: DW4.V2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06456
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/073,873
FILING DATE: 09-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliott M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 23550-89
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: oligonucleotide
PCT-US94-06456-9

Query Match 66.7%; Score 4; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 3.9e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GAGG 6
DB 4 GAGG 1

RESULT 20
PCT-US94-06456-38/c
Sequence 38, Application PC/TUS9406456
GENERAL INFORMATION:
APPLICANT: Beutel, Bruce A.
APPLICANT: Coppola, George R.
APPLICANT: Sherman, Michael I.
TITLE OF INVENTION: Oligonucleotides Which Inhibit HIV Protease Function
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC - DOS
SOFTWARE: DM4 V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06456
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,873
FILING DATE: 09-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliott M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 23550-89
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: oligonucleotide
PCT-US94-06456-38

Query Match 66.7%; Score 4; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 3.9e+08;

APPLICATION NUMBER: 08/247,809A-15
Sequence 15, Application US/08247809A
Patent No. 5569823
GENERAL INFORMATION:
APPLICANT: Peter H. Schreier; Klaus Stenzel; Gunter Adam;
APPLICANT: Edgar Maiss
TITLE OF INVENTION: DEOXYRIBONUCLEIC ACIDS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPRUNG HORN KRAMER & WOODS
STREET: 660 White Plains Road
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-5144

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB
MEDIUM TYPE: storage
COMPUTER: NEC Powermate 1 Plus
OPERATING SYSTEM: DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/247,809A
FILING DATE: May 23, 1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 43 178 45.6 (Germany)
FILING DATE: May 28, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: Bayer 9049-KGB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-247-809A-15

Query Match 66.7%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.1e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GAGG 6
DB 2 GAGG 5

RESULT 22
US-08-381-097A-14
Sequence 14, Application US/08381097A
Patent No. 5643890
GENERAL INFORMATION:
APPLICANT: Iverson, Patrick L.
APPLICANT: Mata, John E.
TITLE OF INVENTION: Synthetic Oligodeoxyribonucleotides
TITLE OF INVENTION: Which Mimic Telomeric Sequences for Use in the Treatment
TITLE OF INVENTION: of Cancer and Other Diseases
NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Zarely, McKee, Thomte, Voorhees, & Sease
 ; STREET: 801 Grand Suite 3200
 ; CITY: Des Moines
 ; STATE: Iowa
 ; COUNTRY: United States
 ; ZIP: 50309
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/381,097A
 ; FILING DATE: 31-JAN-1995
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Nebel, Heidi S
 ; REGISTRATION NUMBER: 37,719
 ; REFERENCE/DOCKET NUMBER: unmc 63092
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 515-288-3667
 ; TELEFAX: 515-288-1338
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: other nucleic acid
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; US-08-381-097A-14

Query Match 66.7%; Score 4; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.1e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GAGG 6
 Db 2 GAGG 5

RESULT 23
 US-08-597-948A-6/c
 ; Sequence 6, Application US/08597948A
 ; Patent No. 595322
 ; GENERAL INFORMATION:
 ; APPLICANT: Guarnieri, Frank
 ; APPLICANT: Bancroft, Frank Carter
 ; TITLE OF INVENTION: A DNA-BASED COMPUTER
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Baker & Botts
 ; STREET: 30 Rockefeller Plaza
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10112
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: Fast SEQ VERSION 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/597,948A
 ; FILING DATE: 7 February 1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION NUMBER:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kole, Lisa B.

; REGISTRATION NUMBER: 35,225
 ; REFERENCE/DOCKET NUMBER: 30372 070165.0385
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-408-2500
 ; TELEFAX: 212-765-2519
 ; TELELEX:
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 bases
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; HYPOTHETICAL:
 ; ANTI-SENSE:
 ; FRAGMENT TYPE:
 ; ORIGINAL SOURCE:
 ; US-08-597-948A-6

Query Match 66.7%; Score 4; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.1e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGAG 5
 Db 5 GGAG 2

RESULT 24
 US-08-711-728-15
 ; Sequence 15, Application US/08711728
 ; Patent No. 5973135
 ; GENERAL INFORMATION:
 ; APPLICANT: Peter H. Schreier; Klaus Stenzel; Gunter Adam;
 ; APPLICANT: Edgar Maiss
 ; TITLE OF INVENTION: DEOXYRIBONUCLEIC ACIDS
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SPRUNG HORN KRAMER & WOODS
 ; STREET: 660 White Plains Road
 ; CITY: Tarrytown
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10591-5144
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB
 ; MEDIUM TYPE: storage
 ; COMPUTER: NEC Powermate 1 Plus
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: WordPerfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/711,728
 ; FILING DATE: 03-SEPT-1996
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION NUMBER:
 ; APPLICATION NUMBER: 08/247,809
 ; FILING DATE: 23-MAY-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DE 43178456
 ; FILING DATE: 28-MAY-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kurt G. Briescoe
 ; REGISTRATION NUMBER: 33,141
 ; REFERENCE/DOCKET NUMBER: Bayer 9049.1-KGB
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (914) 332-1700
 ; TELEFAX: (914) 332-1844
 ; TELELEX:
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-711-728-15

Query Match
Best Local Similarity 66.7%; Score 4; DB 2; Length 5;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GAGG 6
DB 2 GAGG 5

RESULT 25
US-08-873-709-8
; Sequence 8, Application US/08873709
; Patent No. 6037126
; GENERAL INFORMATION:
; APPLICANT: Grossman, Abraham
; TITLE OF INVENTION: COMPOSITIONS, METHODS, KITS AND
; TITLE OF INVENTION: APPARATUS FOR DETERMINING THE PRESENCE OR ABSENCE OF
; TITLE OF INVENTION: PROTEIN COMPONENT OF TELOMERASE ENZYME
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abraham Grossman
; STREET: 666 Washington Avenue
; CITY: Pleasantville
; STATE: NY
; COUNTRY: USA
; ZIP: 10570
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/873,709
; FILING DATE: 12-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Janiuk, Anthony J.
; REGISTRATION NUMBER: 29,809
; REFERENCE/DOCKET NUMBER: Q001/002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 914-747-9108
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
US-08-873-709-8

Query Match
Best Local Similarity 66.7%; Score 4; DB 3; Length 5;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGA 4
DB 1 GGGA 4

RESULT 26
US-08-921-497-12/c
; Sequence 12, Application US/08921497
; Patent No. 6521225
; GENERAL INFORMATION:
; APPLICANT: Srivastava, Arun
; APPLICANT: Ponnazhagan, Selvarangan
; APPLICANT: Chloemer, Robert H.
; APPLICANT: Wang, Xu-Shan
; APPLICANT: Yoder, Mervin C.
; APPLICANT: Zhou, Shang-Zhen
; APPLICANT: Escobedo, Jaime
; APPLICANT: Variavani, Dwaraki
; TITLE OF INVENTION: An AAV Vector Having Two Modified D-Sequences (As Amended)
; FILE REFERENCE: 1242.003
; CURRENT APPLICATION NUMBER: US 60/025,616
; PRIOR FILING DATE: 1996-09-06
; PRIOR APPLICATION NUMBER: US 60/025,649
; PRIOR FILING DATE: 1996-09-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 5
; TYPE: DNA
; ORGANISM: adenoassociated virus
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: D-sequence in ITRs
; OTHER INFORMATION: Antisense strand
US-08-921-497-14

Query Match
Best Local Similarity 66.7%; Score 4; DB 4; Length 5;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAG 5
DB 2 GGAG 5

RESULT 27
US-08-921-497-14
; Sequence 14, Application US/08921497
; Patent No. 6521225
; GENERAL INFORMATION:
; APPLICANT: Srivastava, Arun
; APPLICANT: Ponnazhagan, Selvarangan
; APPLICANT: Chloemer, Robert H.
; APPLICANT: Wang, Xu-Shan
; APPLICANT: Yoder, Mervin C.
; APPLICANT: Zhou, Shang-Zhen
; APPLICANT: Escobedo, Jaime
; APPLICANT: Variavani, Dwaraki
; TITLE OF INVENTION: An AAV Vector Having Two Modified D-Sequences (As Amended)
; FILE REFERENCE: 1242.003
; CURRENT APPLICATION NUMBER: US/08/921,497
; CURRENT FILING DATE: 1997-09-02
; PRIOR APPLICATION NUMBER: US 60/025,616
; PRIOR FILING DATE: 1996-09-06
; PRIOR APPLICATION NUMBER: US 60/025,649
; PRIOR FILING DATE: 1996-09-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 5
; TYPE: DNA
; ORGANISM: adenoassociated virus
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: D-sequence in ITRs
; OTHER INFORMATION: Antisense strand
US-08-921-497-14

Query Match
Best Local Similarity 66.7%; Score 4; DB 4; Length 5;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAG 5
DB 2 GGAG 5
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RESULT 28
PCT-US93-03027-7
; Sequence 7, Application PC/TUS9303027
; GENERAL INFORMATION:
; APPLICANT: LEONARD, WARREN; TOLEDANO,
; APPLICANT: MICHEL
; TITLE OF INVENTION: CONTROL AND/OR
; PREVENTION OF BINDING OF NF- B/REL/DORSAL
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/03027
; FILING DATE: 19930401
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/862,987
; FILING DATE: 06-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: P-36,434
; REFERENCE/DOCKET NUMBER: 2026-4010 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: Unknown
; MOLECULE TYPE: oligonucleotide
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: "A" half of Ig- B binding
; NAME/KEY: site
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
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Query Match 66.7%; Score 4; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.1e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGA 4
DB 1 GGGA 4
RESULT 29
US-08-242-402-20/c
; Sequence 20, Application US/08242402
; Patent No. 5580967
; GENERAL INFORMATION:
; APPLICANT: JOYCE, GERALD F
; TITLE OF INVENTION: OPTIMIZED CATALYTIC DNA-CLEAVING
; TITLE OF INVENTION: RIBOZYMES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE, OFFICE OF
; ADDRESSEE: PATENT COUNSEL
; STREET: 10666 NORTH TORREY PINES ROAD, TPC 8

; CITY: LA JOLLA
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/242,402
; FILING DATE: 13-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LOGAN, APRIL C
; REGISTRATION NUMBER: 33,950
; REFERENCE/DOCKET NUMBER: TSRI 412.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-242-402-20
Query Match 66.7%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.6e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GAGG 6
DB 5 GAGG 2
RESULT 30
US-08-270-180-19/c
; Sequence 19, Application US/08270180
; Patent No. 5595873
; GENERAL INFORMATION:
; APPLICANT: Joyce, Gerald F.
; TITLE OF INVENTION: ENZYMAIC RNA MOLECULES THAT CLEAVE
; TITLE OF INVENTION: AMIDE BONDS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5595873th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/270,180
; FILING DATE: 01-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/242,402
; FILING DATE: 13-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Logan, April C.
; REGISTRATION NUMBER: 33,950
; REFERENCE/DOCKET NUMBER: TSRI 412.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937

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; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 6 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   FEATURE:
;     NAME/KEY: misc_feature
;     LOCATION: 6
;     OTHER INFORMATION: /label= N
;     OTHER INFORMATION: /note= "N SIGNIFIES A NUCLEOTIDE ANALOG"
; US-08-270-180-19

Query Match      66.7%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.6e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 GAGG 6
        ||||
Db      5 GAGG 2
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Search completed: July 21, 2005, 04:29:26
Job time : 58 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:25:43 ; Search time 1348.8 Seconds
(without alignments)
169.325 Million cell updates/sec

Title: US-09-735-363A-45

Perfect score: 6

Sequence: 1 gggagg 6

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 1216

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 3	4	66.7	5	7	CF327578 NACL--02-
C 4	4	66.7	6	7	CF314367 HD--02-N2
C 5	4	66.7	6	7	CF338772 RCL1--02-
C 6	3.4	56.7	5	7	CF327761 NACL--02-
C 7	3.4	56.7	5	7	CF920850 gmrhrw3-
C 8	3.4	56.7	5	9	CL658581 PRI0131d
C 9	3.4	56.7	6	7	CF312755 ABF--08-K
C 10	3.4	56.7	6	9	CL683697 PRI0137c
C 11	3	50.0	3	7	CF282217 14ETL--05-
C 12	3	50.0	3	7	CF300120 7LEAF--04
C 13	3	50.0	3	7	CF315089 HD--03-N2
C 14	3	50.0	3	7	CF315183 HD--04-A0
C 15	3	50.0	3	7	CF339761 RCL1--05-
C 16	3	50.0	3	7	CO790264 NT009A-H0
C 17	3	50.0	3	9	CL674562 PRI0112c
C 18	3	50.0	3	9	CL679821 PRI0127a
C 19	3	50.0	4	1	AL045617 DXFZp4340
C 20	3	50.0	4	6	CA853244 B06A04.se
C 21	3	50.0	4	6	CA853352 B07C08.se
C 22	3	50.0	4	7	CF300913 7LEAF--05
C 23	3	50.0	4	7	CF307853 ABF--01-G
C 24	3	50.0	4	7	CF317789 HD--07-J1

CF338536	RCL1--01-	4	7	CF338536	50.0	3	50.0
CN755098	ID0AAAI4D	4	9	CN755098	50.0	3	50.0
CL651736	PRI0112d	4	9	CL651736	50.0	3	50.0
CK584110	IST_WI5_1	5	7	CK584110	50.0	3	50.0
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CL661701	PRI013c_C	5	9	CL661701	50.0	3	50.0
CL673276	PRI019a-E	5	9	CL673276	50.0	3	50.0
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AL039947	DXFZp434J	6	1	AL039947	50.0	3	50.0
AL042484	DXFZp434F	6	1	AL042484	50.0	3	50.0
CA802833	DXFZp434G	6	1	CA802833	50.0	3	50.0
CA850792	D06E12_E1	6	6	CA850792	50.0	3	50.0
CA850861	D07D05_G1	6	6	CA850861	50.0	3	50.0
CF302557	7LEAF--08	6	7	CF302557	50.0	3	50.0
CF310635	ABF--05-G	6	7	CF310635	50.0	3	50.0
CF332957	JMT--01-K	6	7	CF332957	50.0	3	50.0
CF920971	gmrhrw3-	6	7	CF920971	50.0	3	50.0
CF921483	gmrhrw3-	6	7	CF921483	50.0	3	50.0
CL665420	PRI0149C	6	9	CL665420	50.0	3	50.0
CL65420	PRI0149C	6	9	CL65420	50.0	3	50.0
CL682618	PRI0134C	6	9	CL682618	50.0	3	50.0
CL689395	PRI0151a	6	9	CL689395	50.0	3	50.0
CA850974	D08G08_N2	4	6	CA850974	40.0	2.4	40.0
CF317391	HD--07-B0	4	7	CF317391	40.0	2.4	40.0
CL655267	PRI0122d	4	9	CL655267	40.0	2.4	40.0
CL670570	PRI0182C	4	9	CL670570	40.0	2.4	40.0
CL677539	PRI0120C	4	9	CL677539	40.0	2.4	40.0
CA853329	B07A01.se	5	6	CA853329	40.0	2.4	40.0
CF282401	14ETL--09	5	7	CF282401	40.0	2.4	40.0
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CF314074	HD--02-H0	5	7	CF314074	40.0	2.4	40.0
CF320271	HD--11-B1	5	7	CF320271	40.0	2.4	40.0
CF323326	HDN--03-I	5	7	CF323326	40.0	2.4	40.0
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CF331773	NACL--08-	6	7	CF331773	40.0	2.4	40.0
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AL042337	DXFZp4340	2	1	AL042337	33.3	2	33.3
AL043859	DXFZp434B	2	1	AL043859	33.3	2	33.3
AL047069	DXFZp586P	2	1	AL047069	33.3	2	33.3
BX266185	BX266185	2	5	BX266185	33.3	2	33.3
BX266563	BX266563	2	5	BX266563	33.3	2	33.3
BX267118	BX267118	2	5	BX267118	33.3	2	33.3
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CF280511	14ETL--07	2	7	CF280511	33.3	2	33.3
CF291112	14ROOT--0	2	7	CF291112	33.3	2	33.3
CF299820	7LEAF--03	2	7	CF299820	33.3	2	33.3
CF307123	HDAL--05-	2	7	CF307123	33.3	2	33.3
CF307878	ABF--01-H	2	7	CF307878	33.3	2	33.3
CF311389	ABF--06-J	2	7	CF311389	33.3	2	33.3
CF311851	ABF--07-E	2	7	CF311851	33.3	2	33.3
CF315237	HD--04-B0	2	7	CF315237	33.3	2	33.3
CF329006	NACL--04-	2	7	CF329006	33.3	2	33.3
CF340219	RCL1--07-	2	7	CF340219	33.3	2	33.3
CK632229	AM1-AM000	2	7	CK632229	33.3	2	33.3
CN411958	170005322	2	7	CN411958	33.3	2	33.3
CO788520	NT004B_H0	2	7	CO788520	33.3	2	33.3
CR774574	DXFZp469G	2	7	CR774574	33.3	2	33.3
CR787484	DXFZp469H	2	7	CR787484	33.3	2	33.3
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CL423384	O1S0354-0	2	9	CL423384	33.3	2	33.3
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CL677053	PRI011b_B	2	9	CL677053	33.3	2	33.3
CL681455	PRI0131a	2	9	CL681455	33.3	2	33.3
CL683975	PRI0138b	2	9	CL683975	33.3	2	33.3
CL688890	PRI014d_A	2	9	CL688890	33.3	2	33.3
CL688912	PRI014d_C	2	9	CL688912	33.3	2	33.3
CL690186	PRI0153a	2	9	CL690186	33.3	2	33.3
CL690813	PRI0154d	2	9	CL690813	33.3	2	33.3
CL694963	PRI0165C	2	9	CL694963	33.3	2	33.3

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c 99 2 33.3 3 5 BX267257 BX267257
c 100 2 33.3 3 6 CA850938 CA850938

ALIGNMENTS

RESULT 1
LOCUS CL664862
DEFINITION PRI0148a H04 - PRI0148a.B21 (5) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.
ACCESSION CL664862
VERSION CL664862.1 GI:50155779
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 5)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppADB: an AcedB database for the nematode satellite organism Pristionchus pacificus
JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spenannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: raif.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.

FEATURES
source

1..5 Location/Qualifiers
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus var. California"
/note="Vector: pEpifos-5 Fosmid vector"

ORIGIN

Query Match 83.3%; Score 5; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.6e+09; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6
|||||
Db 1 GGAGG 5

RESULT 2
CK582549/c
LOCUS CK582549
DEFINITION IST W15 41282 AD-wrmcDNA library Caenorhabditis elegans cDNA 5' similar to K07A12.3, mRNA sequence.
ACCESSION CK582549
VERSION CK582549.1 GI:40966478
KEYWORDS EST.
SOURCE Caenorhabditis elegans

ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae; Rhabditidae; Pelodierinae; Caenorhabditis.

REFERENCE 1 (bases 1 to 4)
AUTHORS Li,S., Armstrong,C.M., Bertin,N., Ge,H., Milstein,S., Boxem,M., Vidalain,P.O., Han,J.D., Chesneau,A., Hao,T., Goldberg,D.S., Li,N., Martinez,M., Rual,J.F., Lamesch,P., Xu,L., Tewari,M., Wong,S.L.,

TITLE
JOURNAL
COMMENT

A Map of the Interactome Network of the Metazoan C. elegans
Science (2004) In press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu

For the purpose of protein interaction mapping, we generated a C. elegans cDNA library (AD-wrmcDNA) in which poly(dT)-primed reverse transcribed cDNA are fused to the AD-encoding sequence of the yeast transcription factor GAL4. cDNAs were generated and cloned into the two hybrid vector pPC86 This interacting Sequence Tag IST_W15_41282 (K07A12.3) interacts as a prey with the bait E02H1.7

PCR Primers

FORWARD: CGCGTTGGGAATCACTACAGG

BACKWARD: GGAGCTTGACCAACCTCTGGCG

Insert Length: 4 Std Error: 3.00

Plate: 540 row: 07 column: A

Seq primer: CGCGTTGGGAATCACTACAGG

High quality sequence stop: 3

POLYA=No.

FEATURES
Location/Qualifiers

1..4
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="male, hermaphrodite"
/dev_stage="embryos L1 L2 L3 L4, adult, dauer"
/clone_lib="AD-wrmcDNA library"
/note="Vector: pPC86; For the purpose of protein interaction mapping, we generated a C. elegans cDNA library (AD-wrmcDNA) in which poly(dT)-primed reverse transcribed cDNA are fused to the AD-encoding sequence of the yeast transcription factor GAL4. This library was made with poly(A)+ RNA isolated from mated populations of wild-type (N2 strain) animals of all stages of development including embryonic, larval (L1 to L4 stages), adults and dauer. Approximately equal quantities of RNA from different populations were acquired. cDNAs were generated and cloned into the two hybrid vector pPC86. The library contains ~3x10⁶ clones. Reference - GATEWAY

recombinational cloning: application to the cloning of large numbers of open reading frames or ORFeomes - Walhout AJ, Temple GF, Brasch MA, Hartley JL, Iorson MA, van den Heuvel S, Vidal M - Methods Enzymol. 2000;328:575-92"

ORIGIN

Query Match 66.7%; Score 4; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+09; Mismatches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAG 5
|||||
Db 4 GGAG 1

RESULT 3

CF327578/c

LOCUS

DEFINITION

CF327578

NACU--02-B23.b1 Rice callus plasmid cDNA library (NACL) Oryza

sativa (japonica cultivar-group) cDNA clone NACL--02-B23, mRNA

sequence.

CF327578

ACCESSION


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Query Match      56.7%; Score 3.4; DB 9; Length 5;
Best Local Similarity 80.0%; Pred. No. 7.6e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GGAGG 6
      ||||
Db      1 GAAGG 5

RESULT 9
CF312755      6 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION
ABP--08-K07.b1 ABP3-overexpressing transgenic rice plasmid cDNA
library (ABP) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--08-K07, mRNA sequence.
ACCESSION
CF312755
VERSION
CF312755.1 GI:33684516
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 6)
REFERENCE
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1. .6
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABP--08-K07"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

ORIGIN

Query Match      56.7%; Score 3.4; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGAG 5
      |||
Db      2 GGGTG 6

RESULT 10
CL683697/c
LOCUS
DEFINITION
PR10137c.D12.2 - PR10137c.BR (6) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION
CL683697
VERSION
CL683697.1 GI:50191457
KEYWORDS
GSS.

SOURCE
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nemata; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 6)
REFERENCE
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AppADB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
JOURNAL
COMMENT
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Classes: fosmid ends.
Location/Qualifiers
1. .6
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/notes="Vector: pEpifos-5 Fosmid vector"

ORIGIN

Query Match      56.7%; Score 3.4; DB 9; Length 6;
Best Local Similarity 80.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGAG 5
      ||||
Db      5 GGAAG 1

RESULT 11
CF282217
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-K02,
mRNA sequence.
ACCESSION
CF282217
VERSION
CF282217.1 GI:33659604
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 3)
REFERENCE
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1. .3
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="14ETL--09-K02"

ORIGIN

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/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN
Query Match      50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GGA 4
        |||
Db       1 GGA 3

RESULT 12
CF300120/c
LOCUS
DEFINITION
3 bp mRNA linear EST 15-AUG-2003
7LEAF--04-G11.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--04-G11, mRNA
sequence.
ACCESSION
CF300120
VERSION
CF300120.1 GI:33671881
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 3)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL
COMMENT
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
source
1..3
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--04-G11"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN
Query Match      50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 AGG 6
        |||
Db       3 AGG 1

RESULT 13
CF315089
LOCUS
DEFINITION
3 bp mRNA linear EST 15-AUG-2003

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HD--03-N24.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--03-N24, mRNA sequence.
CF315089
VERSION
CF315089.1 GI:33686850
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 3)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
source
1..3
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--03-N24"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

ORIGIN
Query Match      50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGG 3
        |||
Db       1 GGG 3

RESULT 14
CF315183
LOCUS
DEFINITION
3 bp mRNA linear EST 15-AUG-2003
HD--04-A04.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--04-A04, mRNA sequence.
CF315183
VERSION
CF315183.1 GI:33686944
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 3)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

```

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1. .3
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD-04-A04"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

FEATURES
source
1. .3
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone="HD-04-A04"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGA 4
|||
Db 1 GGA 3

RESULT 15
CF339761
LOCUS
DEFINITION
RCL1--05-N20.g1 Regenerated callus lambda phage cDNA library (RCL1)
Oryza sativa (japonica cultivar-group) cDNA clone RCL1--05-N20,
mRNA sequence.
CF339761
VERSION
CF339761.1 GI:33827892
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoidae; Oryzaceae; Oryza.
1 (bases 1 to 3)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1. .3
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="RCL1-05-N20"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
/notes="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1. .3
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD-04-A04"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

FEATURES
source
1. .3
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD-04-A04"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGA 4
|||
Db 1 GGA 3

RESULT 15
CF339761
LOCUS
DEFINITION
RCL1--05-N20.g1 Regenerated callus lambda phage cDNA library (RCL1)
Oryza sativa (japonica cultivar-group) cDNA clone RCL1--05-N20,
mRNA sequence.
CF339761
VERSION
CF339761.1 GI:33827892
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoidae; Oryzaceae; Oryza.
1 (bases 1 to 3)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1. .3
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="RCL1-05-N20"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
/notes="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was

induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGG 3
|||
Db 1 GGG 3

RESULT 16
CO790264
LOCUS
DEFINITION
NT009A.H05 St18-22 Neural tube (NT) Ambystoma mexicanum cDNA 5',
similar to hypothetical protein, mRNA sequence.
CO790264
ACCESSION
CO790264.1 GI:51006235
VERSION
CO790264.1
SOURCE
EST.
Ambystoma mexicanum (axolotl)
ORGANISM
Ambystoma mexicanum
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
Ambystoma.
1 (bases 1 to 3)
Habermann,B., Bebin,A.G., Herklotz,S., Volkmer,M., Eckelt,K.,
Pehlke,K., Epperlein,H.H., Schackert,H.K., Wiebe,G. and Tanaka,E.M.
An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
expressed sequence tags from embryonic and regenerating blastema
cDNA libraries
Genome Biol. (2004) In press
Contact: Ely M. Tanaka
Tanaka Lab
Max Planck Institute of Molecular Cell Biology and Genetics,
Dresden
Protenhauerstrasse 108, 01307 Dresden, Germany
Tel: 0049 351 210 2620
Fax: 0049 351 210 1489
Email: tanaka@mpi-cbg.de
Plate: NT009A row: 05 column: H
Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
Location/Qualifiers
1. .3
/organism="Ambystoma mexicanum"
/mol_type="mRNA"
/db_xref="taxon:8296"
/tissue_type="Neural Tube, Notochord, Somites"
/cell_type="Includes Neural tube, notochord, somites"
/dev_stage="Stage 18-22"
/clone_lib="St18-22 Neural tube (NT)"
/notes="Vector: pCMVSPORT6; Site 1: NotI; Site 2: SalI;
Unnormalized cDNA plasmid library prepared by Invitrogen.
Size fractionated mRNA was polydt primed and cloned into
NotI-SalI site of pCMVSPORT6. Bacterial host is
EMDH10B-TONA. Average insert size is 1.5 KB.
TAG_LIB=NT"

FEATURES
source
1. .3
/organism="Ambystoma mexicanum"
/mol_type="mRNA"
/db_xref="taxon:8296"
/tissue_type="Neural Tube, Notochord, Somites"
/cell_type="Includes Neural tube, notochord, somites"
/dev_stage="Stage 18-22"
/clone_lib="St18-22 Neural tube (NT)"
/notes="Vector: pCMVSPORT6; Site 1: NotI; Site 2: SalI;
Unnormalized cDNA plasmid library prepared by Invitrogen.
Size fractionated mRNA was polydt primed and cloned into
NotI-SalI site of pCMVSPORT6. Bacterial host is
EMDH10B-TONA. Average insert size is 1.5 KB.
TAG_LIB=NT"

ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGG 6
|||
Db 1 AGG 3

RESULT 17
CL674562/c
LOCUS
DEFINITION
PRI0112c.A06_2 - PRI0112c.BR (3) Mixed stage foemid library of P.

pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.

ACCESSION CL674562
VERSION CL674562.1 GI:50177804

KEYWORDS GSS.

SOURCE Pristionchus pacificus

ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.

REFERENCE 1 (bases 1 to 3)

AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.

TITLE AppADB: an AcedB database for the nematode satellite organism

JOURNAL Pristionchus pacificus

COMMENT Nucleic Acids Res. 32 (1), D421-D422 (2004)

Contact: Sommer RJ

Evolutionary Biology

Max-Planck-Institute for Developmental Biology

Spemannstr. 37-39, Tuebingen D-72076, Germany

Tel: 00497071601371

Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de

This library was generated at Caltech, Pasadena, USA and end

sequenced at Vancouver, Canada.

Seq primer: T7

Class: fosmid ends.

FEATURES Location/Qualifiers

source

1..3

/organism="Pristionchus pacificus"

/mol_type="genomic DNA"

/strain="California"

/db_xref="taxon:54126"

/clone_lib="Mixed stage fosmid library of P. pacificus

var. California"

/note="Vector: pEpifos-5 Fosmid vector"

ORIGIN

Query Match

Best Local Similarity 50.0%; Score 3; DB 9; Length 3;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGA 4

Db |||

3 GGA 1

RESULT 18

CL679821/c

LOCUS

DEFINITION PRI0127a_E01_2 - PRI0127a.BR (3) Mixed stage fosmid library of P.

pacificus var. California Pristionchus pacificus genomic, genomic

survey sequence.

ACCESSION CL679821

VERSION CL679821.1 GI:50186536

KEYWORDS GSS.

SOURCE Pristionchus pacificus

ORGANISM Pristionchus pacificus

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.

REFERENCE 1 (bases 1 to 3)

AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.

TITLE AppADB: an AcedB database for the nematode satellite organism

JOURNAL Pristionchus pacificus

COMMENT Nucleic Acids Res. 32 (1), D421-D422 (2004)

Contact: Sommer RJ

Evolutionary Biology

Max-Planck-Institute for Developmental Biology

Spemannstr. 37-39, Tuebingen D-72076, Germany

Tel: 00497071601371

Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de

This library was generated at Caltech, Pasadena, USA and end

sequenced at Vancouver, Canada.

Seq primer: T7

Class: fosmid ends.

FEATURES Location/Qualifiers

source

1..3

/organism="Pristionchus pacificus"

/mol_type="genomic DNA"

/strain="California"

/db_xref="taxon:54126"

/clone_lib="Mixed stage fosmid library of P. pacificus

var. California"

/note="Vector: pEpifos-5 Fosmid vector"

ORIGIN

Query Match

Best Local Similarity 50.0%; Score 3; DB 9; Length 3;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGG 6

Db |||

3 AGG 1

RESULT 19

AL045617/c

LOCUS

DEFINITION DKFZp4340245_r1 434 (synonym: htes3) Homo sapiens cDNA clone

4 bp mRNA linear EST 06-JUL-2004

ACCESSION DKFZp4340245 mRNA sequence.

VERSION AL045617.1 GI:49682620

KEYWORDS EST.

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4)

AUTHORS Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and

Wiemann,S.

TITLE EST (Duesterhoeft, et al.)

JOURNAL Unpublished (1999)

COMMENT Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES

source

1..4

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp4340245"

/tissue_type="testis"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="434 (synonym: htes3)"

/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN

Query Match

Best Local Similarity 50.0%; Score 3; DB 1; Length 4;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGG 6

Db |||

3 AGG 1

RESULT 20

CA853244

LOCUS

DEFINITION B06A04.seq cDNA Peking library 12hr SCN3 glycine max cDNA clone

4 bp mRNA linear EST 01-AUG-2003

ACCESSION B06A04.5 mRNA sequence.

VERSION CA853244

COMMENT CA853244.1 GI:33390037

EST.

SOURCE Glycine max (soybean)

ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

1 (bases 1 to 4)

Alkharouf, N.W., Khan, R. and Matthews, B.F.

Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode

Unpublished (2002)

Contact: Alkharouf, N.W.

Soybean Genomics and Improvement Laboratory (SGIL)

US Department of Agriculture (USDA), ARS, PSI

Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350, USA

Tel: 301 504 5750

Fax: 301 504 5728

Email: alkharouf@ba.ars.usda.gov.

Location/Qualifiers

FEATURES

source

1..4

/organism="Glycine max"

/mol_type="mRNA"

/cultivar="Peking"

/db_xref="taxon:3847"

/clone="B06A04"

/tissue_type="Roots"

/dev_stage="Seedlings"

/clone_lib="cDNA Peking library 12hr SCN3"

/note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from roots of soybean cv. Peking 12 hrs after infection by SCN race 3. These are cloned in pBluescript SK- phagemid."

ORIGIN

Query Match 50.0%; Score 3; DB 6; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.5e+09;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGG 3

|||

Db 1 GGG 3

RESULT 21

CA853352/c

LOCUS

DEFINITION B07C08.seq cDNA Peking library 12hr SCN3 Glycine max cDNA clone

B07C08 5', mRNA sequence.

CA853352

VERSION

KEYWORDS

SOURCE

ORGANISM

Glycine max (soybean)

Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

Glycine.

1 (bases 1 to 4)

Alkharouf, N.W., Khan, R. and Matthews, B.F.

Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode

Unpublished (2002)

Contact: Alkharouf, N.W.

Soybean Genomics and Improvement Laboratory (SGIL)

US Department of Agriculture (USDA), ARS, PSI

Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350, USA

Tel: 301 504 5750

Fax: 301 504 5728

Email: alkharouf@ba.ars.usda.gov.

Location/Qualifiers

FEATURES

source

1..4

/organism="Glycine max"

/mol_type="mRNA"

/cultivar="Peking"

/db_xref="taxon:3847"

/clone="B07C08"

/tissue_type="Roots"

/dev_stage="Seedlings"

/clone_lib="cDNA Peking library 12hr SCN3"

/note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from roots of soybean cv. Peking 12 hrs after infection by SCN race 3. These are cloned in pBluescript SK- phagemid."

ORIGIN

Query Match 50.0%; Score 3; DB 6; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.5e+09;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGG 3

|||

Db 4 GGG 2

RESULT 22

CF300913/c

LOCUS

DEFINITION

7LEAF--05-J02.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--05-J02, mRNA sequence.

CF300913

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoidae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 4)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Gyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..4

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--05-J02"

/tissue_type="leaf"

/dev_stage="7 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

ORIGIN

Query Match 50.0%; Score 3; DB 7; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.5e+09;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGG 3

|||

Db 3 GGG 1

RESULT 23

```

CF307853/c
LOCUS               CF307853               4 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION          ABF--01-G24.b1 ABF3-overexpressing transgenic rice plasmid cDNA
                    library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ACCESSION            CF307853
VERSION              CF307853.1   GI:33679614
KEYWORDS
SOURCE
ORGANISM              Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 4)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
JOURNAL
COMMENT              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                    of Bioscience and Bioinformatics, Myongji University
                    Yongin, Kyeonggi, Korea
                    Tel: 82 31 330 6193
                    Fax: 82 31 321 6355
                    Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
FEATURES             source
1..4
   /organism="Oryza sativa (japonica cultivar-group)"
   /mol_type="mRNA"
   /cultivar="Nackdong"
   /db_xref="taxon:39947"
   /clone="ABF--01-G24"
   /tissue_type="leaf"
   /dev_stage="14 days after germination"
   /lab_host="E.coli DH10B"
   /clone_lib="ABF3-overexpressing transgenic rice plasmid
   cDNA library (ABF)"
   /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
   for 2hrs. Oligo-capped mRNA was reverse transcribed and
   then used for PCR. mRNA was prepared from ABA-responsive
   element binding transcription factor 3 overexpression
   line."
ORIGIN
Query Match          50.0%; Score 3; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGG 6
   |||
Db 3 AGG 1

RESULT 24
CF317789/c
LOCUS               CF317789               4 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION          HD--07-J18.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
                    library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
ACCESSION            CF317789
VERSION              CF317789.1   GI:33689550
KEYWORDS
SOURCE
ORGANISM              Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 4)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
Contact: Nahm B.H.

CF307853
LOCUS               CF307853               4 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION          ABF--01-G24.b1 ABF3-overexpressing transgenic rice plasmid cDNA
                    library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ACCESSION            CF307853
VERSION              CF307853.1   GI:33679614
KEYWORDS
SOURCE
ORGANISM              Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 4)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
Contact: Nahm B.H.

```

```

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
FEATURES             source
1..4
   /organism="Oryza sativa (japonica cultivar-group)"
   /mol_type="mRNA"
   /cultivar="Nackdong"
   /db_xref="taxon:39947"
   /clone="HD--07-J18"
   /tissue_type="callus"
   /dev_stage="proliferated callus on 2N6 media for 2 weeks"
   /lab_host="E.coli DH10B"
   /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
   cDNA library (HD)"
   /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
   treated with ABA(20um) for 1hr. Oligo-capped mRNA was
   reverse transcribed and then used for PCR. mRNA was
   derived from rice Histone Deacetylase overexpression
   line."
ORIGIN
Query Match          50.0%; Score 3; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGA 4
   |||
Db 3 GGA 1

RESULT 25
CF338536
LOCUS               CF338536               4 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION          RCL1--01-P22.g1 Regenerated callus lambda phage cDNA library (RCL1)
                    Oryza sativa (japonica cultivar-group) cDNA clone RCL1--01-P22,
                    mRNA sequence.
ACCESSION            CF338536
VERSION              CF338536.1   GI:33825460
KEYWORDS
SOURCE
ORGANISM              Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 4)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
Contact: Nahm B.H.
JOURNAL
COMMENT              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                    of Bioscience and Bioinformatics, Myongji University
                    Yongin, Kyeonggi, Korea
                    Tel: 82 31 330 6193
                    Fax: 82 31 321 6355
                    Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
FEATURES             source
1..4
   /organism="Oryza sativa (japonica cultivar-group)"
   /mol_type="mRNA"
   /cultivar="Nackdong"
   /db_xref="taxon:39947"
   /clone="RCL1--01-P22"
   /tissue_type="callus"
   /dev_stage="proliferated callus on 2N6 media for 30 days"
   /lab_host="E.coli SOLR"
   /clone_lib="Regenerated callus lambda phage cDNA library
   (RCL1)"
   /note="Vector: pBluescript SK(+); Site_1: SstI; Site_2:

```

XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

ORIGIN

Query Match 50.0%; Score 3; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGA 4
|||
Db 2 GGA 4

RESULT 26

CN755098/c

LOCUS ID0AAAL4DE08R1 ApMS Acyrthosiphon pisum cDNA clone ID0AAAL4DE08
DEFINITION 5', mRNA sequence.

ACCESSION CN755098
VERSION 1
KEYWORDS EST.

SOURCE Acyrthosiphon pisum (pea aphid)
ORGANISM Acyrthosiphon pisum

REFERENCE 1 (bases 1 to 4)
AUTHORS Hunter, W., Martinez-Torres, D., Rabhe, Y., Sabater-Munoz, B., Stern, D., Tagu, D. and Winkler, P.

TITLE An expressed sequence tags database for the pea aphid Acyrthosiphon pisum
JOURNAL Unpublished (2004)
COMMENT Contact: D. Tagu

INRA Rennes

UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50

Risk of contamination by bacterial sequences from obligatory (Buchnera) or facultative endosymbionts. These sequences were obtained in the frame of the International Consortium of Aphid Genomics in collaboration with Genoscope

PCR Primers

FORWARD: CAGGAACACGCTATGACC

Plate: 14 row: E column: 8.

Location/Qualifiers

1. .4

/organism="Acyrthosiphon pisum"

/mol_type="mRNA"

/cultivar="developmentstage"

/db_xref="taxon:7029"

/clone="ID0AAAL4DE08"

/tissue_type="whole insect"

/dev_stage="nymphs and adults (parthenogenetic females)"

/lab_host="XLI-Blue"

/clone_lib="ApMs"

/notes="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI;

Sample name: ID0AAA; Plant growth place: Department of

Ecology & Evolutionary Biology, Princeton University;

Soil conditions: Soil; Sowing date: 01/06/1999;

Harvesting date: 01/06/1999; Stress date: no stress;

Description: Aphids inoculated on one-week old *Vicia faba*

under non-sterile conditions. All parthenogenetic stages

and both winged and wingless adults were collected for

library construction.; experimental condition: long

photoperiod (16-hr light/8-hr dark at 18 c)"

ORIGIN

Query Match

Best Local Similarity 50.0%; Score 3; DB 7; Length 4;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGA 4
|||
Db 2 GGA 4

RESULT 27

CL651736/c

LOCUS

DEFINITION

CL651736 4 bp DNA linear GSS 09-JUL-2004
PRI0112d.H07 - PRI0112d.B21 (4) Note: Recurring String Mixed stage
fosmid library of *P. pacificus* var. California Pristionchus
CL651736 pacificus genomic, genomic survey sequence.

ACCESSION CL651736

VERSION 1

KEYWORDS GSS.

SOURCE

ORGANISM

Pristionchus pacificus

Pristionchus pacificus

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;

Neodiplogasteridae; Pristionchus.

REFERENCE 1 (bases 1 to 4)

AUTHORS Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.

TITLE AppADB: an AcedB database for the nematode satellite organism

JOURNAL Pristionchus pacificus

COMMENT Nucleic Acids Res. 32 (1), D421-D422 (2004)

Contact: Sommer RJ

Evolutionary Biology

Max-Planck-Institute for Developmental Biology

Spemannstr. 37-39, Tuebingen D-72076, Germany

Tel: 00497071601371

Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de

This library was generated at Caltech, Pasadena, USA and end

sequenced at Vancouver, Canada.

Seq primer: T7

Class: fosmid ends.

Location/Qualifiers

1. .4

/organism="Pristionchus pacificus"

/mol_type="genomic DNA"

/strain="California"

/db_xref="taxon:54126"

/clone_lib="Mixed stage fosmid library of *P. pacificus*

var. California"

/note="Vector: pEpifos-5 Fosmid vector"

ORIGIN

Query Match

Best Local Similarity 50.0%; Score 3; DB 9; Length 4;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGA 4
|||
Db 3 GGA 1

CK584110 5 bp mRNA linear EST 16-JAN-2004
1ST W5.1687 AD-ORFeome1.0 library Caenorhabditis elegans cDNA 5'

CK584110 similar to F44G3.9, mRNA sequence.

CK584110 1 GI:40968039

EST.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;

Rhabditidae; Rhabditidae; Pelodierinae; Caenorhabditis.

REFERENCE 1 (bases 1 to 5)

AUTHORS Li, S., Armstrong, C.M., Bertin, N., Ge, H., Milstein, S., Boxen, M.,

Vidalain, P.O., Han, J.D., Chesneau, A., Hao, T., Goldberg, D.S., Li, N.,

Martinez, M., Rual, J.F., Lamesch, P., Xu, L., Tewari, M., Wong, S.L.,

Zhang, L.V., Beriz, G.F., Jacotot, L., Vaglio, P., Reboul, J.,

Hirozane-Kishikawa, T., Li, Q., Gabel, H.W., Elewa, A., Baumgartner, B.,

Rose, D.J., Yu, H., Bosak, S., Sequerra, R., Fraser, A., Mango, S.E.,

TITLE
JOURNAL
COMMENT

Saxton, W.M., Strome, S., Van Den Heuvel, S., Piano, F., Vandenhaute, J., Sardet, C., Gerstein, M., Doucette-Stamm, L., Gunsalus, K.C., Harper, J.W., Cui, M.E., Roth, F.P., Hill, D.E. and Vidal, M.
 A Map of the Interactome Network of the Metazoan C. elegans
 Science (2004) In press
 Contact: Vidal M
 Marc Vidal Laboratory
 Dana Farber Cancer Institute
 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
 Tel: 617 632 5180
 Fax: 617 632 5739
 Email: Marc.Vidal@dfci.harvard.edu
 For the purpose of protein interaction mapping, we generated a C. elegans a normalized library of ORF fused to the AD-encoding sequence of the yeast transcription factor GAL4. Those ORFs derive from the PCR amplification between the predicted (WS9) initiation and termination codons, using the cDNA library AD-wrmcDNA as template. This Interacting Sequence Tag IST_W15_1687 (F44G3.9) interacts as a prey with the bait F37B1.8
 PCR Primers
 FORWARD: CGCGTTTGGATCACTACAGGG
 BACKWARD: GGAGACTTGACCAACCTCTGGCG
 Insert Length: 5 Std Error: 4.00
 Plate: 22 row: 02 column: G
 Seq primer: CGCGTTTGGATCACTACAGGG
 High quality sequence stop: 4
 POLYA=No.

FEATURES
 source

1. 5
 Location/Qualifiers
 /organism="Caenorhabditis elegans"
 /mol_type="mRNA"
 /strain="N2"
 /db_xref="taxon:6239"
 /sex="male, hermaphrodite"
 /dev_stage="embryos, L1, L2, L3, L4, adult, dauer"
 /clone_lib="AD-ORFeome1.0 library"
 /note="Vector: pDestPC86/Cyb; For the purpose of protein interaction mapping, predicted protein-encoding ORFs were amplified by PCR precisely between the predicted (WS9 version of WormPeP) initiation and termination codons, using a cDNA library (AD-wrmcDNA library - Walhout et al. Methods Enzymol. 2000;328:575-92) as template. The resulting 11,984 Gateway cloned ORFs along with the attempted ones were transferred into a two-hybrid destination vector downstream of the vector sequence encoding the activation domain (AD) of the yeast GAL4 transcription factor. Those constructs were pooled together to constitute a 'normalized' AD-ORFeome1.1 library. Reference - Reboul J, Vaglio P et al. C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression. Nat Genet. 2003 May;34(1):35-41. PMID: 12679813"

ORIGIN

Query Match 50.0%; Score 3; DB 7; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.6e+09;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGG 6
 |||
DB 5 AGG 3

RESULT 29
CL423849/c
LOCUS
DEFINITION
 01S0750-04C1-A12 UniformMu MUTAIL Library Zea mays genomic clone
 01S0750-04C1-A12, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
GSS.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CL423849 5 bp DNA linear GSS 16-MAR-2004
 01S0750-04C1-A12 UniformMu MUTAIL Library Zea mays genomic clone
 01S0750-04C1-A12, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
GSS.

CL423849.1 GI:45501893

SOURCE
ORGANISM

Zea mays
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 5)
 Latshaw, S., Tan, B.-C., Settles, A.M. and McCarty, D.R.
 Sequence tagged transposon insertions from the UniformMu maize population
 Unpublished (2003)
 Contact: Donald R. McCarty
 Plant Molecular and Cellular Biology Program
 University of Florida
 PO 110690 Gainesville, FL 32611-0690, USA
 Tel: 352-392-1928 x322
 Email: drmc@ufl.edu
 Sequence Sequence flanking probable Mu insertion site in UniformMu line: 01S0750-04, Primer set: C
 Class: transposon insertion site.

FEATURES
 Location/Qualifiers
 1. 5
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="W22 (ACR, bz1-m9)"
 /cultivar="UniformMu"
 /db_xref="taxon:4577"
 /clone="01S0750-04C1-A12"
 /clone_lib="UniformMu MUTAIL Library"
 /note="Vector: TOPO-PCR4; DNA flanking Mu transposon insertions in Mu inactive lines were extracted from the UniformMu maize population by the thermo asymmetric interlaced PCR (TAIL) protocol using primers specific for the Mu terminal inverted repeat and a set of 16 arbitrary primers. Amplicons were size enriched using Sepharose 400 spin columns and cloned into the TOPO PCR4 vector."

ORIGIN

Query Match 50.0%; Score 3; DB 9; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.6e+09;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GAG 5
 |||
DB 5 GAG 3

RESULT 30
CL661701/c
LOCUS
DEFINITION
 CL661701 5 bp DNA linear GSS 09-JUL-2004
 PRI013c.C05 - PRI013c.B21 (5) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
GSS.

SOURCE
ORGANISM

Pristionchus pacificus
 Pristionchus pacificus
 Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.
 1 (bases 1 to 5)
 Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
 AppaDB: an AcedB database for the nematode satellite organism Pristionchus pacificus
 Pristionchus pacificus
 Nucleic Acids Res. 32 (1), D421-D422 (2004)
 Contact: Sommer RJ
 Evolutionary Biology
 Max-Planck-Institute for Developmental Biology
 Spemannstr. 37-39, Tuebingen D-72076, Germany
 Tel: 00497071601371
 Fax: 00497071601498
 Email: raif.sommer@tuebingen.mpg.de
 This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.

```

Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1. .5
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/notes="Vector: pEpifos-5 Fosmid vector"

ORIGIN

Query Match          50.0%; Score 3; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.6e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GGA 4
      |||
Db       3 GGA 1

Search completed: July 21, 2005, 01:54:38
Job time : 1349.8 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 21:46:09 ; Search time 187.4 Seconds
(without alignments)
189.533 Million cell updates/sec

Title: US-09-735-363A-45

Perfect score: 6

Sequence: 1 999agg 6

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 1582

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : N_Geneseq_16Dec04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	83.3	6	2	AAQ61541 TDT promo
2	5	83.3	6	2	AAV45399 TDT promo
3	5	83.3	6	3	AAAG2709 PNA clamp
4	5	83.3	6	12	ADJ35621 Stabilisi
5	4.4	73.3	6	2	AAT04935 Anti-HIV
6	4.4	73.3	6	6	ABK877547 Angiogene
7	4.4	73.3	6	6	ABK877320 Mammalian
8	4.4	73.3	6	9	ACD99345 Immunosti
9	4.4	73.3	6	12	ADJ35665 Stabilisi
10	4.4	73.3	6	13	ADR32691 Human nic
11	4.4	66.7	5	1	AAAG60771 Restricti
12	4	66.7	5	4	AAH56407 Synthetic
13	4	66.7	5	12	ADP90315 NEO ribos
14	4	66.7	5	12	AD161783 NEO ribos
15	4	66.7	6	2	AAQ38797 PCR prime
16	4	66.7	6	2	AAV61657 Fusarium
17	4	66.7	6	3	AAZ89322 Human UCP
18	4	66.7	6	4	AAZ24321 Human NFA
19	4	66.7	6	8	AAAF24321 Self asse
20	4	66.7	6	10	AAE383304 Immune mo

21	4	66.7	6	10	ADJ35308	Immune mo
22	4	66.7	6	10	ADJ35300	Immune mo
23	4	66.7	6	12	ADJ35691	Stabilisi
24	4	66.7	6	12	ADJ35735	Stabilisi
25	4	66.7	6	12	ADJ35654	Stabilisi
26	4	66.7	6	12	ADL09191	T7 promot
27	4	66.7	6	12	ADL09189	T7 promot
28	4	66.7	6	12	ADL09220	T3 promot
29	4	66.7	6	12	ADQ89354	Acute pha
30	4	66.7	6	13	ADR32741	Human nic
31	4	66.7	6	13	ADR32677	Human nic
32	4	66.7	6	13	ADR32553	Human nic
33	4	66.7	6	13	ADN33273	E. coli 2
34	4	66.7	6	13	ADN33281	E. coli 2
35	4	66.7	6	13	ADN33272	E. coli 2
36	4	66.7	6	13	ADN33282	E. coli 2
37	3.4	56.7	5	3	AAA56981	Human col
38	3.4	56.7	5	6	ABT12403	Orestes s
39	3.4	56.7	5	8	ABZ75664	Helicase-
40	3.4	56.7	5	8	ABZ75665	Helicase-
41	3.4	56.7	5	8	ABZ75667	Helicase-
42	3.4	56.7	5	8	ABZ75663	Helicase-
43	3.4	56.7	5	10	ADH60372	Myctophid
44	3.4	56.7	5	10	ACD91697	Human col
45	3.4	56.7	6	2	AAQ53911	Portion o
46	3.4	56.7	6	2	AAAT96305	Fungal te
47	3.4	56.7	6	4	AAF91686	Breast-ca
48	3.4	56.7	6	6	ABK87321	Mammalian
49	3.4	56.7	6	8	ABX50029	Telomere
50	3.4	56.7	6	10	ACA88957	Selection
51	3.4	56.7	6	12	ADJ35353	Stabilisi
52	3.4	56.7	6	12	ADJ35694	Stabilisi
53	3.4	56.7	6	12	ADJ35808	Stabilisi
54	3.4	56.7	6	12	ADJ35593	Stabilisi
55	3.4	56.7	6	12	ADJ35427	Stabilisi
56	3.4	56.7	6	12	ADJ35500	Stabilisi
57	3.4	56.7	6	12	ADJ35723	Stabilisi
58	3.4	56.7	6	12	ADJ35355	Stabilisi
59	3.4	56.7	6	12	ADJ35463	Stabilisi
60	3.4	56.7	6	13	ADR32744	Human nic
61	3.4	56.7	6	13	ADR32766	Human nic
62	3.4	56.7	6	13	ADR32491	Human nic
63	3.4	56.7	6	13	ADR32505	Human nic
64	3.4	56.7	6	13	ADR32508	Human nic
65	3	50.0	3	3	AAA94655	Human TUB
66	3	50.0	3	10	ADE58066	Human gen
67	3	50.0	4	10	ADB99580	Sequence
68	3	50.0	5	2	AAZ11611	DNA enhan
69	3	50.0	5	4	AAI19176	Human bre
70	3	50.0	5	6	ABK878153	Angiogene
71	3	50.0	5	6	ABK89732	Oestrogen
72	3	50.0	5	8	ACC49721	Template
73	3	50.0	5	9	ACD99926	Immunosti
74	3	50.0	5	11	ADL99555	Single ch
75	3	50.0	5	12	ADO05794	Telomere-
76	3	50.0	5	12	ADP86477	mini-attn
77	3	50.0	6	1	AAAG60769	Core sequ
78	3	50.0	6	1	AAAG60771	Restricti
79	3	50.0	6	1	AAAG60771	Restricti
80	3	50.0	6	1	AAAG60771	Restricti
81	3	50.0	6	1	AAAG60771	Restricti
82	3	50.0	6	2	AAQ27868	Cfr91 rec
83	3	50.0	6	2	AAQ27868	Cfr91 rec
84	3	50.0	6	2	AAQ50333	Ribozyme
85	3	50.0	6	2	AAQ47786	Mammalian
86	3	50.0	6	2	AAQ57115	Chromosom
87	3	50.0	6	2	AAQ70690	Triplex f
88	3	50.0	6	2	AAQ56535	Nucleic a
89	3	50.0	6	2	AAQ58444	Sequencin
90	3	50.0	6	2	AAQ58447	Sequencin
91	3	50.0	6	2	AAQ58448	Sequencin
92	3	50.0	6	2	AAQ97988	Peptide n
93	3	50.0	6	2	AAQ5734	Telomeras

c 94 3 50.0 6 2 AAQ85606 Aaq85606 T-DNA Vir
 95 3 50.0 6 2 AAQ86731 Aaq86731 Mung bean
 c 96 3 50.0 6 2 AAQ86731 Aaq86731 Mung bean
 97 3 50.0 6 2 AAQ86737 Aaq86737 Mung bean
 c 98 3 50.0 6 2 AAQ86737 Aaq86737 Mung bean
 99 3 50.0 6 2 AAQ86741 Aaq86741 Mung bean
 c 100 3 50.0 6 2 AAQ86741 Aaq86741 Mung bean

ALIGNMENTS

RESULT 1
 AAQ61541
 ID AAQ61541 standard; cDNA; 6 BP.
 XX
 AC AAQ61541;
 XX 25-MAR-2003 (revised)
 DT 10-MAR-2003 (revised)
 DT 21-OCT-1994 (first entry)
 XX
 DE TDT promoter/LYF sequence comprising Ikaros binding site.
 XX
 KW Ikaros; zinc finger; protein; immune disorder; therapy; treatment;
 KW corpus striatum; regulatory gene; enhancer; regulatory element;
 KW gene expression; ss.
 XX
 OS Mus sp.
 XX
 PN WO9406814-A1.
 XX
 PD 31-MAR-1994.
 XX
 PF 14-SEP-1993; 93WO-US008743.
 XX
 PR 14-SEP-1992; 92US-00946233.
 XX
 PA (GEO) GEN HOSPITAL CORP.
 XX
 PI Georgopoulos K;
 XX
 DR WPI; 1994-118387/14.
 XX
 PT I-cell pathway regulatory gene, Ikaros - encodes family of unique zinc
 PT finger proteins, useful for treating immune system disorders.
 XX
 PS Disclosure; Page 28; 112pp; English.
 XX
 CC The Ikaros gene encodes a zinc finger protein which can be used in a
 CC therapeutic composition to treat animals with an immune system disorder.
 CC It may also be used for assessing whether a subject is at risk for an
 CC immune disorder. It is of particular use in treating a disorder of the
 CC corpus striatum. Heterologous genes may be expressed by placing them
 CC under the control of an Ikaros responsive control element and contacting
 CC the element with an Ikaros protein. Potential high affinity binding sites
 CC for the Ikaros proteins were found in the enhancer and promoter regions
 CC of the TCR-alpha, -beta and -delta, the CD3-delta, -epsilon and -gamma
 CC genes, the SL3 and HIV long terminal repeat and in the regulatory domains
 CC of other T cell restricted antigens. Related sequences to the Ikaros
 CC motif were also found in the purine boxes of the IL2 gene in the
 CC LYF site of the TPT promoter as well as in the NFkB variant sites of the
 CC HIV long terminal repeat. See also AAQ61504-Q61543. (Updated on 10-MAR-
 CC 2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 6 BP; 1 A; 0 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 83.3%; Score 5; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGAG 5

Db 2 GGGAG 6
 RESULT 2
 AA45399
 ID AA45399 standard; DNA; 6 BP.
 XX
 AC AA45399;
 XX 11-JAN-1999 (first entry)
 DT
 DE TDT promoter/LYF binding site for Ikaros.
 XX
 KW Ikaros; mIK; transcription factor; mouse; lymphocyte;
 KW cell differentiation; T cell; cancer; immunodeficiency;
 KW Alzheimer's disease; therapy; diagnosis; TDT; promoter; LYF; ss.
 XX
 OS Synthetic.
 XX
 PN CA2194256-A.
 XX
 PD 05-MAR-1998.
 XX
 PF 02-JAN-1997; 97CA-02194256.
 XX
 PR 05-SEP-1996; 96US-00711417.
 XX
 PA (GEO) GEN HOSPITAL CORP.
 XX
 PI Georgopoulos K;
 XX
 DR WPI; 1998-378292/33.
 XX
 PT New nucleic acid encoding Ikaros protein involved in early
 PT differentiation of lymphocytes - existing in several isoforms, and
 PT related products, used to treat e.g. immune diseases or cancer and to
 PT control cell differentiation.
 XX
 PS Disclosure; Page 38; 158pp; English.
 XX
 CC This oligonucleotide from the TDT promoter/LYF site was identified as a
 CC potential high affinity binding site for Ikaros proteins (see AAW70963-
 CC 71). It partially includes the core motif GGGAA found in consensus
 CC recognition sequences for murine Ikaros protein isoforms mIk-1, mIk-2 and
 CC mIk-3 (see AAV52830-32). High affinity binding sites for Ikaros have been
 CC found in enhancer and promoter regions of the regulatory domains of the
 CC TCR antigen complex, the CD3 genes, the SL3 and HIV long terminal repeat
 CC and in the regulatory domains of other T cell restricted antigens (see
 CC AAV45358-402) by gel retardation assay. Ikaros is involved in early
 CC differentiation of lymphocytes. The invention provides Ikaros nucleic
 CC acids (see AAV42805-11 and AAV42840) and polypeptides, vectors and host
 CC cells. These are used to treat T and B cell diseases, to control
 CC expression of heterologous genes placed under control of an Ikaros-
 CC responsive element, to treat nervous system diseases and to modulate cell
 CC division, amplification or differentiation, especially in haematopoietic
 CC cells
 XX
 SQ Sequence 6 BP; 1 A; 0 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 83.3%; Score 5; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGAG 5

Db 2 GGGAG 6
 RESULT 3
 AAA62709/c
 ID AAA62709 standard; DNA; 6 BP.
 XX

```

AC AAA62709;
XX
DT 02-JAN-2001 (first entry)
XX
DE PNA clamp oligonucleotide #3.
XX
KW Quencher-PNA clamp; fluorescent dye-PNA clamp; probe;
XX target hybridisation detection; ss.
XX
OS Synthetic.
XX
PN WO200041549-A2.
XX
PD 20-JUL-2000.
XX
PF 14-JAN-2000; 2000WO-US000972.
XX
PR 15-JAN-1999; 99US-00232000.
XX
PA (PEKE ) PERKIN-ELMER CORP.
XX
PI Livak KJ, Egholm M, Hunkapiller MW;
XX
DR WPI; 2000-499036/44.
XX
PT Binary composition comprising probe and labeled clamp, useful e.g. for
XX detecting polymerase chain reaction products, with probe containing parts
XX specific for a target and the clamp used e.g. for detecting polymerase
XX chain reaction products.
XX
PS Example 4; Page 28; 68pp; English.
XX
CC The present sequence forms part of a number of PNA clamps, including
XX quencher PNA-clamps and fluorescent dye-PNA clamps, used in a binary
XX composition for target hybridisation detection. The PNA clamps generally
XX comprise two oligonucleotides, including the present sequence, which are
XX linked through 2-[2-(2-aminethoxy)acetic acid spacer units. One or both
XX oligonucleotides are labelled through a spacer at the free end. Some PNA
XX clamps also contain internal or carboxy-terminal lysine residues. The
XX binary composition comprises a PNA clamp with a probe-specific part and
XX at least one label, and a probe with target-specific and clamp-specific
XX parts. The probe and clamp remain bound during detection of the label.
XX The composition can be used for quantitation, detection and labelling of
XX PCR products. Probes and clamps may be labelled with fluorescent dyes, and
XX quenchers, hybridisation-stabilising moieties, chemiluminescent dyes, and
XX affinity ligands. A single clamp may be used with several different
XX probes, thus eliminating the need to prepare expensive labelled probes.
XX By using different labels, many loci in a single target sequence can be
XX assayed in a single reaction vessel
XX
SQ Sequence 6 BP; 0 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 83.3%; Score 5; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6
Db |||||
6 GGAGG 2

RESULT 4
ADJ35621/c
ID ADJ35621 standard; DNA; 6 BP.
XX
AC ADJ35621;
XX
XX
XX
DT 22-APR-2004 (first entry)
XX
DE Stabilising anti-repression, STAR, element dyad sequence #287.
XX
KW STAR affilitated proteinaceous molecule; post translational modification;
XX stabilising anti-repression; STAR; STAR element; ds; dyad.
XX

Unidentified.
XX
WO2003106674-A2.
XX
24-DEC-2003.
XX
30-MAY-2003; 2003WO-NL000410.
XX
14-JUN-2002; 2002EP-00077344.
XX
(CHRO-) CHROMAGENICS BV.
XX
Otte AP, Kruckeberg AL, Satiijn DPE;
XX
WPI; 2004-082195/08.
XX
Producing proteinaceous molecules in cells by selecting a cell, providing
XX a nucleic acid encoding a proteinaceous molecule with an stabilizing Anti
XX -Repression sequence and expressing proteinaceous molecule.
XX
Disclosure; Page 101; 177pp; English.
XX
The invention relates to a method of producing a proteinaceous molecule
XX (I) in a cell comprising selecting a cell for its suitability for
XX producing (I), providing a nucleic acid encoding (I) with a nucleic acid
XX comprising a Stabilising Anti-Repression (STAR) sequence, expressing the
XX resulting nucleic acid in the cell and collecting (I). The method is
XX useful for producing (I). A cell line (II) provided with a nucleic acid
XX comprising a STAR sequence is useful for producing (I). (II) Enables
XX production of affilitated proteinaceous molecule, as cell carries out
XX proper post-translational modifications of produced proteins. The present
XX sequence represents a stabilising anti-repression, STAR, element primer
XX dyad sequence.
XX
SQ Sequence 6 BP; 0 A; 5 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 83.3%; Score 5; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6
Db |||||
6 GGAGG 2

RESULT 5
AAT04935
ID AAT04935 standard; DNA; 6 BP.
XX
AC AAT04935;
XX
DT 10-MAY-1996 (first entry)
XX
DE Anti-HIV oligodeoxynucleotide.
XX
KW Anti-HIV; AIDS; ARC; treatment; ss.
XX
OS Synthetic.
XX
PN WO9526190-A1.
XX
PD 05-OCT-1995.
XX
PF 24-MAR-1995; 95WO-JP000543.
XX
PR 25-MAR-1994; 94JP-00092809.
XX 25-MAR-1994; 94JP-00092810.
XX
PA (KAJI/) KAJI A.
XX
PI Kaji A;
XX

```

DR WPI; 1995-351196/45.
XX Anti HIV agents useful for the treatment of HIV, AIDS and ARC - comprise
PT a phosphodiester linked oligonucleotide deriv.
XX Example 3; Page 11; 19pp; Japanese.
XX The oligodeoxynucleotides AAT04934/35 are anti-HIV agents, useful for
CC treating HIV, AIDS and ARC. They are pref. given in a dosage of 1-100
CC mg/day parenterally, or 0.1- 6g/day orally
XX Sequence 6 BP; 0 A; 0 C; 6 G; 0 T; 0 U; 0 Other;
SQ Query Match 73.3%; Score 4.4; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 9.7e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGG 6
Db |||||
1 GGGGGG 6

RESULT 6
ID ABS77547/c
XX ABS77547 standard; DNA; 6 BP.
AC ABS77547;
XX 13-DEC-2002 (first entry)
XX Angiogenesis inhibitory oligonucleotide #31.
XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophiliac joint;
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX Synthetic.
XX WO200253141-A2.
PN 14-DEC-2001; 2001WO-US048458.
XX 11-JUL-2002.
PD 14-DEC-2001; 2001WO-US048458.
XX 14-DEC-2000; 2000US-0255534P.
PR (COLE-) COLEY PHARM GROUP INC.
PA Bratzler RL;
PI WPI; 2002-566690/60.
XX Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX Claim 2; Page 20; 276pp; English.
XX The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,

CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention
XX Sequence 6 BP; 0 A; 6 C; 0 G; 0 T; 0 U; 0 Other;
SQ Query Match 73.3%; Score 4.4; DB 6; Length 6;
Best Local Similarity 83.3%; Pred. No. 9.7e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGG 6
Db |||||
6 GGGGGG 1

RESULT 7
ID ABK87320
XX ABK87320 standard; DNA; 6 BP.
AC ABK87320;
XX 24-SEP-2002 (first entry)
XX Mammalian SP1 recognition sequence #1.
DE Nucleic acid detection; Sp1; ss.
KW Mammalia.
XX WO200244326-A2.
PN 06-JUN-2002.
PD 26-NOV-2001; 2001WO-US044215.
XX 30-NOV-2000; 2000US-00728574.
PR (STRA-) STRATAGENE.
PA Sorge JA, Whalen AM;
PI WPI; 2002-508503/54.
XX Detecting/measuring target nucleic acid, by forming cleavage structure by
PT incubating target nucleic acid with probe having binding moiety, cleaving
PT structure to release nucleic acid and detecting released fragments.
XX Disclosure; Page 75; 157pp; English.
XX This invention relates to a novel method for detecting/measuring a target
CC nucleic acid. The method comprises forming a cleavage structure by
CC incubating the target sequence with a probe comprising a binding moiety
CC and a secondary structure that changes upon binding of the probe to the
CC target, cleaving the cleavage structure to release a nucleic acid
CC fragment, and detecting and/or measuring the fragment captured by binding
CC of the binding moiety to a capture element on a solid support. The method
CC of the invention is useful for detecting or measuring a target nucleic
CC acid and are useful for generating a signal indicative of the presence of
CC the target nucleic acid in a sample. Another method of the invention is
CC useful for simultaneously forming a cleavage structure, amplifying the
CC target nucleic acid in a sample and cleaving the cleavage structure. The
CC method does not require multiple steps, subsequent amplification process,
CC and allows for concurrent amplification and detection of target nucleic
CC acid in a sample. The present sequence represents the Mammalian SP1
CC recognition sequence shown in the specification
XX Sequence 6 BP; 0 A; 1 C; 5 G; 0 T; 0 U; 0 Other;
SQ Query Match 73.3%; Score 4.4; DB 6; Length 6;
Best Local Similarity 83.3%; Pred. No. 9.7e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGG 6

```

Db      |||||
      1 GGGCGG 6

RESULT 8
ACD99345/c
ID ACD99345 standard; DNA; 6 BP.
XX
AC ACD99345;
XX
XX
DT 25-SEP-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #31.
XX
KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW antulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS Synthetic.
XX
XX US2003050268-A1.
PN
XX
PD 13-MAR-2003.
XX
XX 29-MAR-2002; 2002US-00112653.
XX
XX 29-MAR-2001; 2001US-0279642P.
PR
PA (KRIE/) KRIEG A M.
PA (BERG/) BERG D J.
XX
PI Krieg AM, Berg DJ;
XX
DR WPI; 2003-521815/49.
XX
XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT disease by administering an immunostimulatory nucleic acid.
XX
XX Disclosure; Page 9; 229pp; English.
XX
CC The invention describes a method of treating non-allergic inflammatory
CC disease comprising administering to a subject having or at risk of
CC developing a non-allergic inflammatory disease an immunostimulatory
CC nucleic acid for prevention or treatment of the disease. The method is
CC useful for treating non-allergic inflammatory diseases, such as
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC This sequence represents an immunostimulatory nucleic acid
XX
SQ Sequence 6 BP; 0 A; 6 C; 0 G; 0 T; 0 U; 0 Other;
      Query Match      73.3%; Score 4.4; DB 9; Length 6;
      Best Local Similarity 83.3%; Pred. No. 9.7e+08;
      Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGGAGG 6
Db      |||||
      6 GGGCGG 1

RESULT 10
ADR32691/c
ID ADR32691 standard; DNA; 6 BP.
XX
XX ADR32691;
AC
XX
DT 04-NOV-2004 (first entry)
XX
DE Human nicking agent target DNA #232.
XX
KW ss; nicking agent; assay panel; diagnosis; expression pattern;
KW DNA fingerprinting; nosocomial infection; microbiological assay;
KW bacterial contamination; genome mapping; bioremediation.
XX
XX Homo sapiens.
XX
XX WO2004067765-A2.
PN
XX
PD 12-AUG-2004.
XX
XX 29-JAN-2004; 2004WO-US002720.
PF
XX 29-JAN-2003; 2003US-0443811P.
PR
PA (KECK-) KECK GRADUATE INST.
XX

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KW stabilising anti-repression; STAR; STAR element; ds; dyad.
XX Unidentified.
OS
XX WO2003106674-A2.
PN
XX
XX 24-DEC-2003.
PD
XX
XX 30-MAY-2003; 2003WO-NL000410.
PF
XX
XX 14-JUN-2002; 2002EP-00077344.
PR
XX (CHRO-) CHROMAGENICS BV.
PA
XX
XX Otte AP, Kruckeberg AL, Satiijn DPE;
PI WPI; 2004-082195/08.
DR
XX Producing proteinaceous molecules in cells by selecting a cell, providing
XX a nucleic acid encoding a proteinaceous molecule with an Stabilising Anti
XX -Repression sequence and expressing proteinaceous molecule.
XX
XX Disclosure; Page 101; 177pp; English.
XX
CC The invention relates to a method of producing a proteinaceous molecule
CC (I) in a cell comprising selecting a cell for its suitability for
CC producing (I), providing a nucleic acid encoding (I) with a nucleic acid
CC comprising a Stabilising Anti-Repression (STAR) sequence, expressing the
CC resulting nucleic acid in the cell and collecting (I). The method is
CC useful for producing (I). A cell line (II) provided with a nucleic acid
CC comprising a STAR sequence is useful for producing (I). (II) Enables
CC production of affiliated proteinaceous molecule, as cell carries out
CC proper post-translational modifications of produced proteins. The present
CC sequence represents a stabilising anti-repression, STAR, element primer
CC dyad sequence.
XX
SQ Sequence 6 BP; 0 A; 5 C; 1 G; 0 T; 0 U; 0 Other;
      Query Match      73.3%; Score 4.4; DB 12; Length 6;
      Best Local Similarity 83.3%; Pred. No. 9.7e+08;
      Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGGAGG 6
Db      |||||
      6 GGGCGG 1

RESULT 10
ADR32691/c
ID ADR32691 standard; DNA; 6 BP.
XX
XX ADR32691;
AC
XX
DT 04-NOV-2004 (first entry)
XX
DE Human nicking agent target DNA #232.
XX
KW ss; nicking agent; assay panel; diagnosis; expression pattern;
KW DNA fingerprinting; nosocomial infection; microbiological assay;
KW bacterial contamination; genome mapping; bioremediation.
XX
XX Homo sapiens.
XX
XX WO2004067765-A2.
PN
XX
PD 12-AUG-2004.
XX
XX 29-JAN-2004; 2004WO-US002720.
PF
XX 29-JAN-2003; 2003US-0443811P.
PR
PA (KECK-) KECK GRADUATE INST.
XX

```

```

Db      |||||
      1 GGGCGG 6

RESULT 8
ACD99345/c
ID ACD99345 standard; DNA; 6 BP.
XX
AC ACD99345;
XX
XX
DT 25-SEP-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #31.
XX
KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW antulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS Synthetic.
XX
XX US2003050268-A1.
PN
XX
PD 13-MAR-2003.
XX
XX 29-MAR-2002; 2002US-00112653.
XX
XX 29-MAR-2001; 2001US-0279642P.
PR
PA (KRIE/) KRIEG A M.
PA (BERG/) BERG D J.
XX
PI Krieg AM, Berg DJ;
XX
DR WPI; 2003-521815/49.
XX
XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT disease by administering an immunostimulatory nucleic acid.
XX
XX Disclosure; Page 9; 229pp; English.
XX
CC The invention describes a method of treating non-allergic inflammatory
CC disease comprising administering to a subject having or at risk of
CC developing a non-allergic inflammatory disease an immunostimulatory
CC nucleic acid for prevention or treatment of the disease. The method is
CC useful for treating non-allergic inflammatory diseases, such as
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC This sequence represents an immunostimulatory nucleic acid
XX
SQ Sequence 6 BP; 0 A; 6 C; 0 G; 0 T; 0 U; 0 Other;
      Query Match      73.3%; Score 4.4; DB 9; Length 6;
      Best Local Similarity 83.3%; Pred. No. 9.7e+08;
      Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGGAGG 6
Db      |||||
      6 GGGCGG 1

RESULT 9
ADJ35665/c
ID ADJ35665 standard; DNA; 6 BP.
XX
AC ADJ35665;
XX
XX
DT 22-APR-2004 (first entry)
XX
DE Stabilising anti-repression, STAR, element dyad sequence #331.
XX
KW STAR affiliated proteinaceous molecule; post translational modification;

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PI Van Ness J, Galas DJ, Van Ness LK;
 XX WPI; 2004-581010/56.
 XX Identifying nucleic acid sample source, useful for identifying bacterial
 PT strains involved in nosocomial infections, comprises treating the nucleic
 PT acid sample with components comprising a nicking agent under nicking
 PT conditions.
 XX
 XX Example 1; Page 75; 238pp; English.
 XX The invention relates to a method of treating a nucleic acid sample with
 CC components under nicking conditions, where the components comprise a
 CC nicking agent, and the conditions cause the nicking agent to nick the
 CC nucleic acid sample to thus produce a family of initiating
 CC oligonucleotide fragments, and subjecting one or more members of the
 CC family of initiating oligonucleotide fragments to a characterization
 CC process to thus provide results. The method is useful for creating an
 CC assay panel of diagnostic oligonucleotides that can identify any organism
 CC or individual. The method is useful for characterizing other DNA
 CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
 CC The method kit or composition is useful for identifying the source
 CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
 CC non-human animal or human. The method is particularly useful for rapidly
 CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
 CC subspecies, and especially strains or individuals of the subspecies. It
 CC is especially useful for identifying different bacterial strains involved
 CC in e.g., nosocomial infections. Furthermore, the method is useful for
 CC diagnosing bacterial disease in plants and humans, monitoring for
 CC bacterial content and/or contamination in the environment, monitoring
 CC food for bacterial contamination, monitoring quality assurance/processes for
 CC bacterial contamination, monitoring quality assurance/quality control of
 CC laboratory tests involving microbiological assays, tracing bacterial
 CC contamination and/or outbreaks of bacterial infections, genome mapping,
 CC monitoring bioremediation sites, and for monitoring agricultural sites
 CC for test crops, bacteria and recombinant molecules. This sequence
 CC corresponds to nucleic acid used in the method of the invention.
 XX
 SQ Sequence 6 BP; 1 A; 5 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 73.3%; Score 4.4; DB 13; Length 6;
 Best Local Similarity 83.3%; Pred. No. 9.7e+08;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGGAGG 6
 DB |||||
 6 GGGTGG 1
 RESULT 11
 AA93676/c
 ID AA93676 standard; DNA; 5 BP.
 XX
 AC AA93676;
 XX
 XX 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 24-JUN-1990 (first entry)
 XX
 XX Synthetic probe for hop growth retarding viroid (HSV), HSV cucumber
 DE variant (HSV-c) and HSV grape variant (HSV-g).
 DE
 KW Hop growth retarding viroid; cucumber variant; grape variant; probe; ss.
 XX
 OS Hop growth retardant viroid.
 XX
 XX JP01040000-A.
 PN
 PD 10-FEB-1989.
 XX
 XX 05-AUG-1987; 87JP-00194377.
 PF
 XX 05-AUG-1987; 87JP-00194377.
 PR

XX (YUKI) YUKI GOSHI YAKUHI KOGYO KK.
 XX WPI; 1989-089715/12.
 XX Fractionating and detecting of hop growth retarding viroids - using
 PT synthetic DNA probe contg. specified base sequence.
 PT
 XX Disclosure; Page 3; 5pp; Japanese.
 PS
 XX The synthetic probes is complementary to the RNA of HSV-g bases 53-59.
 CC HSV, HSV-c and HSV-g are fractionated and detected using the synthetic
 CC probe. The probe is 15-25mer. The probe can be used to diagnose HSV
 CC infections in plants. (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 27-AUG-2003 to
 CC correct OS field.)
 CC
 SQ Sequence 5 BP; 1 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
 Query Match 66.7%; Score 4; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.2e+09;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GAGG 6
 DB |||||
 5 GAGG 2
 RESULT 12
 AAH56407
 ID AAH56407 standard; DNA; 5 BP.
 XX
 AC AAH56407;
 XX
 XX 06-SEP-2001 (first entry)
 DT
 XX Escherichia coli groE operon antisense oligonucleotide SEQ ID NO:55.
 DE
 KW Antisense oligonucleotide; groE; groEL; groES; inhibitor; growth;
 KW microorganism; Escherichia coli; Streptococcus pneumoniae; diagnosis;
 KW Streptococcus pyogenes; Staphylococcus aureus; Pseudomonas aeruginosa;
 KW antibacterial; antiviral; antiproliferative; antisense therapy;
 KW microbial infection; ss.
 XX
 OS Escherichia coli.
 XX
 XX WO200136625-A2.
 PN
 PD 25-MAY-2001.
 XX
 XX 20-NOV-2000; 2000WO-CA001347.
 PF
 XX 18-NOV-1999; 99US-0166249P.
 PR
 XX (GENE-) GENESENSE TECHNOLOGIES INC.
 PA
 XX Wright JA, Young AH, Dugourd D;
 PI
 XX WPI; 2001-355633/37.
 DR
 XX Novel antisense compounds targeting nucleic acid encoding groEL or groES
 PT gene of microorganism, which hybridize with and inhibit expression of the
 PT genes, useful to inhibit growth of microorganism having the genes.
 PT
 XX Claim 3; Page 41; 110pp; English.
 PS
 XX The present invention specifically claims AAH56368 to AAH56832 which are
 CC antisense oligonucleotides to nucleotide sequences encoding groE. More
 CC generally, antisense compounds (I) comprising antisense oligonucleotides
 CC of 5-50 bases targeted to a nucleotide sequence encoding groEL (heat
 CC shock protein (HSP)60) (GL) and groES (HSP10) (GS) gene from a
 CC microorganism, where the antisense compound is complementary to GL or GS
 CC of a microorganism and specifically hybridizes with and inhibits the

CC expression of GL or GS, is claimed. (I) have antibacterial, antiviral and
 CC antiproliferative activities, and can be used in antisense therapy and
 CC for inhibition of expression of groES or groEL. (I) are useful for
 CC inhibiting expression of GL or GS in cells or tissues in vitro. (I) are
 CC also useful for inhibiting the growth of a microorganism, or inhibiting
 CC the expression of GL or GS gene in a microorganism (a bacterial cell or a
 CC virus) having a GL or GS gene which involves administering to the
 CC microorganism or to a cell infected with the microorganism, (I). (I) are
 CC also useful for treating a mammalian pathological condition mediated by
 CC the microorganisms which involves identifying a eukaryotic organism
 CC having a pathological condition mediated by microorganisms having a GL or
 CC GS gene and administering (I) such that the growth of microorganism is
 CC inhibited. The antisense compounds are utilised for diagnostics,
 CC therapeutics, prophylaxis and as research reagents and kits, e.g., to
 CC prevent or delay microbial infections in humans. They are also useful as
 CC molecular weight markers. AAH56362 to AAH56367 and AAH56833 to AAH56854
 CC represent PCR primers for groE sequences which are used in the
 CC exemplification of the present invention. AAH56855 to AAH56870 represent
 CC groE nucleotide sequence given in the present invention
 XX
 SQ Sequence 5 BP; 2 A; 0 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 4; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.2e+09;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GGAG 5
 DB 2 GGAG 5
 ||||
 2 GGAG 5

RESULT 13
 ADF90315/c
 ID ADF90315 standard; DNA; 5 BP.
 XX
 AC ADF90315;
 DT 26-FEB-2004 (first entry)
 XX
 DE NEO ribosomal binding site SEQ ID NO:24.
 XX
 KW charged transfection-facilitating polypeptide;
 KW growth hormone releasing hormone; GHRH; poly-L-glutamate; antidiabetic;
 KW gene therapy; diabetes; gene; ds.
 XX
 OS Synthetic.
 XX
 PN WO2003099341-A1.
 XX
 PD 04-DEC-2003.

PF 23-MAY-2003; 2003WO-US016541.
 XX
 PR 28-MAY-2002; 2002US-00156670.
 PR 24-MAR-2003; 2003US-00395709.
 XX
 PA (ADVI-) ADVISYS INC.
 XX
 PI Draghia-Akli R, Carpenter RH, Kern DR, Hill LA, Attra H, Hebel H;
 XX
 DR WPI; 2004-062023/06.

XX Composition useful for delivering isolated nucleic acid constructs for
 PT correcting genetic deficiencies, such as diabetes, comprises a nucleic
 PT acid expression construct, and a charged transfection-facilitating
 PT polypeptide.
 XX

PS Disclosure; SEQ ID NO 24; 80pp; English.

XX The present invention describes a composition (I) comprising a nucleic
 CC acid expression construct, and a charged transfection-facilitating
 CC polypeptide associated with it, where a ratio in moles of the charged
 CC transfection-facilitating polypeptide to nucleic acid expression

CC construct comprises from 1 mole to 5000 moles of the charged transfection
 CC -facilitating polypeptide per mole of nucleic acid expression construct.
 CC Also described is a composition (II) comprising a nucleic acid expression
 CC construct encoding a growth hormone releasing hormone (GHRH) or its
 CC functional biological equivalent, and a charged transfection-facilitating
 CC polypeptide or a poly-L-glutamate polypeptide associated with it. (I) and
 CC (II) have antidiabetic activities, and can be used in gene therapy. The
 CC methods and compositions of the present invention are useful for
 CC delivering isolated nucleic acid constructs for correcting genetic
 CC deficiencies, such as diabetes. The present sequence is used in an
 CC example from the present invention.

SQ Sequence 5 BP; 0 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 12; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.2e+09;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GAGG 6
 DB 5 GAGG 2
 ||||
 5 GAGG 2

RESULT 14
 ADI61783/c
 ID ADI61783 standard; DNA; 5 BP.
 XX
 AC ADI61783;
 DT 22-APR-2004 (first entry)
 XX
 DE NEO ribosomal binding site SEQ ID NO:13.

XX mammalian expression plasmid; eukaryotic promoter;
 KW codon-optimised-eukaryotic therapeutic gene; poly adenylation signal;
 KW selectable marker gene promoter; ribosomal binding site;
 KW selectable marker gene; origin of replication;
 KW plasmid mediated gene supplementation; growth hormone releasing hormone;
 KW GHRH; gene; ds.

XX Synthetic.

PN WO2004007678-A2.

XX 22-JAN-2004.

XX 15-JUL-2003; 2003WO-US021917.

XX 16-JUL-2002; 2002US-0396247P.

XX (ADVI-) ADVISYS INC.

XX Draghia-Akli R, Abruzzese RV, Kern DR;

XX WPI; 2004-122918/12.

XX New codon optimized synthetic mammalian expression plasmids having
 PT operatively linked therapeutic and replication elements, useful for
 PT plasmid mediated gene supplementation.

PS Claim 6; SEQ ID NO 13; 76pp; English.

XX The present invention describes a synthetic mammalian expression plasmid
 CC (I) comprising a synthetic or eukaryotic promoter, a codon-optimised-
 CC eukaryotic therapeutic gene sequence, a poly adenylation signal, a
 CC selectable marker gene promoter, a ribosomal binding site, a selectable
 CC marker gene sequence and an origin of replication. Also described: (1) a
 CC synthetic mammalian expression plasmid comprising a fully defined
 CC sequence of 2722, 2725, 2716, 2716 or 2725 bp (ADI61787, ADI61788,
 CC ADI61789, ADI61790 or ADI61791); and (2) a method for plasmid mediated
 CC gene supplementation, comprising delivering into a subject a codon
 CC optimised synthetic mammalian expression plasmid, wherein the codon
 CC optimised synthetic mammalian expression plasmid encodes a growth hormone

CC releasing hormone (GHRH) or its functional biological equivalent in the
 CC subject. The methods and compositions of the present invention are useful
 CC for producing an optimised nucleic acid delivery vehicle or synthetic
 CC expression plasmid containing many structural elements necessary for the
 CC in vitro amplification of the plasmid in a bacterial host, and for
 CC plasmid mediated gene supplementation. The present sequence represents a
 CC NEO ribosomal binding site, which is used in the exemplification of the
 CC present invention.

XX Sequence 5 BP; 0 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

SQ Query Match 66.7%; Score 4; DB 12; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.2e+09;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GAGG 6
 DB ||||
 5 GAGG 2

RESULT 15

AAQ38797
 ID AAQ38797 standard; DNA; 6 BP.

XX AC

XX AC

XX 25-MAR-2003 (revised)

XX 26-JUL-1993 (first entry)

XX PCR primer #11 for analysis of lower TCR Vbeta gene usage in RA SILs.

XX TCR; T cell receptor; autoimmune disease; rheumatoid arthritis; RA;

XX J beta domain; V beta domain; T-cell mediated autoimmune disease;

XX antagonists.

XX Homo sapiens.

XX WO9306135-A1.

XX PD

XX 01-APR-1993.

XX 23-SEP-1992; 92WO-US08094.

XX 23-SEP-1991; 91US-00765222.

XX 18-OCT-1991; 91US-00779445.

XX 18-MAR-1992; 92US-00853362.

XX (GETH) GENENTECH INC.

XX Amento EP;

XX WPI; 1993-117475/14.

XX T-cell receptor antagonising polypeptide(s) - used in the diagnosis and

XX treatment of auto-immune disorders, partic. rheumatoid arthritis.

XX Example 1; Page 22; 51pp; English.

XX This 5' PCR primer was used with a 3' primer designated a constant region

XX sequence common to all TCR beta transcripts. It was used for the PCR

XX analysis of lower TCR usage in synovial Vbetas. This primer was used for

XX Vbeta family 2, subfamily 4.1, Jbeta 2.7. Cbeta 2 and corresponds to D &

XX J translation AAR34165. (Updated on 25-MAR-2003 to correct FN field.)

XX Sequence 6 BP; 2 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

SQ Query Match 66.7%; Score 4; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.7e+08;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGA 4

DB ||||

1 GGGA 4

CC releasing hormone (GHRH) or its functional biological equivalent in the
 CC subject. The methods and compositions of the present invention are useful
 CC for producing an optimised nucleic acid delivery vehicle or synthetic
 CC expression plasmid containing many structural elements necessary for the
 CC in vitro amplification of the plasmid in a bacterial host, and for
 CC plasmid mediated gene supplementation. The present sequence represents a
 CC NEO ribosomal binding site, which is used in the exemplification of the
 CC present invention.

XX Sequence 5 BP; 0 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

SQ Query Match 66.7%; Score 4; DB 12; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.2e+09;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GAGG 6
 DB ||||
 5 GAGG 2

RESULT 16

AAV61657/c
 ID AAV61657 standard; DNA; 6 BP.

XX AC

XX AAV61657;

XX 03-DEC-1998 (first entry)

XX Fusarium sp. 18S rRNA DNA fragment #1.

XX 18S rRNA; detection; identification; fungus; ss.

XX Fusarium sp.

XX JP10234380-A.

XX 08-SEP-1998.

XX 28-FEB-1997; 97JP-00062104.

XX 28-FEB-1997; 97JP-00062104.

XX (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.

XX WPI; 1998-535034/46.

XX Use of oligo:nucleotide for detecting and identification of fungus of

XX Fusarium genus - as primer or probe to detect of identify microbes

XX rapidly and exactly.

XX Claim 1; Page 6; 20pp; Japanese.

XX AAV61657-V61664 are fragments of a Fusarium sp. 18S rRNA gene which are

XX used in a method for the detection and identification of a fungus of

XX Fusarium genus. The process can be used to detect or identify microbes

XX rapidly and exactly

XX Sequence 6 BP; 1 A; 3 C; 1 G; 1 T; 0 U; 0 Other;

SQ Query Match 66.7%; Score 4; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.7e+08;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GAGG 6

DB ||||

4 GAGG 1

RESULT 17

AAZ89322/c
 ID AAZ89322 standard; DNA; 6 BP.

XX AC

XX AAZ89322;

XX 13-JUN-2000 (first entry)

XX Human UCP3 promoter fragment #2.

XX UCP3; uncoupling protein 3; human; promoter; fat cell; transcription;

XX fat metabolism; ss.

XX Homo sapiens.

XX DE19838837-A1.

XX 02-MAR-2000.

XX 27-AUG-1998; 98DE-01038837.

XX 27-AUG-1998; 98DE-01038837.

XX

PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 XX (NOVO) NOVO-NORDISK AS.
 PI Esterbauer H, Oberkofler H, Patsch W;
 XX WPI; 2000-272214/24.
 DR
 XX Recombinant fat and muscle tissue specific uncoupling protein 3 promoters
 PT useful for identifying UCP3 modulators.
 XX
 PS Claim 2; Page 10; 38pp; German.
 XX
 XX This invention describes novel recombinant DNA molecules containing an
 CC uncoupling protein 3 (UCP-3) promoter DNA sequence active in fat cells
 CC but not functional in muscle cells or vice versa. The recombinant DNA
 CC molecules are useful for transcription of genes and, with host cells, to
 CC test for substances that can influence transcription. They can also be
 CC used to identify modulators of UCP3 promoters. UCP3 plays a role in fat
 CC metabolism and control of the promoter is useful in combating diseases
 CC with inappropriate fat tissue metabolism. This sequence represents a
 CC fragment of the human UCP-3 promoter which is used to illustrate the
 CC method of the invention
 XX
 XX Sequence 6 BP; 1 A; 4 C; 0 G; 1 T; 0 U; 0 Other;
 SQ
 Query Match 66.7%; Score 4; DB 3; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 3 GAGG 6
 Db |||||
 6 GAGG 3
 XX
 RESULT 18
 AAF24321
 ID AAF24321 standard; DNA; 6 BP.
 XX
 AC AAF24321;
 XX
 DT 09-APR-2001 (first entry)
 XX
 DE Human NFAR-1/NFAR-2 intron/exon junction sequence #21.
 XX
 XX Human; nuclear factor associated with dsRNA; NFAR-1; NFAR-2;
 KW transcription regulator; chromosome 19p13.1-13.2; apoptosis;
 KW tumorigenesis; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200077205-A1.
 XX
 XX 21-DEC-2000.
 XX
 PF 09-JUN-1999; 99US-0138612P.
 XX
 PR 11-JUN-1999; 99US-0138612P.
 XX
 PA (BARB/) BARBER G N.
 PA (SAUN/) SAUNDERS L.
 PA (PERK/) PERKINS D J.
 XX
 PI Barber GN, Saunders L, Perkins DJ;
 XX
 DR WPI; 2001-080688/09.
 XX
 XX Novel isolated human nuclear factor associated with dsRNA polypeptide
 PT useful for determining structure-function relationships and as affinity
 PT tag to identify and isolate interacting proteins that bind to the factor.
 XX
 PS Disclosure; Page 62; 73pp; English.
 XX
 CC The present invention provides the protein and coding sequences of two

CC human nuclear factors associated with dsRNA (NFAR-1 and NFAR-2). These
 CC are transcriptional regulators and are thought to play a role in
 CC apoptosis and tumorigenesis. The coding sequence (found on chromosome
 CC 19p13.1-13.2) is useful as a probe to detect rearrangements in tumour
 CC cells and the protein is useful for determining structure-function
 CC relationships
 XX
 SQ Sequence 6 BP; 1 A; 1 C; 3 G; 1 T; 0 U; 0 Other;
 Query Match 66.7%; Score 4; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GAGG 6
 Db |||||
 1 GAGG 4
 XX
 RESULT 19
 ACA63330
 ID ACA63330 standard; RNA; 6 BP.
 XX
 AC ACA63330;
 XX
 DT 26-AUG-2003 (first entry)
 XX
 DE Self assembly ribozyme system 6 nucleotide component.
 XX
 KW Ribozyme; Pneumocystis carinii infection; chronic hepatitis D; ss;
 KW delta hepatitis virus infection; group I intron RNA.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT misc_binding 1..6
 FT /tag= b
 FT /bound moiety= "28 nucleotide component"
 FT /note= "Forms a Watson-Crick duplex with nucleotides 28-
 FT 23 of sequence in ACA63331"
 FT modified_base 1
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= 32P labelled"
 XX
 XX US2003040114-A1.
 PN
 XX 27-FEB-2003.
 PD
 XX
 PF 07-JUN-1999; 99US-00326956.
 XX
 PR 05-SEP-1996; 96US-0024685P.
 PR 04-SEP-1997; 97US-00923487.
 XX
 PA (WARN) WARNER LAMBERT CO.
 XX
 PI Cui M, Czarnik AW, Mei H;
 XX
 DR WPI; 2003-492174/46.
 XX
 XX Selecting compounds that modulate ribozyme activity or that bind ribozyme
 PT in vivo in an organism, for use in diagnosing or treating microbial
 PT infections, by using a biological assay.
 XX
 PS Example 2; Fig 9; 20pp; English.
 XX
 CC The invention relates to a method of selecting a compound that modulates
 CC the activity of ribozyme, or that detects the ribozyme in an organism,
 CC comprising measuring in an assay the ability of the compound to modulate
 CC the function of or to selectively bind to the ribozyme and selecting the
 CC assayed compound for use in modulating the activity of the ribozyme or
 CC detecting the ribozyme in the organism. The method is useful for
 CC selecting a compound, preferably a small organic molecule having a
 CC molecular weight of less than 1000 Daltons, that modulates the activity

CC of a ribozyme or that detects the presence of a ribozyme in an organism
CC that is pathogenic for an animal or plant. The selected compound which
CC modulates ribozyme activity is useful for treating an infection caused by
CC a microorganism containing the ribozyme, especially for treating
CC Pneumocystis carinii infections, delta hepatitis virus infections and
CC chronic hepatitis B and selected compounds which binds to ribozyme are
CC useful for diagnosing the conditions. The method allows rapid
CC determination of small organic modulators that regulate the function of
CC ribozymes. The present sequence represents the self assembly ribozyme
CC system 6 nucleotide component
XX
SQ Sequence 6 BP; 1 A; 1 C; 3 G; 0 T; 1 U; 0 Other;
Query Match 66.7%; Score 4; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GAGG 6
Db ||||
1 GAGG 4
RESULT 20
ADE38304
ID ADE38304 standard; DNA; 6 BP.
XX
AC ADE38304;
XX
DT 29-JAN-2004 (first entry)
XX
DE Immune modulatory sequence (IMS) hexamer oligonucleotide SEQ ID NO:43.
XX
KW autoimmune disease; statin; antigen-specific immunomodulatory agent;
KW non-antigen-specific immunomodulatory agent; immunomodulatory;
KW antidiabetic; antiarthritic; vasotropic; gene therapy;
KW multiple sclerosis; insulin dependent diabetes mellitus; IDDM;
KW rheumatoid arthritis; autoimmune uveitis; ss.
XX
OS Synthetic.
XX
FN WO2003082269-A1.
XX
PD 09-OCT-2003.
XX
PF 31-MAR-2003; 2003WO-US009807.
XX
PR 29-MAR-2002; 2002US-0368803P.
XX
PA (STRD) UNIV LELAND STANFORD JUNIOR.
XX (BAYH-) BAYHILL THERAPEUTICS INC.
XX
PI Garren H, Steinman L;
XX
DR WPI; 2003-803953/75.
XX
PT Treating an autoimmune disease by co-administering to a patient a statin
PT and an antigen-specific non-antigen-specific immunomodulatory agent.
XX
PS Disclosure; SEQ ID NO 43; 90pp; English.
XX
CC The present invention describes a method for treating an autoimmune
CC disease comprising co-administering to a patient a statin and an antigen-
CC specific/non-antigen-specific immunomodulatory agent. The
CC immunomodulatory agent has antidiabetic, antiarthritic and vasotropic
CC activities, and can be used in gene therapy. The method is useful for
CC treating autoimmune disease e.g., multiple sclerosis, insulin dependent
CC diabetes mellitus (IDDM), rheumatoid arthritis or autoimmune uveitis. The
CC present sequence is used in the exemplification of the present invention.
XX
SQ Sequence 6 BP; 1 A; 1 C; 3 G; 1 T; 0 U; 0 Other;
Query Match 66.7%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GAGG 6
Db ||||
1 GAGG 4
RESULT 22
ADE38300
ID ADE38300 standard; DNA; 6 BP.
XX
AC ADE38300;
XX
DT 29-JAN-2004 (first entry)
XX

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GAGG 6
Db ||||
1 GAGG 4
RESULT 21
ADE38308
ID ADE38308 standard; DNA; 6 BP.
XX
AC ADE38308;
XX
DT 29-JAN-2004 (first entry)
XX
DE Immune modulatory sequence (IMS) hexamer oligonucleotide SEQ ID NO:47.
XX
KW autoimmune disease; statin; antigen-specific immunomodulatory agent;
KW non-antigen-specific immunomodulatory agent; immunomodulatory;
KW antidiabetic; antiarthritic; vasotropic; gene therapy;
KW multiple sclerosis; insulin dependent diabetes mellitus; IDDM;
KW rheumatoid arthritis; autoimmune uveitis; ss.
XX
OS Synthetic.
XX
FN WO2003082269-A1.
XX
PD 09-OCT-2003.
XX
PF 31-MAR-2003; 2003WO-US009807.
XX
PR 29-MAR-2002; 2002US-0368803P.
XX
PA (STRD) UNIV LELAND STANFORD JUNIOR.
XX (BAYH-) BAYHILL THERAPEUTICS INC.
XX
PI Garren H, Steinman L;
XX
DR WPI; 2003-803953/75.
XX
PT Treating an autoimmune disease by co-administering to a patient a statin
PT and an antigen-specific non-antigen-specific immunomodulatory agent.
XX
PS Disclosure; SEQ ID NO 47; 90pp; English.
XX
CC The present invention describes a method for treating an autoimmune
CC disease comprising co-administering to a patient a statin and an antigen-
CC specific/non-antigen-specific immunomodulatory agent. The
CC immunomodulatory agent has antidiabetic, antiarthritic and vasotropic
CC activities, and can be used in gene therapy. The method is useful for
CC treating autoimmune disease e.g., multiple sclerosis, insulin dependent
CC diabetes mellitus (IDDM), rheumatoid arthritis or autoimmune uveitis. The
CC present sequence is used in the exemplification of the present invention.
XX
SQ Sequence 6 BP; 1 A; 1 C; 3 G; 1 T; 0 U; 0 Other;
Query Match 66.7%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GAGG 6
Db ||||
1 GAGG 4
RESULT 22
ADE38300
ID ADE38300 standard; DNA; 6 BP.
XX
AC ADE38300;
XX
DT 29-JAN-2004 (first entry)
XX

DE Immune modulatory sequence (IMS) hexamer oligonucleotide SEQ ID NO:39.
XX autoimmune disease; statin; antigen-specific immunomodulatory agent;
KW non-antigen-specific immunomodulatory agent; immunomodulatory;
KW anti-diabetic; antiarthritic; vasotropic; gene therapy;
KW multiple sclerosis; insulin dependent diabetes mellitus; IDDM;
KW rheumatoid arthritis; autoimmune uveitis; ss.
XX Synthetic.
OS
XX WO2003082269-A1.
XX PN
XX PD 09-OCT-2003.
XX PF 31-MAR-2003; 2003WO-US009807.
XX PR 29-MAR-2002; 2002US-0368803P.
XX PA (STRD) UNIV LELAND STANFORD JUNIOR.
PA (BAYH-) BAYHILL THERAPEUTICS INC.
XX PI Garren H, Steinman L;
XX DR WPI; 2003-803953/75.
XX PT Treating an autoimmune disease by co-administering to a patient a statin
PT and an antigen-specific non-antigen-specific immunomodulatory agent.
XX PS Disclosure; SEQ ID NO 39; 90pp; English.
XX CC The present invention describes a method for treating an autoimmune
CC disease comprising co-administering to a patient a statin and an antigen-
CC specific/non-antigen-specific immunomodulatory agent. The
CC immunomodulatory agent has antidiabetic, antiarthritic and vasotropic
CC activities, and can be used in gene therapy. The method is useful for
CC treating autoimmune disease e.g., multiple sclerosis, insulin dependent
CC diabetes mellitus (IDDM), rheumatoid arthritis or autoimmune uveitis. The
CC present sequence is used in the exemplification of the present invention.
XX SQ Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 66.7%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GAGG 6
Db ||||
1 GAGG 4
RESULT 23
ADJ35691/c
ID ADJ35691 standard; DNA; 6 BP.
XX AC ADJ35691;
XX DT 22-APR-2004 (first entry)
XX DE Stabilising anti-repression, STAR, element dyad sequence #357.
XX KW STAR affiliated proteinaceous molecule; post translational modification;
XX KW stabilising anti-repression; STAR; STAR element; ds; dyad.
XX OS Unidentified.
XX PN WO2003106674-A2.
XX PD 24-DEC-2003.
XX PF 30-MAY-2003; 2003WO-NL000410.
XX PR 14-JUN-2002; 2002EP-00077344.
XX PA (CHRO-) CHROMAGENICS BV.
XX PI Otte AP, Kruckeberg AL, Satijn DPE;
XX DR WPI; 2004-082195/08.
XX PT Producing proteinaceous molecules in cells by selecting a cell, providing
XX PT a nucleic acid encoding a proteinaceous molecule with an Stabilizing Anti
XX PT -Repression sequence and expressing proteinaceous molecule.
XX PS Disclosure; Page 103; 177pp; English.
XX CC The invention relates to a method of producing a proteinaceous molecule
CC (I) in a cell comprising selecting a cell for its suitability for
CC producing (I), providing a nucleic acid encoding (I) with a nucleic acid
CC comprising a Stabilising Anti-Repression (STAR) sequence, expressing the
CC resulting nucleic acid in the cell and collecting (I). The method is
CC useful for producing (I). A cell line (II) provided with a nucleic acid
CC comprising a STAR sequence is useful for producing (I). (II) Enables
CC production of affiliated proteinaceous molecule, as cell carries out
CC proper post-translational modifications of produced proteins. The present
CC sequence represents a stabilising anti-repression, STAR, element primer
CC dyad sequence.
XX SQ Sequence 6 BP; 0 A; 5 C; 0 G; 1 T; 0 U; 0 Other;
Query Match 66.7%; Score 4; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GAGG 6
Db ||||
6 GAGG 3
RESULT 24
ADJ35735
ID ADJ35735 standard; DNA; 6 BP.
XX AC ADJ35735;
XX DT 22-APR-2004 (first entry)
XX DE Stabilising anti-repression, STAR, element dyad sequence #401.
XX KW STAR affiliated proteinaceous molecule; post translational modification;
XX KW stabilising anti-repression; STAR; STAR element; ds; dyad.
XX OS Unidentified.
XX PN WO2003106674-A2.
XX PD 24-DEC-2003.
XX PF 30-MAY-2003; 2003WO-NL000410.
XX PR 14-JUN-2002; 2002EP-00077344.
XX PA (CHRO-) CHROMAGENICS BV.
XX PI Otte AP, Kruckeberg AL, Satijn DPE;
XX DR WPI; 2004-082195/08.
XX PT Producing proteinaceous molecules in cells by selecting a cell, providing
XX PT a nucleic acid encoding a proteinaceous molecule with an Stabilizing Anti
XX PT -Repression sequence and expressing proteinaceous molecule.
XX PS Disclosure; Page 103; 177pp; English.
XX CC The invention relates to a method of producing a proteinaceous molecule
CC (I) in a cell comprising selecting a cell for its suitability for
CC producing (I), providing a nucleic acid encoding (I) with a nucleic acid

PA (CHRO-) CHROMAGENICS BV.
XX Otte AP, Kruckeberg AL, Satijn DPE;
XX WPI; 2004-082195/08.
XX PT Producing proteinaceous molecules in cells by selecting a cell, providing
XX PT a nucleic acid encoding a proteinaceous molecule with an Stabilizing Anti
XX PT -Repression sequence and expressing proteinaceous molecule.
XX PS Disclosure; Page 102; 177pp; English.
XX CC The invention relates to a method of producing a proteinaceous molecule
CC (I) in a cell comprising selecting a cell for its suitability for
CC producing (I), providing a nucleic acid encoding (I) with a nucleic acid
CC comprising a Stabilising Anti-Repression (STAR) sequence, expressing the
CC resulting nucleic acid in the cell and collecting (I). The method is
CC useful for producing (I). A cell line (II) provided with a nucleic acid
CC comprising a STAR sequence is useful for producing (I). (II) Enables
CC production of affiliated proteinaceous molecule, as cell carries out
CC proper post-translational modifications of produced proteins. The present
CC sequence represents a stabilising anti-repression, STAR, element primer
CC dyad sequence.
XX SQ Sequence 6 BP; 0 A; 5 C; 0 G; 1 T; 0 U; 0 Other;
Query Match 66.7%; Score 4; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GAGG 6
Db ||||
6 GAGG 3
RESULT 24
ADJ35735
ID ADJ35735 standard; DNA; 6 BP.
XX AC ADJ35735;
XX DT 22-APR-2004 (first entry)
XX DE Stabilising anti-repression, STAR, element dyad sequence #401.
XX KW STAR affiliated proteinaceous molecule; post translational modification;
XX KW stabilising anti-repression; STAR; STAR element; ds; dyad.
XX OS Unidentified.
XX PN WO2003106674-A2.
XX PD 24-DEC-2003.
XX PF 30-MAY-2003; 2003WO-NL000410.
XX PR 14-JUN-2002; 2002EP-00077344.
XX PA (CHRO-) CHROMAGENICS BV.
XX PI Otte AP, Kruckeberg AL, Satijn DPE;
XX DR WPI; 2004-082195/08.
XX PT Producing proteinaceous molecules in cells by selecting a cell, providing
XX PT a nucleic acid encoding a proteinaceous molecule with an Stabilizing Anti
XX PT -Repression sequence and expressing proteinaceous molecule.
XX PS Disclosure; Page 103; 177pp; English.
XX CC The invention relates to a method of producing a proteinaceous molecule
CC (I) in a cell comprising selecting a cell for its suitability for
CC producing (I), providing a nucleic acid encoding (I) with a nucleic acid

CC comprising a Stabilising Anti-Repression (STAR) sequence, expressing the
 CC resulting nucleic acid in the cell and collecting (I). The method is
 CC useful for producing (I). A cell line (II) provided with a nucleic acid
 CC comprising a STAR sequence is useful for producing (I). (II) Enables
 CC production of affiliated proteinaceous molecule, as cell carries out
 CC proper post-translational modifications of produced proteins. The present
 CC sequence represents a stabilising anti-repression, STAR, element primer
 CC dyad sequence.
 XX
 SQ Sequence 6 BP; 1 A; 1 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 12; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGA 4
 ||||
 Db 3 GGGA 6

RESULT 25

ADJ35654

ID ADJ35654 standard; DNA; 6 BP.

XX

AC

ADJ35654;

XX

DT 22-APR-2004 (first entry)

XX

DE

XX

KW

XX

OS

XX

PN

WO2003106674-A2.

XX

PD

24-DEC-2003.

XX

PF

30-MAY-2003; 2003WO-NL000410.

XX

PR

14-JUN-2002; 2002BP-00077344.

XX

PA

(CHRO-) CHROMAGENICS BV.

XX

PI

Otte AP, Kruckeberg AL, Satiijn DPE;

XX

DR

WPI; 2004-082195/08.

XX

PT

Producing proteinaceous molecules in cells by selecting a cell, providing

XX

PT

a nucleic acid encoding a proteinaceous molecule with an stabilizing Anti

XX

PT

-Repression sequence and expressing proteinaceous molecule.

XX

PS

Disclosure; Page 101; 177pp; English.

XX

CC

The invention relates to a method of producing a proteinaceous molecule

XX

CC

(I) in a cell comprising selecting a cell for its suitability for

XX

CC

producing (I), providing a nucleic acid encoding (I) with a nucleic acid

CC comprising a Stabilising Anti-Repression (STAR) sequence, expressing the
 CC resulting nucleic acid in the cell and collecting (I). The method is
 CC useful for producing (I). A cell line (II) provided with a nucleic acid
 CC comprising a STAR sequence is useful for producing (I). (II) Enables
 CC production of affiliated proteinaceous molecule, as cell carries out
 CC proper post-translational modifications of produced proteins. The present
 CC sequence represents a stabilising anti-repression, STAR, element primer
 CC dyad sequence.
 XX
 SQ Sequence 6 BP; 1 A; 1 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 12; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGA 4
 ||||
 Db 3 GGGA 6

RESULT 26

ADL09191

ID ADL09191 standard; DNA; 6 BP.

XX

AC

ADL09191;

XX

DT 20-MAY-2004 (first entry)

XX

DE

XX

KW

T7 promoter DNA fragment #3.

XX

OS

amplification; primer; promoter; RNA polymerase; ds.

XX

PN

Enterobacteria phage T7.

XX

PD

WO2004016757-A2.

XX

PF

26-FEB-2004.

XX

PR

15-AUG-2003; 2003WO-US025564.

XX

PR

16-AUG-2002; 2002US-0404075P.

XX

PA

(REGC) UNIV CALIFORNIA.

XX

PI

Karin M, Park JM;

XX

DR

WPI; 2004-203788/19.

XX

PT

Producing a nucleic acid sequence comprises amplifying double stranded

XX

PT

DNA sequence in the presence of first and second primers to produce a

XX

PT

first nucleic acid molecule having the double stranded DNA sequence in a

XX

PT

head to head orientation.

XX

PS

Disclosure; SEQ ID NO 7; 55pp; English.

CC comprising a Stabilising Anti-Repression (STAR) sequence, expressing the
 CC resulting nucleic acid in the cell and collecting (I). The method is
 CC useful for producing (I). A cell line (II) provided with a nucleic acid
 CC comprising a STAR sequence is useful for producing (I). (II) Enables
 CC production of affiliated proteinaceous molecule, as cell carries out
 CC proper post-translational modifications of produced proteins. The present
 CC sequence represents a stabilising anti-repression, STAR, element primer
 CC dyad sequence.
 XX
 SQ Sequence 6 BP; 1 A; 1 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 12; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGA 4
 ||||
 Db 3 GGGA 6

RESULT 25

ADJ35654

ID ADJ35654 standard; DNA; 6 BP.

XX

AC

ADJ35654;

XX

DT 22-APR-2004 (first entry)

XX

DE

XX

KW

STAR affiliated proteinaceous molecule; post translational modification;

XX

KW

stabilising anti-repression; STAR; STAR element; ds; dyad.

XX

OS

Unidentified.

XX

PN

WO2003106674-A2.

XX

PD

24-DEC-2003.

XX

PF

30-MAY-2003; 2003WO-NL000410.

XX

PR

14-JUN-2002; 2002BP-00077344.

XX

PA

(CHRO-) CHROMAGENICS BV.

XX

PI

Otte AP, Kruckeberg AL, Satiijn DPE;

XX

DR

WPI; 2004-082195/08.

XX

PT

Producing proteinaceous molecules in cells by selecting a cell, providing

XX

PT

a nucleic acid encoding a proteinaceous molecule with an stabilizing Anti

XX

PT

-Repression sequence and expressing proteinaceous molecule.

XX

PS

Disclosure; Page 101; 177pp; English.

XX

CC

The invention relates to a method of producing a proteinaceous molecule

CC comprising a Stabilising Anti-Repression (STAR) sequence, expressing the
 CC resulting nucleic acid in the cell and collecting (I). The method is
 CC useful for producing (I). A cell line (II) provided with a nucleic acid
 CC comprising a STAR sequence is useful for producing (I). (II) Enables
 CC production of affiliated proteinaceous molecule, as cell carries out
 CC proper post-translational modifications of produced proteins. The present
 CC sequence represents a stabilising anti-repression, STAR, element primer
 CC dyad sequence.
 XX
 SQ Sequence 6 BP; 1 A; 1 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 12; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGA 4
 ||||
 Db 3 GGGA 6

RESULT 25

ADJ35654

ID ADJ35654 standard; DNA; 6 BP.

XX

AC

ADJ35654;

XX

DT 22-APR-2004 (first entry)

XX

DE

XX

KW

STAR affiliated proteinaceous molecule; post translational modification;

XX

KW

stabilising anti-repression; STAR; STAR element; ds; dyad.

XX

OS

Unidentified.

XX

PN

WO2003106674-A2.

XX

PD

24-DEC-2003.

XX

PF

30-MAY-2003; 2003WO-NL000410.

XX

PR

14-JUN-2002; 2002BP-00077344.

XX

PA

(CHRO-) CHROMAGENICS BV.

XX

PI

Otte AP, Kruckeberg AL, Satiijn DPE;

XX

DR

WPI; 2004-082195/08.

XX

PT

Producing proteinaceous molecules in cells by selecting a cell, providing

XX

PT

a nucleic acid encoding a proteinaceous molecule with an stabilizing Anti

XX

PT

-Repression sequence and expressing proteinaceous molecule.

XX

PS

Disclosure; Page 101; 177pp; English.

XX

CC

The invention relates to a method of producing a proteinaceous molecule

CC comprising a Stabilising Anti-Repression (STAR) sequence, expressing the
 CC resulting nucleic acid in the cell and collecting (I). The method is
 CC useful for producing (I). A cell line (II) provided with a nucleic acid
 CC comprising a STAR sequence is useful for producing (I). (II) Enables
 CC production of affiliated proteinaceous molecule, as cell carries out
 CC proper post-translational modifications of produced proteins. The present
 CC sequence represents a stabilising anti-repression, STAR, element primer
 CC dyad sequence.
 XX
 SQ Sequence 6 BP; 1 A; 1 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 12; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGA 4
 ||||
 Db 3 GGGA 6

RESULT 25

ADJ35654

ID ADJ35654 standard; DNA; 6 BP.

XX

AC

ADJ35654;

XX

DT 22-APR-2004 (first entry)

XX

DE

XX

KW

STAR affiliated proteinaceous molecule; post translational modification;

XX

KW

stabilising anti-repression; STAR; STAR element; ds; dyad.

XX

OS

Unidentified.

XX

PN

WO2003106674-A2.

XX

PD

24-DEC-2003.

XX

PF

30-MAY-2003; 2003WO-NL000410.

XX

PR

14-JUN-2002; 2002BP-00077344.

XX

PA

(CHRO-) CHROMAGENICS BV.

XX

PI

Otte AP, Kruckeberg AL, Satiijn DPE;

XX

DR

WPI; 2004-082195/08.

XX

PT

Producing proteinaceous molecules in cells by selecting a cell, providing

XX

PT

a nucleic acid encoding a proteinaceous molecule with an stabilizing Anti

XX

PT

-Repression sequence and expressing proteinaceous molecule.

XX

PS

Disclosure; Page 101; 177pp; English.

XX

CC

The invention relates to a method of producing a proteinaceous molecule

CC comprising a Stabilising Anti-Repression (STAR) sequence, expressing the
 CC resulting nucleic acid in the cell and collecting (I). The method is
 CC useful for producing (I). A cell line (II) provided with a nucleic acid
 CC comprising a STAR sequence is useful for producing (I). (II) Enables
 CC production of affiliated proteinaceous molecule, as cell carries out
 CC proper post-translational modifications of produced proteins. The present
 CC sequence represents a stabilising anti-repression, STAR, element primer
 CC dyad sequence.
 XX
 SQ Sequence 6 BP; 1 A; 1 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 12; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGA 4
 ||||
 Db 3 GGGA 6

RESULT 25

ADJ35654

ID ADJ35654 standard; DNA; 6 BP.

XX

AC

ADJ

Query Match 66.7%; Score 4; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGA 4
| | | |
Db 1 GGGA 4

RESULT 27
ADL09189/c
ID ADL09189 standard; DNA; 6 BP.
XX
AC ADL09189;
XX
DT 20-MAY-2004 (first entry)
XX
DE T7 promoter DNA fragment #2.
XX
KW amplification; primer; promoter; RNA polymerase; ds.
XX
OS Enterobacteria phage T7.
XX
PN WO2004016757-A2.
XX
PD 26-FEB-2004.
XX
PF 15-AUG-2003; 2003WO-US025564.
XX
PR 16-AUG-2002; 2002US-0404075P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Karin M, Park JM;
XX
DR WPI; 2004-203788/19.
XX
PT Producing a nucleic acid sequence comprises amplifying double stranded
DNA sequence in the presence of first and second primers to produce a
first nucleic acid molecule having the double stranded DNA sequence in a
head to head orientation.
XX
PS Disclosure; SEQ ID NO 5; 55pp; English.
XX
CC This invention describes a novel method for producing a nucleic acid
sequence comprising amplifying the double stranded DNA sequence of
interest in the presence of the first primer and the second primer to
produce a first nucleic acid molecule comprising the double stranded DNA
sequence of interest flanked by at least a portion of the first promoter
in a head to head orientation. The method involves providing RNA
polymerase that specifically binds to the first promoter and contacting
the first nucleic acid molecule with the RNA polymerase to produce double
stranded DNA sequence of interest flanked by the first promoter in a head
to head orientation. The method further comprises providing RNA
polymerase that specifically binds to the first promoter and contacting
the second nucleic acid molecule with the RNA polymerase to produce
double stranded RNA that is complementary to the double stranded DNA
sequence of interest. The second strand of the double-stranded DNA
sequence of interest comprises at least a portion of a second promoter.
The second promoter is different from the first promoter. The first
stranded DNA comprises a nucleotide sequence linked to the 3' end of the
first promoter, and the first primer further comprises a second sequence
complementary to the nucleotide sequence, where the second sequence is
linked to the 3' end of the first sequence of the first primer. The first
primer comprises a sequence complementary to T7, T3 or SP6 promoter. The
first sequence comprises a second primer complementary to at least a

CC portion of a promoter. The methods and kits are useful for producing
nucleic acid sequences as powerful alternative tools for functional
genomics.
XX
SQ Sequence 6 BP; 1 A; 3 C; 0 G; 2 T; 0 U; 0 Other;
Query Match 66.7%; Score 4; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGA 4
| | | |
Db 6 GGGA 3

RESULT 28
ADL09220
ID ADL09220 standard; DNA; 6 BP.
XX
AC ADL09220;
XX
DT 20-MAY-2004 (first entry)
XX
DE T3 promoter DNA fragment #15.
XX
KW amplification; primer; promoter; RNA polymerase; ds.
XX
OS Bacteriophage T3.
XX
PN WO2004016757-A2.
XX
PD 26-FEB-2004.
XX
PF 15-AUG-2003; 2003WO-US025564.
XX
PR 16-AUG-2002; 2002US-0404075P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Karin M, Park JM;
XX
DR WPI; 2004-203788/19.
XX
PT Producing a nucleic acid sequence comprises amplifying double stranded
DNA sequence in the presence of first and second primers to produce a
first nucleic acid molecule having the double stranded DNA sequence in a
head to head orientation.
XX
PS Disclosure; SEQ ID NO 36; 55pp; English.
XX
CC This invention describes a novel method for producing a nucleic acid
sequence comprising amplifying the double stranded DNA sequence of
interest in the presence of the first primer and the second primer to
produce a first nucleic acid molecule comprising the double stranded DNA
sequence of interest flanked by at least a portion of the first promoter
in a head to head orientation. The method involves providing RNA
polymerase that specifically binds to the first promoter and contacting
the first nucleic acid molecule with the RNA polymerase to produce double
stranded RNA that is complementary to the double stranded DNA sequence of
interest. This method further comprises providing a third primer
complementary to at least a portion of the first promoter and amplifying
the first nucleic acid molecule produced in the presence of the third
primer to produce a second nucleic acid molecule comprising the double
stranded DNA sequence of interest flanked by the first promoter in a head
to head orientation. The method further comprises providing RNA
polymerase that specifically binds to the first promoter and contacting
the second nucleic acid molecule with the RNA polymerase to produce
double stranded RNA that is complementary to the double stranded DNA
sequence of interest. The second strand of the double-stranded DNA
sequence of interest comprises at least a portion of a second promoter.
The second promoter is different from the first promoter. The first
stranded DNA comprises a nucleotide sequence linked to the 3' end of the
first promoter, and the first primer further comprises a second sequence
complementary to the nucleotide sequence, where the second sequence is
linked to the 3' end of the first sequence of the first primer. The first
primer comprises a sequence complementary to T7, T3 or SP6 promoter. The
first sequence comprises a second primer complementary to at least a

CC first promoter, and the first primer further comprises a second sequence
 CC complementary to the nucleotide sequence, where the second sequence is
 CC linked to the 3' end of the first sequence of the first primer. The first
 CC primer comprises a sequence complementary to T7, T3 or SP6 promoter. The
 CC first sequence comprises a second primer complementary to at least a
 CC portion of a promoter. The methods and kits are useful for producing
 CC nucleic acid sequences as powerful alternative tools for functional
 CC genomics.

XX Sequence 6 BP; 3 A; 0 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 12; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGA 4
 DB ||||
 3 GGGA 6

RESULT 29
 ADQ89354
 ID ADQ89354 standard; DNA; 6 BP.

XX AC ADQ89354;
 XX 07-OCT-2004 (first entry)

XX DE Acute phase response factor consensus binding site.
 XX ds; diarrhoea; infectious disease; necrotising enterocolitis;
 KW urinary tract infection; acute phase response factor.

XX OS Synthetic.
 XX US2004142415-A1.
 XX 22-JUL-2004.

XX PF 21-JAN-2003; 2003US-00348304.
 XX 21-JAN-2003; 2003US-00348304.

XX PA (UYNE-) UNIV NEBRASKA.
 XX Mcdonald TL, Larson MA, Weber A;
 XX WPI; 2004-579907/56.

XX New isolated nucleic acid molecule encoding a polypeptide having serum
 PT amyloid A3 (SAA3) activity, useful for preventing or treating diarrhea,
 PT infectious diseases, necrotizing enterocolitis, or urinary tract
 PT infections.

XX Example; SEQ ID NO 12; 25pp; English.

XX The invention relates to an isolated nucleic acid molecule that encodes a
 CC polypeptide having serum amyloid A3 (SAA3) activity. The nucleic acid
 CC encoding the proteins having SAA3 activity is useful as probes to detect
 CC the presence of and/or expression of the genes. They are also useful for
 CC producing transgenic cells, tissues, or organs. They are also useful for
 CC preventing or treating diarrhoea, infectious diseases, necrotising
 CC enterocolitis or urinary tract infections. The present sequence
 CC represents the acute phase response factor consensus binding site. Note:
 CC SEQ ID Nos 1 and 2 are not disclosed in the specification.

XX Sequence 6 BP; 1 A; 1 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 12; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGA 4

DB ||||
 3 GGGA 6

RESULT 30
 ADR32741
 ID ADR32741 standard; DNA; 6 BP.

XX AC ADR32741;
 XX 04-NOV-2004 (first entry)

XX DE Human nicking agent target DNA #282.

XX ss; nicking agent; assay panel; diagnosis; expression pattern;
 KW DNA fingerprinting; nosocomial infection; microbiological assay;
 KW bacterial contamination; genome mapping; bioremediation.

XX OS Homo sapiens.

XX PN WO2004067765-A2.

XX PD 12-AUG-2004.

XX PF 29-JAN-2004; 2004WO-US002720.

XX PR 29-JAN-2003; 2003US-0443811P.

XX PA (KECK-) KECK GRADUATE INST.

XX PI Van Ness J, Galas DJ, Van Ness LK;

XX WPI; 2004-581010/56.

XX Identifying nucleic acid sample source, useful for identifying bacterial
 PT strains involved in nosocomial infections, comprises treating the nucleic
 PT acid sample with components comprising a nicking agent under nicking
 PT conditions.

XX Example 1; Page 76; 238pp; English.

XX The invention relates to a method of treating a nucleic acid sample with
 CC components under nicking conditions, where the components comprise a
 CC nicking agent, and the conditions cause the nicking agent to nick the
 CC nucleic acid sample to thus produce a family of initiating
 CC oligonucleotide fragments, and subjecting one or more members of the
 CC family of initiating oligonucleotide fragments to a characterization
 CC process to thus provide results. The method is useful for creating an
 CC assay panel of diagnostic oligonucleotides that can identify any organism
 CC or individual. The method is useful for characterizing other DNA
 CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
 CC The method, kit or composition is useful for identifying the source
 CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
 CC non-human animal or human. The method is particularly useful for rapidly
 CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
 CC subspecies, and especially strains or individuals of the subspecies. It
 CC is especially useful for identifying different bacterial strains involved
 CC in e.g., nosocomial infections. Furthermore, the method is useful for
 CC diagnosing bacterial disease in plants and humans, monitoring for
 CC bacterial content and/or contamination in the environment, monitoring
 CC food for bacterial contamination, monitoring manufacturing processes for
 CC bacterial contamination, monitoring quality assurance/quality control of
 CC laboratory tests involving microbiological assays, tracing bacterial
 CC contamination and/or outbreaks of bacterial infections, genome mapping,
 CC monitoring bioremediation sites, and for monitoring agricultural sites
 CC for test crops, bacteria and recombinant molecules. This sequence
 CC corresponds to nucleic acid used in the method of the invention.

XX Sequence 6 BP; 2 A; 0 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 13; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGA 4
|
|
|
|
Db 3 GGA 6

Search completed: July 20, 2005, 22:59:09
Job time : 189.4 secs

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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 21:47:48 ; Search time 738.2 Seconds
(without alignments)
393.838 Million cell updates/sec

Title: US-09-735-363A-45

Perfect score: 6

Sequence: 1 99gagg 6

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 4754

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

GenEmbl:.*
1: gb_ba:.*
2: gb_hcg:.*
3: gb_in:.*
4: gb_om:.*
5: gb_ov:.*
6: gb_pat:.*
7: gb_ph:.*
8: gb_pl:.*
9: gb_pr:.*
10: gb_ro:.*
11: gb_sts:.*
12: gb_sy:.*
13: gb_un:.*
14: gb_vi:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	6	100.0	6	6	AX175281 Sequence
2	6	100.0	6	6	AX743310 Sequence
3	6	100.0	6	6	AX743314 Sequence
C 4	6	100.0	6	6	AX805866 Sequence
5	6	100.0	6	6	AX816715 Sequence
C 6	5	83.3	5	6	A70976 Sequence 30
C 7	5	83.3	5	6	BD244758 Isolation
C 8	5	83.3	5	6	AX805860 Sequence
C 9	5	83.3	6	6	A93563 Sequence 1
C 10	5	83.3	6	6	CQ755704 Sequence
C 11	5	83.3	6	6	CQ755766 Sequence
C 12	5	83.3	6	6	CQ755813 Sequence
C 13	5	83.3	6	6	CQ755818 Sequence
C 14	5	83.3	6	6	CQ756128 Sequence
C 15	5	83.3	6	6	CQ757942 Sequence
C 16	5	83.3	6	6	CQ758004 Sequence
C 17	5	83.3	6	6	CQ758051 Sequence
C 18	5	83.3	6	6	CQ758056 Sequence
C 19	5	83.3	6	6	CQ758366 Sequence

20	5	83.3	6	6	E08990	E08990 Oligo DNA m
21	5	83.3	6	6	E09173	E09173 Synthetic o
22	5	83.3	6	6	E09489	E09489 Phosphoroth
23	5	83.3	6	6	AX093419	AX093419 Sequence
24	5	83.3	6	6	AX175283	AX175283 Sequence
25	5	83.3	6	6	AX361080	AX361080 Sequence
26	5	83.3	6	6	AX391507	AX391507 Sequence
27	5	83.3	6	6	AX574433	AX574433 Sequence
C 28	5	83.3	6	6	AX764742	AX764742 Sequence
C 29	5	83.3	6	6	AX764804	AX764804 Sequence
C 30	5	83.3	6	6	AX764851	AX764851 Sequence
C 31	5	83.3	6	6	AX764856	AX764856 Sequence
C 32	5	83.3	6	6	AX765166	AX765166 Sequence
C 33	4.4	73.3	6	6	CQ755693	CQ755693 Sequence
C 34	4.4	73.3	6	6	CQ755744	CQ755744 Sequence
C 35	4.4	73.3	6	6	CQ755745	CQ755745 Sequence
C 36	4.4	73.3	6	6	CQ756172	CQ756172 Sequence
C 37	4.4	73.3	6	6	CQ756501	CQ756501 Sequence
C 38	4.4	73.3	6	6	CQ757931	CQ757931 Sequence
C 39	4.4	73.3	6	6	CQ757982	CQ757982 Sequence
C 40	4.4	73.3	6	6	CQ757983	CQ757983 Sequence
C 41	4.4	73.3	6	6	CQ758410	CQ758410 Sequence
C 42	4.4	73.3	6	6	CQ758739	CQ758739 Sequence
C 43	4.4	73.3	6	6	AX063645	AX063645 Sequence
C 44	4.4	73.3	6	6	AX103839	AX103839 Sequence
C 45	4.4	73.3	6	6	AX175261	AX175261 Sequence
C 46	4.4	73.3	6	6	AX175278	AX175278 Sequence
C 47	4.4	73.3	6	6	AX175280	AX175280 Sequence
C 48	4.4	73.3	6	6	AX175282	AX175282 Sequence
C 49	4.4	73.3	6	6	AX175310	AX175310 Sequence
C 50	4.4	73.3	6	6	AX175315	AX175315 Sequence
C 51	4.4	73.3	6	6	AX189456	AX189456 Sequence
C 52	4.4	73.3	6	6	AX207279	AX207279 Sequence
C 53	4.4	73.3	6	6	AX235310	AX235310 Sequence
C 54	4.4	73.3	6	6	AX285288	AX285288 Sequence
C 55	4.4	73.3	6	6	AX355137	AX355137 Sequence
C 56	4.4	73.3	6	6	AX428534	AX428534 Sequence
C 57	4.4	73.3	6	6	AX546892	AX546892 Sequence
C 58	4.4	73.3	6	6	AX574435	AX574435 Sequence
C 59	4.4	73.3	6	6	AX743309	AX743309 Sequence
C 60	4.4	73.3	6	6	AX743311	AX743311 Sequence
C 61	4.4	73.3	6	6	AX743313	AX743313 Sequence
C 62	4.4	73.3	6	6	AX743315	AX743315 Sequence
C 63	4.4	73.3	6	6	AX764731	AX764731 Sequence
C 64	4.4	73.3	6	6	AX764782	AX764782 Sequence
C 65	4.4	73.3	6	6	AX764783	AX764783 Sequence
C 66	4.4	73.3	6	6	AX765210	AX765210 Sequence
C 67	4.4	73.3	6	6	AX765539	AX765539 Sequence
C 68	4.4	73.3	6	6	AX816714	AX816714 Sequence
C 69	4.4	73.3	6	6	AX827233	AX827233 Sequence
C 70	4.4	73.3	6	6	BD080743	BD080743 Presenili
C 71	4.4	73.3	6	6	BD080744	BD080744 Presenili
C 72	4.2	70.0	6	6	AX557115	AX557115 Sequence
C 73	4.2	70.0	6	6	AX711257	AX711257 Sequence
C 74	4	66.7	4	6	AX794771	AX794771 Sequence
C 75	4	66.7	4	6	AX805855	AX805855 Sequence
C 76	4	66.7	4	6	AX805859	AX805859 Sequence
C 77	4	66.7	5	6	CQ787899	CQ787899 Sequence
C 78	4	66.7	5	6	CQ787900	CQ787900 Sequence
C 79	4	66.7	5	6	CQ854736	CQ854736 Sequence
C 80	4	66.7	5	6	CQ868987	CQ868987 Sequence
C 81	4	66.7	5	6	CQ868999	CQ868999 Sequence
C 82	4	66.7	5	6	CQ869006	CQ869006 Sequence
C 83	4	66.7	5	6	CQ869010	CQ869010 Sequence
C 84	4	66.7	5	6	CQ869136	CQ869136 Sequence
C 85	4	66.7	5	6	CQ869148	CQ869148 Sequence
C 86	4	66.7	5	6	CQ869155	CQ869155 Sequence
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 99 4 66.7 6 6 CQ755742 Sequence
 100 4 66.7 6 6 CQ755749 Sequence

ALIGNMENTS

RESULT 1
 AX175281
 LOCUS AX175281 6 bp DNA linear PAT 03-JUL-2001
 DEFINITION Sequence 45 from Patent WO0144465.
 ACCESSION AX175281
 VERSION AX175281.1 GI:14598649
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1 (bases 1 to 6)
 AUTHORS Phillips,N.C. and Filion,M.C.
 TITLE Therapeutically useful synthetic oligonucleotides
 JOURNAL Patent: WO 0144465-A 45 21-JUN-2001;
 Bioniche Life Sciences Inc. (CA)
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 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

ORIGIN

Query Match 100.0%; Score 6; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 8.1e+09;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAGG 6
 |||||
 Db 1 GGGAGG 6

RESULT 2
 AX743310
 LOCUS AX743310 6 bp DNA linear PAT 12-MAY-2003
 DEFINITION Sequence 2 from Patent WO03028764.
 ACCESSION AX743310
 VERSION AX743310.1 GI:30577236
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Phillips,N.C., Filion,M.C. and Herrera-Gayol,A.C.
 TITLE Therapeutically useful triethyleneglycol cholesteryl oligonucleotides
 JOURNAL Patent: WO 03028764-A 2 10-APR-2003;
 Bioniche Life Sciences Inc. (CA) ; Phillips, Nigel C. (CA)
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 /organism="synthetic construct"
 /mol_type="genomic DNA"
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 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAGG 6

Db 1 GGGAGG 6
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RESULT 3
 AX743314
 LOCUS AX743314 6 bp DNA linear PAT 12-MAY-2003
 DEFINITION Sequence 6 from Patent WO03028764.
 ACCESSION AX743314
 VERSION AX743314.1 GI:30577240
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.

REFERENCE 1
 AUTHORS Phillips,N.C., Filion,M.C. and Herrera-Gayol,A.C.
 TITLE Therapeutically useful triethyleneglycol cholesteryl oligonucleotides
 JOURNAL Patent: WO 03028764-A 6 10-APR-2003;
 Bioniche Life Sciences Inc. (CA) ; Phillips, Nigel C. (CA)
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ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 8.1e+09;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAGG 6
 |||||
 Db 1 GGGAGG 6

RESULT 4
 AX805866/c
 LOCUS AX805866 6 bp DNA linear PAT 25-NOV-2003
 DEFINITION Sequence 12 from Patent WO03060163.
 ACCESSION AX805866
 VERSION AX805866.1 GI:38522777
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS van Eijk,M.J. and van Schaik,C.
 TITLE Discrimination and detection of target nucleotide sequences using mass spectrometry
 JOURNAL Patent: WO 03060163-A 12 24-JUL-2003;
 Keygene N.V. (NL)
 FEATURES
 source
 1..6
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 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="stuffer sequence"

ORIGIN

Query Match 100.0%; Score 6; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 8.1e+09;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAGG 6
 |||||
 Db 6 GGGAGG 1

RESULT 5
 AX816715

LOCUS AX816715 6 bp DNA linear PAT 09-DEC-2003
 DEFINITION Sequence 3 from Patent WO02085340.
 ACCESSION AX816715
 VERSION AX816715.1 GI:39647044
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Filion, M.C. and Phillips, N.C.
 TITLE Oligonucleotide compositions and their use to induce differentiation of cells
 JOURNAL Patent: WO 02085340-A 3 31-OCT-2002;
 Bioniche Life Sciences Inc. (CA)
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 Matches 6; Conservative 0; Mismatches 0;
 QY 1 GGGAGG 6
 |||||
 Db 1 GGGAGG 6
 RESULT 6
 A70976/c
 LOCUS A70976 5 bp DNA linear PAT 07-MAY-1999
 DEFINITION Sequence 30 from Patent WO9813522.
 ACCESSION A70976
 VERSION A70976.1 GI:4774961
 KEYWORDS unidentified
 SOURCE unidentified
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 5)
 AUTHORS Uhlen, M. and Lundberg, J.
 TITLE THE USE OF MODULAR OLIGONUCLEOTIDES AS PROBES OR PRIMERS IN NUCLEIC ACID BASED ASSAY
 JOURNAL Patent: WO 9813522-A 30 02-APR-1998;
 DZIEGLEWSKA HANNA EVA (GB)
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 /mol_type="genomic DNA"
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 Matches 5; Conservative 0; Mismatches 0;
 QY 2 GGGAG 6
 |||||
 Db 5 GGGAG 1
 RESULT 7
 BD244758/c
 LOCUS BD244758 5 bp DNA linear PAT 17-JUL-2003
 DEFINITION Isolation method of primer extension products by modular oligonucleotide.
 ACCESSION BD244758
 VERSION BD244758.1 GI:33054528
 KEYWORDS JP 2002525076-A/37.
 SOURCE synthetic construct
 ORGANISM synthetic construct

other sequences; artificial sequences.
 1 (bases 1 to 5)
 REFERENCE
 AUTHORS Lundberg, J. and Uhlen, M.
 TITLE Isolation method of primer extension products by modular
 JOURNAL Patent: JP 2002525076-A 37 13-AUG-2002;
 DYNAL AS
 COMMENT OS Artificial Sequence
 PN JP 2002525076-A/37
 PD 13-AUG-2002
 PF 15-SEP-1999 JP 2000570369
 PR 15-SEP-1998 US 09/153242,16-SEP-1998 GB 9820185.8 PI
 JOAKIM LUNDBERG, MATHIAS UHLEN
 PC C12N15/09, C12Q1/68, C12N15/00
 CC Description of Artificial Sequence: Synthetic oligonucleotide
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 CC H1-5 Location/Qualifiers
 FH Key source 1..5
 FT /organism="Artificial Sequence".
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 source Location/Qualifiers
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 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
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 Best Local Similarity 100.0%; Pred. No. 9.7e+09; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;
 QY 2 GGGAG 6
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 Db 5 GGGAG 1
 RESULT 8
 AX805860/c
 LOCUS AX805860 5 bp DNA linear PAT 25-NOV-2003
 DEFINITION Sequence 6 from Patent WO03060163.
 ACCESSION AX805860
 VERSION AX805860.1 GI:38522771
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS van Eijk, M.J. and van Schaik, C.
 TITLE Discrimination and detection of target nucleotide sequences using mass spectrometry
 JOURNAL Patent: WO 03060163-A 6 24-JUL-2003;
 Keygene N.V. (NL)
 FEATURES
 source Location/Qualifiers
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 /organism="synthetic construct"
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 /db_xref="taxon:32630"
 /note="stuffer sequence"
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 QY 1 GGGAG 5
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 Db 5 GGGAG 1
 RESULT 9
 A93563/c
 LOCUS A93563 6 bp DNA linear PAT 22-JAN-2000
 DEFINITION Sequence 1 from Patent WO9737040.
 ACCESSION A93563

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VERSION A93563.1 GI:6741768
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 6)
AUTHORS Goudsmit,J. and Beld,M.G.
TITLE ISOLATION AND/OR AMPLIFICATION OF HEPATITIS C VIRUS (HCV) NUCLEIC
JOURNAL ACIDS FROM SAMPLES SUSPECTED TO CONTAIN HCV
FEATURES Patent: WO 9737040-A 1 09-OCT-1997;
SOURCE AMSTERDAM SUPPORT DIAGNOSTICS (NL); GOUDSMIT JAAP (NL)
1. .6
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6
Db |||||
6 GGAGG 2

RESULT 10
LOCUS CQ755704/c 6 bp DNA linear PAT 01-MAR-2004
DEFINITION Sequence 205 from Patent WO2003106674.
ACCESSION CQ755704
VERSION CQ755704.1 GI:44846509
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Otte,A.P., Kruckeberg,A.L. and Satiijn,D.P.
TITLE Means and methods for regulating gene expression
JOURNAL Patent: WO 2003106674-A 205 24-DEC-2003;
FEATURES Chromagenics B.V. (NL)
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Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/Note="oligonucleotide patterns over-represented in STAR
elements"

ORIGIN
Query Match 83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6
Db |||||
6 GGAGG 2

RESULT 11
LOCUS CQ755766/c 6 bp DNA linear PAT 01-MAR-2004
DEFINITION Sequence 267 from Patent WO2003106674.
ACCESSION CQ755766
VERSION CQ755766.1 GI:44846571
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Otte,A.P., Kruckeberg,A.L. and Satiijn,D.P.
TITLE Means and methods for regulating gene expression

JOURNAL Patent: WO 2003106674-A 267 24-DEC-2003;
FEATURES Chromagenics B.V. (NL)
1. .6
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/Note="oligonucleotide patterns over-represented in STAR
elements"

ORIGIN
Query Match 83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGG 6
Db |||||
6 GGAGG 2

RESULT 12
LOCUS CQ755813/c 6 bp DNA linear PAT 01-MAR-2004
DEFINITION Sequence 314 from Patent WO2003106674.
ACCESSION CQ755813
VERSION CQ755813.1 GI:44846618
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Otte,A.P., Kruckeberg,A.L. and Satiijn,D.P.
TITLE Means and methods for regulating gene expression
JOURNAL Patent: WO 2003106674-A 314 24-DEC-2003;
FEATURES Chromagenics B.V. (NL)
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Location/Qualifiers
/organism="synthetic construct"
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/db_xref="taxon:32630"
/Note="oligonucleotide patterns over-represented in STAR
elements"

ORIGIN
Query Match 83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5
Db |||||
5 GGGAG 1

RESULT 13
LOCUS CQ755818/c 6 bp DNA linear PAT 01-MAR-2004
DEFINITION Sequence 319 from Patent WO2003106674.
ACCESSION CQ755818
VERSION CQ755818.1 GI:44846623
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Otte,A.P., Kruckeberg,A.L. and Satiijn,D.P.
TITLE Means and methods for regulating gene expression
JOURNAL Patent: WO 2003106674-A 319 24-DEC-2003;
FEATURES Chromagenics B.V. (NL)
1. .6
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/Note="oligonucleotide patterns over-represented in STAR
elements"

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/note="oligonucleotide patterns over-represented in STAR elements"

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ORIGIN
Query Match      83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
Db 6 GGGAG 2

RESULT 14
CQ756128/c
LOCUS      CQ756128      6 bp      DNA      linear      PAT 01-MAR-2004
DEFINITION Sequence 629 from Patent WO2003106674.
ACCESSION  CQ756128
VERSION    CQ756128.1 GI:44846933
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
            other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
TITLE      Means and methods for regulating gene expression
JOURNAL    Patent: WO 2003106674-A 629 24-DEC-2003;
            Chromagenics B.V. (NL)
FEATURES   Location/Qualifiers
            1..6
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            /note="Dyad patterns over-represented in STAR elements"

ORIGIN
Query Match      83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGAG 6
Db 6 GGGAG 2

RESULT 15
CQ757942/c
LOCUS      CQ757942      6 bp      DNA      linear      PAT 01-MAR-2004
DEFINITION Sequence 246 from Patent WO2003106684.
ACCESSION  CQ757942
VERSION    CQ757942.1 GI:44847963
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
            other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
TITLE      A method for the simultaneous production of multiple proteins;
            vectors and cells for use therein
JOURNAL    Patent: WO 2003106684-A 246 24-DEC-2003;
            Chromagenics B.V. (NL)
FEATURES   Location/Qualifiers
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            /db_xref="taxon:32630"
            /note="oligonucleotide patterns over-represented in STAR elements"

ORIGIN
Query Match      83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGAG 6
Db 6 GGGAG 2

RESULT 16
CQ758004/c
LOCUS      CQ758004      6 bp      DNA      linear      PAT 01-MAR-2004
DEFINITION Sequence 308 from Patent WO2003106684.
ACCESSION  CQ758004
VERSION    CQ758004.1 GI:44848025
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
            other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
TITLE      A method for the simultaneous production of multiple proteins;
            vectors and cells for use therein
JOURNAL    Patent: WO 2003106684-A 308 24-DEC-2003;
            Chromagenics B.V. (NL)
FEATURES   Location/Qualifiers
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            /db_xref="taxon:32630"
            /note="oligonucleotide patterns over-represented in STAR elements"

ORIGIN
Query Match      83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGAG 6
Db 6 GGGAG 2

RESULT 17
CQ758051/c
LOCUS      CQ758051      6 bp      DNA      linear      PAT 01-MAR-2004
DEFINITION Sequence 355 from Patent WO2003106684.
ACCESSION  CQ758051
VERSION    CQ758051.1 GI:44848072
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
            other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
TITLE      A method for the simultaneous production of multiple proteins;
            vectors and cells for use therein
JOURNAL    Patent: WO 2003106684-A 355 24-DEC-2003;
            Chromagenics B.V. (NL)
FEATURES   Location/Qualifiers
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ORIGIN
Query Match      83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGAG 6
Db 5 GGGAG 1
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RESULT 18
LOCUS       CQ758056/c
DEFINITION  Sequence 360 from Patent WO2003106684.
ACCESSION   CQ758056
VERSION     CQ758056.1 GI:44848077
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
TITLE       A method for the simultaneous production of multiple proteins;
JOURNAL     vectors and cells for use therein
JOURNAL     Patent: WO 2003106684-A 360 24-DEC-2003;
JOURNAL     Chromagenics B.V. (NL)
FEATURES    Location/Qualifiers
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               /note="oligonucleotide patterns over-represented in STAR
               elements"
ORIGIN
Query Match      83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
        |||||
Db      6 GGGAG 2

RESULT 19
LOCUS       CQ758366/c
DEFINITION  Sequence 670 from Patent WO2003106684.
ACCESSION   CQ758366
VERSION     CQ758366.1 GI:44848387
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
TITLE       A method for the simultaneous production of multiple proteins;
JOURNAL     vectors and cells for use therein
JOURNAL     Patent: WO 2003106684-A 670 24-DEC-2003;
JOURNAL     Chromagenics B.V. (NL)
FEATURES    Location/Qualifiers
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ORIGIN
Query Match      83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GGAGG 6
        |||||
Db      6 GGAGG 2

RESULT 20
LOCUS       E08990
DEFINITION  Oligo DNA modified to inhibit Hrv proliferation.
ACCESSION   E08990

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VERSION     E08990.1 GI:22024628
KEYWORDS    JP 1995087982-A/1.
SOURCE      unidentified
ORGANISM    unidentified.
REFERENCE   1 (bases 1 to 6)
AUTHORS     Furukawa,H., Momota,K., Hotoda,H., Koizumi,M. and Kaneko,M.
TITLE       MODIFIED OLIGODEOXYRIBONUCLEOTIDE
JOURNAL     Patent: JP 1995087982-A 1 04-APR-1995;
JOURNAL     SANKYO CO LTD
COMMENT     OS None
            OC Artificial sequences.
            PN JP 1995087982-A/1
            PD 04-APR-1995
            PF 31-JAN-1994 JP 1994009772
            PR 23-JAN-1993 JP 93P 13509, 10-JUN-1993 JP 93P 138517 PI
            FURUKAWA HIDEHIKO, MOMOTA KENJI, HOTODA HITOSHI, PI KOIZUMI
            MAKOTO,
            PI KANEKO MASAKATSU
            PC C12N15/11,A61K31/70,C07H21/04;
            CC strandedness: Single;
            CC topology: Linear;
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            FT tg99gc,tg99gt'.
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Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
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Db      2 GGGAG 6

RESULT 21
E09173
LOCUS       E09173
DEFINITION  Synthetic oligonucleotides for anti-HIV agent.
ACCESSION   E09173
VERSION     E09173.1 GI:22025799
KEYWORDS    JP 1995118289-A/15.
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 6)
AUTHORS     Azuma,T., Momota,K. and Furukawa,H.
TITLE       OLIGODEOXYNUCLEOTIDE BOUND WITH SHORT PHOSPHOROTHIOATE
JOURNAL     Patent: JP 1995118289-A 15 09-MAY-1995;
JOURNAL     SANKYO CO LTD
COMMENT     OS None

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OC Artificial sequences.
PN JP 1995118289-A/15
PD 09-MAY-1995
PF 19-OCT-1993 JP 1993260581
PI AZUMA TOSHINORI, MOMOTA KENJI, FURUKAWA HIDEHIKO PC
C07H21/04/A61K31/70;
CC strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
FT source 1..6
FT misc_feature 1..6 /organism='Artificial sequences' FT
FT /note='Anti-HIV agent'.
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Query Match 83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGAG 5
DB 1 11111
2 GGGAG 6
RESULT 23
AX093419
LOCUS AX093419 6 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 1 from Patent WO0118195.
ACCESSION AX093419
VERSION AX093419.1 GI:13509869
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 6)
AUTHORS Francis,K.P., Contag,P.R. and Joh,D.J.
TITLE Luciferase expression cassettes and methods of use
JOURNAL Patent: WO 0118195-A 1 15-MAR-2001;
Xenogen Corporation (US)
FEATURES
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    /db_xref="taxon:32630"
    /note="Gram-positive ribosome binding site"
ORIGIN
Query Match 83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGGAG 6
DB 2 11111
2 GGGAG 6
RESULT 24
AX175283
LOCUS AX175283 6 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 47 from Patent WO0144465.
ACCESSION AX175283
VERSION AX175283.1 GI:14598651
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 6)
AUTHORS Phillips,N.C. and Fillion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 47 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
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    Location/Qualifiers
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    /mol_type="genomic DNA"
    /db_xref="taxon:32630"
ORIGIN
Query Match 83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGGAG 6
DB 1 11111
1 GGGAG 5
RESULT 25
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OC Artificial sequences.
PN JP 1995118289-A/15
PD 09-MAY-1995
PF 19-OCT-1993 JP 1993260581
PI AZUMA TOSHINORI, MOMOTA KENJI, FURUKAWA HIDEHIKO PC
C07H21/04/A61K31/70;
CC strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
FT source 1..6
FT misc_feature 1..6 /organism='Artificial sequences' FT
FT /note='Phosphorothioate-bound oligodeoxynucleotide which inhibits HIV-1 growth'.
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    /mol_type="genomic DNA"
    /db_xref="taxon:32644"
ORIGIN
Query Match 83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGAG 5
DB 2 11111
2 GGGAG 6
RESULT 22
E09489
LOCUS E09489 6 bp DNA linear PAT 29-SEP-1997
DEFINITION Phosphorothioate-bound oligodeoxynucleotide which inhibits HIV-1 growth.
ACCESSION E09489
VERSION E09489.1 GI:22026116
KEYWORDS JP 1995157498-A/15.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 6)
AUTHORS Azuma,T., Momota,K. and Furukawa,H.
TITLE SHORT-CHAIN OLIGODEOXYNUCLEOTIDE BONDED THROUGH PHOSPHOROTHIOATE LINKAGES
JOURNAL Patent: JP 1995157498-A 15 20-JUN-1995;
SANKYO CO LTD
COMMENT
OS None
OC Artificial sequences.
PN JP 1995157498-A/15
PD 20-JUN-1995
PF 07-DEC-1993 JP 1993306213
PI AZUMA TOSHINORI, MOMOTA KENJI, FURUKAWA HIDEHIKO PC
C07H21/04,A61K31/70,C12N15/09;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: Yes;
FH Key Location/Qualifiers
FT source 1..6
FT misc_feature 1..6 /organism='Artificial sequences' FT
FT /note='Phosphorothioate-bound FT
FT oligodeoxynucleotide which inhibits HIV-1 growth'.
FEATURES
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    /mol_type="genomic DNA"
    /db_xref="taxon:32644"
ORIGIN
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AX361080
LOCUS AX361080 6 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 1 from Patent WO0208431.
ACCESSION AX361080
VERSION AX361080.1 GI:18693739
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Francis, K.P. and Purchio, A.P.
TITLE Compositions and methods for use thereof in modifying the genomes of microorganisms
JOURNAL Patent: WO 0208431-A 1 31-JAN-2002;
Xenogen Corporation (US)
FEATURES
source Location/Qualifiers
1..6
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Gram-positive ribosome binding site (RBS)"
ORIGIN
Query Match 83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGAGG 6
Db |||||
2 GGAGG 6
RESULT 26
AX391507
LOCUS AX391507 6 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 1 from Patent EP1184462.
ACCESSION AX391507
VERSION AX391507.1 GI:19700115
KEYWORDS
SOURCE Staphylococcus aureus
ORGANISM Staphylococcus aureus
REFERENCE 1
AUTHORS Fan, F.G., He, Y.G., Huang, J.G., Jiang, X.G., Mcdevitt, D.G., Rosenberg, M.G. and St John, A.G.
TITLE Identification of targets of antimicrobial compounds
JOURNAL Patent: EP 1184462-A 1 06-MAR-2002;
SmithKline Beecham Corporation (US); SMITHKLINE BEECHAM PLC (GB)
FEATURES
source Location/Qualifiers
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/organism="Staphylococcus aureus"
/mol_type="genomic DNA"
/db_xref="taxon:1280"
ORIGIN
Query Match 83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGAGG 6
Db |||||
2 GGAGG 6
RESULT 27
AX574433
LOCUS AX574433 6 bp mRNA linear PAT 07-JAN-2003
DEFINITION Sequence 5 from Patent WO02068629.
ACCESSION AX574433
VERSION AX574433.1 GI:27551757
KEYWORDS
SOURCE unidentified
ORGANISM unidentified

unclassified.
REFERENCE 1
AUTHORS Pachuk, C.J. and McCallus, D.E.
TITLE Dna constructs for cytoplasmic and mitochondrial expression and methods of making and using same
JOURNAL Patent: WO 02068629-A 5 06-SEP-2002;
Wyeth (US)
FEATURES
source Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:32644"
/note="Shine-Dalgarno"
ORIGIN
Query Match 83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGAGG 6
Db |||||
2 GGAGG 6
RESULT 28
AX764742/c
LOCUS AX764742 6 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 212 from Patent WO03004704.
ACCESSION AX764742
VERSION AX764742.1 GI:32258950
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Otte, A.P. and Kruckeberg, A.L.
TITLE Dna sequences comprising gene transcription regulatory qualities and methods for detecting and using such dna sequences
JOURNAL Patent: WO 03004704-A 212 16-JAN-2003;
Chromagenics B.V. (NL)
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Best Local Similarity 100.0%; Pred. No. 8.1e+09;
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QY 2 GGAGG 6
Db |||||
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RESULT 29
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LOCUS AX764804 6 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 274 from Patent WO03004704.
ACCESSION AX764804
VERSION AX764804.1 GI:32259012
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Otte, A.P. and Kruckeberg, A.L.
TITLE Dna sequences comprising gene transcription regulatory qualities and methods for detecting and using such dna sequences
JOURNAL Patent: WO 03004704-A 274 16-JAN-2003;

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    AX764851.1 GI:32259059
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      other sequences; artificial sequences.
  REFERENCE
    1
  AUTHORS
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  TITLE
    Dna sequences comprising gene transcription regulatory qualities
    and methods for detecting and using such dna sequences
  JOURNAL
    Patent: WO 03004704-A 321 16-JAN-2003;
    Chromagenics B.V. (NL)
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  Best Local Similarity 100.0%; Pred. No. 8.1e+09;
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  Db 5 GGAGG 1
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Job time : 740.2 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 21, 2005, 00:00:54 ; Search time 710.6 Seconds
(without alignments)
53.568 Million cell updates/sec

Title: US-09-735-363A-43

Perfect score: 6

Sequence: 1 g9ccgg 6

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7173243 seqs, 3172129809 residues

Total number of hits satisfying chosen parameters: 6704

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications NA:*

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- 26: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	6	100.0	6	9	US-09-879-668-15
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4	6	100.0	6	18	US-10-420-513A-4
5	6	100.0	6	19	US-10-716-029-169
6	5	83.3	5	13	US-10-027-632-175366
7	5	83.3	5	13	US-10-027-632-175371

5	17	US-10-027-632-175366	Sequence 175366,
5	17	US-10-027-632-175371	Sequence 175371,
6	15	US-10-269-790-14	Sequence 14, Appl
6	15	US-10-187-264A-109	Sequence 109, App
6	16	US-10-306-522-109	Sequence 109, App
6	16	US-10-190-312A-198	Sequence 198, App
6	16	US-10-190-312A-204	Sequence 204, App
6	16	US-10-190-312A-204	Sequence 204, App
6	16	US-10-190-312A-219	Sequence 219, App
6	16	US-10-190-312A-220	Sequence 220, App
6	16	US-10-190-312A-230	Sequence 230, App
6	16	US-10-190-312A-275	Sequence 275, App
6	16	US-10-190-312A-282	Sequence 282, App
6	16	US-10-190-312A-332	Sequence 332, App
6	16	US-10-190-312A-385	Sequence 385, App
6	16	US-10-190-312A-385	Sequence 385, App
6	16	US-10-190-312A-412	Sequence 412, App
6	16	US-10-190-312A-531	Sequence 531, App
6	18	US-10-719-493-109	Sequence 109, App
6	19	US-10-666-022-14	Sequence 14, Appl
6	19	US-10-666-022-14	Sequence 14, Appl
6	19	US-10-627-331-109	Sequence 109, App
6	19	US-10-296-085A-78	Sequence 78, Appl
6	19	US-10-296-085A-79	Sequence 79, Appl
6	21	US-10-627-413-109	Sequence 109, App
6	21	US-10-921-086-109	Sequence 109, App
6	9	US-09-735-363A-28	Sequence 28, Appl
6	9	US-09-735-363A-46	Sequence 46, Appl
6	9	US-09-879-668-8	Sequence 8, Appl
6	9	US-09-879-668-18	Sequence 18, Appl
6	9	US-09-824-346-6	Sequence 6, Appl
6	9	US-09-728-574-20	Sequence 20, Appl
6	9	US-09-728-574-21	Sequence 21, Appl
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6	15	US-10-280-274-18	Sequence 18, Appl
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6	16	US-10-109-363-5	Sequence 5, Appl
6	16	US-10-190-312A-201	Sequence 201, App
6	16	US-10-190-312A-238	Sequence 238, App
6	17	US-10-190-312A-680	Sequence 680, App
6	17	US-10-182-329-4	Sequence 4, Appl
6	18	US-10-420-513A-7	Sequence 7, Appl
6	19	US-10-071-411-61	Sequence 61, Appl
6	19	US-10-716-029-165	Sequence 165, App
6	21	US-10-914-799-61	Sequence 61, Appl
4	19	US-10-686-317-34	Sequence 34, Appl
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5	13	US-10-027-632-175366	Sequence 175366,
5	13	US-10-027-632-175371	Sequence 175371,
5	17	US-10-027-632-175366	Sequence 175366,
5	17	US-10-027-632-175371	Sequence 175371,
5	19	US-10-681-818-218	Sequence 218, App
5	19	US-10-681-818-218	Sequence 218, App
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5	20	US-10-483-538-22	Sequence 22, Appl
5	20	US-10-483-538-23	Sequence 23, Appl
6	8	US-08-887-505-109	Sequence 109, App
6	9	US-09-735-363A-43	Sequence 43, Appl
6	9	US-09-785-269-16	Sequence 16, Appl
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6	9	US-09-785-269-18	Sequence 18, Appl
6	9	US-09-785-269-18	Sequence 18, Appl
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6	10	US-09-731-289B-4	Sequence 4, Appl
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6	10	US-09-798-883B-36	Sequence 36, Appl
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Sequence 199, App
Sequence 203, App
Sequence 209, App

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ALIGNMENTS

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; Sequence 43, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide

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US-09-879-668-15
; Sequence 15, Application US/09879668
; Patent No. US20020091095A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Fillion, Mario C.
; TITLE OF INVENTION: Modulation of Fas and FasL Expression
; FILE REFERENCE: 02811-0241 42368-256931
; CURRENT APPLICATION NUMBER: US/09/879,668
; CURRENT FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: PCT/CA00/01467
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/228,925

; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: US 60/266,229
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 09/735,363
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/170,325
; PRIOR FILING DATE: 1999-12-13
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide
US-09-879-668-15

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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGCCGG 6

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; Sequence 15, Application US/10280274
; Publication No. US20030119776A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Fillion, Mario C.
; TITLE OF INVENTION: Modulation of Fas and FasL Expression
; FILE REFERENCE: 02811-0242 42368-279803
; CURRENT APPLICATION NUMBER: US/10/280,274
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: PCT/CA00/01467
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 09/879,668
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: US 60/228,925
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: US 60/266,229
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 09/735,363
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/170,325
; PRIOR FILING DATE: 1999-12-13
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 6
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide
US-10-280-274-15

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QY 1 GGCCGG 6
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US-10-420-513A-4
; Sequence 4, Application US/10420513A
; Publication No. US2004005883A1
; GENERAL INFORMATION:

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; APPLICANT: Phillips, Nigel C.
; APPLICANT: Fallon, Mario C.
; TITLE OF INVENTION: Oligonucleotide Compositions and Their Use for the Modulation of
; FILE OF INVENTION: Immune Response
; FILE REFERENCE: 02811-0301 (42368-283135)
; CURRENT APPLICATION NUMBER: US/10/420,513A
; CURRENT FILING DATE: 2003-04-22
; PRIOR APPLICATION NUMBER: US 60/374,540
; PRIOR FILING DATE: 2002-04-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
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US-10-420-513A-4

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Db 1 GGCCGG 6

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; Sequence 169, Application US/10716029
; Publication No. US2004017038A1
; GENERAL INFORMATION:
; APPLICANT: Nicklin, Martin
; APPLICANT: Duff, Gordon
; APPLICANT: Kornman, Kenneth
; APPLICANT: Kolpin, Maryam R
; APPLICANT: Hsieh, Chung-Ming
; APPLICANT: Govindaraju, Raju
; APPLICANT: Aziz, Nazneen
; TITLE OF INVENTION: The IL-1 Gene Cluster and Associated Inflammatory Polymorphisms
; FILE OF INVENTION: and Haplotypes
; FILE REFERENCE: 24299-524 CON
; CURRENT APPLICATION NUMBER: US/10/716,029
; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: 10/351,702
; PRIOR FILING DATE: 2003-01-25
; PRIOR APPLICATION NUMBER: 60/351,951
; PRIOR FILING DATE: 2002-01-25
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; SEQ ID NO 169
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-716-029-169

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Db 1 GGCCGG 6

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; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
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; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175366
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175366

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; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175371
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175371

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; OTHER INFORMATION: Sequence for Spacer C accessory region
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Best Local Similarity 100.0%; Pred. No. 1.1e+09;
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Db 5 GCCGG 1

RESULT 12

US-10-187-264A-109

; Sequence 109, Application US/10187264A

; Publication No. US20030162734A1

; GENERAL INFORMATION:

; APPLICANT: Krieg, Arthur M.

; APPLICANT: Klinman, Dennis

; APPLICANT: Steinberg, Alfred D.

; TITLE OF INVENTION: Methods for Treating and Preventing

; TITLE OF INVENTION: Infectious Disease

; FILE REFERENCE: C01039.70062.US

; CURRENT APPLICATION NUMBER: US/10/187,264A

; CURRENT FILING DATE: 2002-06-28

; PRIOR APPLICATION NUMBER: US 09/630,319

; PRIOR FILING DATE: 2000-07-31

; PRIOR APPLICATION NUMBER: US 08/960,774

; PRIOR FILING DATE: 1997-10-30

; PRIOR APPLICATION NUMBER: US 08/738,652

; PRIOR FILING DATE: 1996-10-30

; PRIOR APPLICATION NUMBER: US 08/386,063

; PRIOR FILING DATE: 1995-02-07

; PRIOR APPLICATION NUMBER: US 08/276,358

; PRIOR FILING DATE: 1994-07-15

; NUMBER OF SEQ ID NOS: 124

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 109

; LENGTH: 6

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Oligonucleotide

US-10-187-264A-109

Query Match 83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GCCGG 5

RESULT 13

US-10-306-522-109

; Sequence 109, Application US/10306522

; Publication No. US20030191079A1

; GENERAL INFORMATION:

; APPLICANT: Krieg, Arthur M.

; APPLICANT: Klinman, Dennis

; APPLICANT: Steinberg, Alfred D.

; TITLE OF INVENTION: Methods for Treating and Preventing

; TITLE OF INVENTION: Infectious Disease

; FILE REFERENCE: C01039.70062.US

; CURRENT APPLICATION NUMBER: US/10/306,522

; CURRENT FILING DATE: 2002-11-27

; PRIOR APPLICATION NUMBER: US 09/630,319

; PRIOR FILING DATE: 2000-07-31

; PRIOR APPLICATION NUMBER: US 08/960,774

; PRIOR FILING DATE: 1997-10-30

; PRIOR APPLICATION NUMBER: US 08/738,652

; PRIOR FILING DATE: 1996-10-30

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; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-306-522-109

Query Match 83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6
|||
Db 1 GCCGG 5

RESULT 14

US-10-190-312A-198/c

; Sequence 198, Application US/10190312A

; Publication No. US20030199468A1

; GENERAL INFORMATION:

; APPLICANT: Chromagenics B.V.

; APPLICANT: Otte, Arie P.

; APPLICANT: Kruckeberg, Arthur L.

; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities

; TITLE OF INVENTION: Methods for detecting and using such DNA sequences

; FILE REFERENCE: 2183-4993.1

; CURRENT APPLICATION NUMBER: US/10/190,312A

; CURRENT FILING DATE: 2002-07-05

; PRIOR APPLICATION NUMBER: 60/303,199

; PRIOR FILING DATE: 2001-07-05

; NUMBER OF SEQ ID NOS: 1079

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 198

; LENGTH: 6

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements

US-10-190-312A-198

Query Match 83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6
|||
Db 5 GCCGG 1

RESULT 15

US-10-190-312A-204

; Sequence 204, Application US/10190312A

; Publication No. US20030199468A1

; GENERAL INFORMATION:

; APPLICANT: Chromagenics B.V.

; APPLICANT: Otte, Arie P.

; APPLICANT: Kruckeberg, Arthur L.

; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities

; TITLE OF INVENTION: Methods for detecting and using such DNA sequences

; FILE REFERENCE: 2183-4993.1

; CURRENT APPLICATION NUMBER: US/10/190,312A

; CURRENT FILING DATE: 2002-07-05

; PRIOR APPLICATION NUMBER: 60/303,199

; PRIOR FILING DATE: 2001-07-05

; NUMBER OF SEQ ID NOS: 1079

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 204
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements
US-10-190-312A-204

Query Match      83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6
Db 1 GCCGG 5

RESULT 16
US-10-190-312A-204/c
; Sequence 204, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; TITLE OF INVENTION: methods for detecting and using such DNA sequences
; FILE REFERENCE: 2183-4993.1
; CURRENT APPLICATION NUMBER: US/10/190,312A
; PRIOR FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/303,199
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 204
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements
US-10-190-312A-204

Query Match      83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6
Db 6 GCCGG 2

RESULT 17
US-10-190-312A-219/c
; Sequence 219, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; TITLE OF INVENTION: methods for detecting and using such DNA sequences
; FILE REFERENCE: 2183-4993.1
; CURRENT APPLICATION NUMBER: US/10/190,312A
; CURRENT FILING DATE: 2002-07-05
; PRIOR FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/303,199
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 219
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
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```
; FEATURE:
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements
US-10-190-312A-219

Query Match      83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6
Db 5 GCCGG 1

RESULT 18
US-10-190-312A-220
; Sequence 220, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; TITLE OF INVENTION: methods for detecting and using such DNA sequences
; FILE REFERENCE: 2183-4993.1
; CURRENT APPLICATION NUMBER: US/10/190,312A
; PRIOR FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/303,199
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 220
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements
US-10-190-312A-220

Query Match      83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6
Db 2 GCCGG 6

RESULT 19
US-10-190-312A-230/c
; Sequence 230, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; TITLE OF INVENTION: methods for detecting and using such DNA sequences
; FILE REFERENCE: 2183-4993.1
; CURRENT APPLICATION NUMBER: US/10/190,312A
; CURRENT FILING DATE: 2002-07-05
; PRIOR FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/303,199
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 230
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements
US-10-190-312A-230

Query Match      83.3%; Score 5; DB 16; Length 6;
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Best Local Similarity 100.0%; Pred. No. 1.1e+09; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGCG 5
|||||

Db 5 GCGCG 1

RESULT 20
US-10-190-312A-275/c
; Sequence 275, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; TITLE OF INVENTION: methods for detecting and using such DNA sequences
; FILE REFERENCE: 2183-4993.1
; CURRENT APPLICATION NUMBER: US/10/190,312A
; CURRENT FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/303,199
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 275
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements
US-10-190-312A-275

Query Match 83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGCG 5
|||||

Db 6 GCGCG 2

RESULT 21
US-10-190-312A-282/c
; Sequence 282, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; TITLE OF INVENTION: methods for detecting and using such DNA sequences
; FILE REFERENCE: 2183-4993.1
; CURRENT APPLICATION NUMBER: US/10/190,312A
; CURRENT FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/303,199
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 282
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements
US-10-190-312A-282

Query Match 83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGCG 6
|||||

Db 6 GCGCG 2

RESULT 22
US-10-190-312A-332/c
; Sequence 332, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; TITLE OF INVENTION: methods for detecting and using such DNA sequences
; FILE REFERENCE: 2183-4993.1
; CURRENT APPLICATION NUMBER: US/10/190,312A
; CURRENT FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/303,199
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 332
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements
US-10-190-312A-332

Query Match 83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGCG 6
|||||

Db 6 GCGCG 2

RESULT 23
US-10-190-312A-385
; Sequence 385, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; TITLE OF INVENTION: methods for detecting and using such DNA sequences
; FILE REFERENCE: 2183-4993.1
; CURRENT APPLICATION NUMBER: US/10/190,312A
; CURRENT FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/303,199
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 385
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Dyad patterns over-represented in STAR elements
US-10-190-312A-385

Query Match 83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGCG 6
|||||

Db 1 GCGCG 5

RESULT 24
US-10-190-312A-385/c

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; Sequence 385, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; FILE REFERENCE: 2183-4993.1
; CURRENT FILING DATE: 2002-07-05
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 385
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Dyad patterns over-represented in STAR elements
US-10-190-312A-385

Query Match      83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 GCCGG 6
Db   6 GCCGG 2

RESULT 25
US-10-190-312A-412/c
; Sequence 412, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; FILE REFERENCE: 2183-4993.1
; CURRENT FILING DATE: 2002-07-05
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 412
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Dyad patterns over-represented in STAR elements
US-10-190-312A-412

Query Match      83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 GCCGG 6
Db   5 GCCGG 1

RESULT 26
US-10-190-312A-531/c
; Sequence 531, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
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; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; FILE REFERENCE: 2183-4993.1
; CURRENT FILING DATE: 2002-07-05
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 531
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Dyad patterns over-represented in STAR elements
US-10-190-312A-531

Query Match      83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 GCCGG 6
Db   5 GCCGG 1

RESULT 27
US-10-719-493-109
; Sequence 109, Application US/10719493
; Publication No. US20040087538A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Methods of Treating Cancer Using
; FILE REFERENCE: C1039/7021/HCL
; CURRENT FILING DATE: 2003-11-21
; PRIOR FILING DATE: 1997-10-30
; PRIOR FILING DATE: 1996-10-30
; PRIOR FILING DATE: 1995-02-07
; PRIOR FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-719-493-109

Query Match      83.3%; Score 5; DB 18; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 GCCGG 6
Db   1 GCCGG 5

RESULT 28
US-10-666-022-14
; Sequence 14, Application US/10666022
; Publication No. US20040105872A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by the
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: Klinman, Dennis M.
```

```
; APPLICANT: Verthelyi, Daniela
; TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
; FILE OF INVENTION: SUBJECTS WITH IMMUNOSTIMULATORY CPG
; FILE REFERENCE: 4239-66899
; CURRENT APPLICATION NUMBER: US/10/666,022
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,944
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-666-022-14

Query Match      83.3%; Score 5; DB 19; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GCCGG 6
Db      1 GCCGG 5

RESULT 29
US-10-666-022-14/c
; Sequence 14, Application US/10666022
; Publication No. US20040105872A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by the
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: Klimman, Dennis M.
; APPLICANT: Verthelyi, Daniela
; TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
; FILE OF INVENTION: SUBJECTS WITH IMMUNOSTIMULATORY CPG
; FILE REFERENCE: 4239-66899
; CURRENT APPLICATION NUMBER: US/10/666,022
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,944
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-666-022-14

Query Match      83.3%; Score 5; DB 19; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GCCGG 6
Db      6 GCCGG 2

RESULT 30
US-10-627-331-109
; Sequence 109, Application US/10627331
; Publication No. US20040106586A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Klimman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: Methods for Treating and Preventing
; TITLE OF INVENTION: Infectious Disease
; FILE REFERENCE: C01039.70062.US
```

```
; CURRENT APPLICATION NUMBER: US/10/627,331
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 09/630,319
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 08/960,774
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PastSeq for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-627-331-109
```

```
Query Match      83.3%; Score 5; DB 19; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      2 GCCGG 6
Db      1 GCCGG 5
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Search completed: July 21, 2005, 07:13:21
Job time : 712.6 secs
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:43:13 ; Search time 57 Seconds
(without alignments)
172.240 Million cell updates/sec

Title: US-09-735-363A-43

Perfect score: 6

Sequence: 1 ggcggg 6

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2678

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents NA:*

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3: /cgn2_6/prodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/prodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/prodata/1/ina/PCUS_COMB.seq.*
6: /cgn2_6/prodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	83.3	6	1	US-07-627-538-1
2	5	83.3	6	1	US-07-627-538-1
3	5	83.3	6	1	US-08-128-369-1
4	5	83.3	6	1	US-08-128-369-1
5	5	83.3	6	2	US-08-692-825-24
6	5	83.3	6	2	US-08-692-825-24
7	5	83.3	6	3	US-08-895-495-24
8	5	83.3	6	3	US-08-895-495-24
9	5	83.3	6	3	US-09-337-619-109
10	4.4	73.3	6	3	US-08-920-422-15
11	4.4	73.3	6	3	US-08-920-422-16
12	4.4	73.3	6	3	US-09-593-323-29
13	4.4	73.3	6	3	US-09-594-108-29
14	4.4	73.3	6	3	US-09-344-300-29
15	4.4	73.3	6	4	US-09-924-346-6
16	4.4	73.3	6	4	US-10-071-411A-61
17	4.4	73.3	6	4	US-09-483-184A-6
18	4	66.7	4	1	US-08-169-950-6
19	4	66.7	4	1	US-08-169-950-6
20	4	66.7	4	1	US-07-630-288A-14
21	4	66.7	4	1	US-07-630-288A-14
22	4	66.7	4	1	US-08-468-049-14
23	4	66.7	4	1	US-08-468-049-14
24	4	66.7	4	3	US-09-193-792-19
25	4	66.7	4	3	US-09-193-792-19
26	4	66.7	4	3	US-08-357-399-2
27	4	66.7	5	1	US-08-357-399-2
28	4	66.7	5	1	US-08-357-399-2
29	4	66.7	5	1	US-08-357-399-2
30	4	66.7	5	1	US-08-357-399-2
31	4	66.7	5	1	US-08-357-399-2
32	4	66.7	5	1	US-08-357-399-2
33	4	66.7	5	1	US-08-357-399-2
34	4	66.7	5	1	US-08-357-399-2
35	4	66.7	5	1	US-08-357-399-2
36	4	66.7	5	1	US-08-357-399-2
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45	4	66.7	5	1	US-08-357-399-2
46	4	66.7	5	1	US-08-357-399-2
47	4	66.7	5	1	US-08-357-399-2
48	4	66.7	5	1	US-08-357-399-2
49	4	66.7	5	1	US-08-357-399-2
50	4	66.7	5	1	US-08-357-399-2
51	4	66.7	5	1	US-08-357-399-2
52	4	66.7	5	1	US-08-357-399-2
53	4	66.7	5	1	US-08-357-399-2
54	4	66.7	5	1	US-08-357-399-2
55	4	66.7	5	1	US-08-357-399-2
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58	4	66.7	5	1	US-08-357-399-2
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63	4	66.7	5	1	US-08-357-399-2
64	4	66.7	5	1	US-08-357-399-2
65	4	66.7	5	1	US-08-357-399-2
66	4	66.7	5	1	US-08-357-399-2
67	4	66.7	5	1	US-08-357-399-2
68	4	66.7	5	1	US-08-357-399-2
69	4	66.7	5	1	US-08-357-399-2
70	4	66.7	5	1	US-08-357-399-2
71	3.4	56.7	3	4	US-08-140-349-7
72	3.4	56.7	3	4	US-08-140-349-7
73	3.4	56.7	3	4	US-08-475-236-7
74	3.4	56.7	3	4	US-08-475-236-16
75	3.4	56.7	3	4	US-08-475-236-16
76	3.4	56.7	3	4	US-08-717-526-53
77	3.4	56.7	3	4	US-09-107-708-1
78	3.4	56.7	3	4	US-09-449-581-1
79	3.4	56.7	3	4	US-09-449-581-1
80	3.4	56.7	3	4	US-09-449-581-1
81	3.4	56.7	3	4	US-09-449-581-1
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88	3.4	56.7	3	4	US-09-449-581-1
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90	3.4	56.7	3	4	US-09-449-581-1
91	3.4	56.7	3	4	US-09-449-581-1
92	3.4	56.7	3	4	US-09-449-581-1
93	3.4	56.7	3	4	US-09-449-581-1
94	3.4	56.7	3	4	US-09-449-581-1
95	3.4	56.7	3	4	US-09-449-581-1
96	3.4	56.7	3	4	US-09-449-581-1
97	3.4	56.7	3	4	US-09-449-581-1
98	3.4	56.7	3	4	US-09-449-581-1
99	3.4	56.7	3	4	US-09-449-581-1
100	3.4	56.7	3	4	US-09-449-581-1

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Sequence 28, Appli
Sequence 22, Appli
Sequence 6, Appli
Sequence 10, Appli
Sequence 11, Appli
Sequence 110, Appli

ALIGNMENTS

RESULT 1
US-07-627-538-1
; Sequence 1, Application US/07627538
; Patent No. 5248600
; GENERAL INFORMATION:
; APPLICANT: Topal, Michael D.
; APPLICANT: Conrad, Michael
; TITLE OF INVENTION: Method of Cleaving DNA
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Kenneth D. Sibley; Bell, Seltzer, Park and Gibson
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5248600th Carolina
; COUNTRY: U.S.A.
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/627,538
; FILING DATE: 19901214
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5052-24
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
US-07-627-538-1
Query Match 83.3%; Score 5; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GCCGG 6
Db 1 GCCGG 5

RESULT 2
US-07-627-538-1/c
; Sequence 1, Application US/07627538
; Patent No. 5248600
; GENERAL INFORMATION:
; APPLICANT: Topal, Michael D.
; APPLICANT: Conrad, Michael
; TITLE OF INVENTION: Method of Cleaving DNA
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Kenneth D. Sibley; Bell, Seltzer, Park and Gibson
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5248600th Carolina
; COUNTRY: U.S.A.

; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/627,538
; FILING DATE: 19901214
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5052-24
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
US-07-627-538-1
Query Match 83.3%; Score 5; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GCCGG 6
Db 6 GCCGG 2

RESULT 3
US-08-128-369-1
; Sequence 1, Application US/08128369
; Patent No. 5418150
; GENERAL INFORMATION:
; APPLICANT: Topal, Michael D.
; APPLICANT: Conrad, Michael J.
; TITLE OF INVENTION: METHOD OF CLEAVING DNA
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Kenneth D. Sibley; Bell, Seltzer, Park and
; ADDRESSEE: Gibson
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: No. 5418150th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/128,369
; FILING DATE: 21-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-5A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-128-369-1
Query Match      83.3%; Score 5; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GCCGG 6
Db      1 GCCGG 5

RESULT 4
US-08-128-369-1/c
; Sequence 1, Application US/08128369
; Patent No. 5418150
; GENERAL INFORMATION:
; APPLICANT: Topal, Michael D.
; APPLICANT: Conrad, Michael J.
; TITLE OF INVENTION: METHOD OF CLEAVING DNA
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park and
; ADDRESSEE: Gibson
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: No. 5418150th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/128,369
; FILING DATE: 21-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-5A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-128-369-1
Query Match      83.3%; Score 5; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GCCGG 6
Db      6 GCCGG 2

RESULT 5
US-08-692-825-24
; Sequence 24, Application US/08692825
; Patent No. 5858665
; GENERAL INFORMATION:
; APPLICANT: Hepp, Jozsef
```

```
; APPLICANT: Lengyel, Zsolt
; APPLICANT: Pande, Rajiv
; TITLE OF INVENTION: HOMOGENEOUS DIAGNOSTIC ASSAY
; TITLE OF INVENTION: METHOD UTILIZING SIMULTANEOUS TARGET AND SIGNAL AMPL
; TITLE OF INVENTION: IFICATION
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/692,825
; FILING DATE: 25-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Axford, Laurie A
; REGISTRATION NUMBER: 35,053
; REFERENCE/DOCKET NUMBER: 32260-20002.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-692-825-24
Query Match      83.3%; Score 5; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GCCGG 6
Db      1 GCCGG 5

RESULT 6
US-08-692-825-24/c
; Sequence 24, Application US/08692825
; Patent No. 5858665
; GENERAL INFORMATION:
; APPLICANT: Hepp, Jozsef
; APPLICANT: Lengyel, Zsolt
; APPLICANT: Pande, Rajiv
; TITLE OF INVENTION: HOMOGENEOUS DIAGNOSTIC ASSAY
; TITLE OF INVENTION: METHOD UTILIZING SIMULTANEOUS TARGET AND SIGNAL AMPL
; TITLE OF INVENTION: IFICATION
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
```

;
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/692,825
; FILING DATE: 25-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Axford, Laurie A
; REGISTRATION NUMBER: 35,053
; REFERENCE/DOCKET NUMBER: 32260-20002.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-692-825-24

Query Match 83.3%; Score 5; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6
Db 6 GCCGG 2

RESULT 7

US-08-895-495-24
; Sequence 24, Application US/08895495
; Patent No. 6114117
; GENERAL INFORMATION:
; APPLICANT: Hepp, Jozsef
; APPLICANT: Lengyel, Zsolt
; APPLICANT: Pande, Rajiv
; TITLE OF INVENTION: HOMOGENEOUS DIAGNOSTIC ASSAY
; TITLE OF INVENTION: METHOD UTILIZING SIMULTANEOUS TARGET AND SIGNAL AMPL
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/895,495
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Axford, Laurie A
; REGISTRATION NUMBER: 35,053
; REFERENCE/DOCKET NUMBER: 32260-20002.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 24:

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-895-495-24

Query Match 83.3%; Score 5; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6
Db 1 GCCGG 5

RESULT 8

US-08-895-495-24/c
; Sequence 24, Application US/08895495
; Patent No. 6114117
; GENERAL INFORMATION:
; APPLICANT: Hepp, Jozsef
; APPLICANT: Lengyel, Zsolt
; APPLICANT: Pande, Rajiv
; TITLE OF INVENTION: HOMOGENEOUS DIAGNOSTIC ASSAY
; TITLE OF INVENTION: METHOD UTILIZING SIMULTANEOUS TARGET AND SIGNAL AMPL
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/895,495
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Axford, Laurie A
; REGISTRATION NUMBER: 35,053
; REFERENCE/DOCKET NUMBER: 32260-20002.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-895-495-24

Query Match 83.3%; Score 5; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6
Db 6 GCCGG 2

RESULT 9

US-09-337-619-109
; Sequence 109, Application US/09337619
; Patent No. 6653292
; GENERAL INFORMATION:
; APPLICANT: Kriegl, Arthur M.
; TITLE OF INVENTION: Methods of Treating Cancer Using
; TITLE OF INVENTION: Immunostimulatory Oligonucleotides
; FILE REFERENCE: C1039/7021/HCL
; CURRENT APPLICATION NUMBER: US/09/337,619
; CURRENT FILING DATE: 1999-06-21
; EARLIER APPLICATION NUMBER: US 08/960,774
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: US 08/738,652
; EARLIER FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-337-619-109

Query Match 83.3%; Score 5; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCCG 6
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Db 1 GCCCG 5

RESULT 10
US-08-920-422-15
; Sequence 15, Application US/08920422A
; Patent No. 6255473
; GENERAL INFORMATION:
; APPLICANT: Vitek, Michael P.
; APPLICANT: Mitsuda, No. 6255473iaki
; APPLICANT: Roses, Allen D.
; TITLE OF INVENTION: Presenilin-1 Gene Promoter
; FILE REFERENCE: VITEKPRESENTILIN
; CURRENT APPLICATION NUMBER: US/08/920,422A
; CURRENT FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-920-422-15

Query Match 73.3%; Score 4.4; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.7e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCG 6
|||
Db 1 GCCCG 6

RESULT 11
US-08-920-422-16/c
; Sequence 16, Application US/08920422A
; Patent No. 6255473
; GENERAL INFORMATION:

; APPLICANT: Vitek, Michael P.
; APPLICANT: Mitsuda, No. 6255473iaki
; APPLICANT: Roses, Allen D.
; TITLE OF INVENTION: Presenilin-1 Gene Promoter
; FILE REFERENCE: VITEKPRESENTILIN
; CURRENT APPLICATION NUMBER: US/08/920,422A
; CURRENT FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-920-422-16

Query Match 73.3%; Score 4.4; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.7e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCG 6
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Db 6 GCCCG 1

RESULT 12
US-09-593-323-29
; Sequence 29, Application US/09593323
; Patent No. 6265213
; GENERAL INFORMATION:
; APPLICANT: Morgan, Antony R.
; APPLICANT: Severini, Alberto
; TITLE OF INVENTION: Compositions and Methods for Determining the Activity
; TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of
; TITLE OF INVENTION: Transcription
; FILE REFERENCE: DNAB-02921
; CURRENT APPLICATION NUMBER: US/09/593,323
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: 09/344,300
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-593-323-29

Query Match 73.3%; Score 4.4; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.7e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCCG 6
|||
Db 1 GCCCG 6

RESULT 13
US-09-594-108-29
; Sequence 29, Application US/09594108
; Patent No. 6284468
; GENERAL INFORMATION:
; APPLICANT: Morgan, Antony R.
; APPLICANT: Severini, Alberto
; TITLE OF INVENTION: Compositions and Methods for Determining the Activity
; TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of
; TITLE OF INVENTION: Transcription
; FILE REFERENCE: DNAB-02921
; CURRENT APPLICATION NUMBER: US/09/594,108
; CURRENT FILING DATE: 2000-06-13

; PRIOR APPLICATION NUMBER: 09/344,300
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-594-108-29

Query Match 73.3%; Score 4.4; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.7e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCCGG 6
|||
Db 1 GGCCGG 6

RESULT 14
US-09-344-300-29
; Sequence 29, Application US/09344300B
; Patent No. 6297013
; GENERAL INFORMATION:
; APPLICANT: Morgan, Antony R.
; APPLICANT: Severini, Alberto
; TITLE OF INVENTION: Compositions and Methods for Determining the Activity
; TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of
; TITLE OF INVENTION: Transcription
; FILE REFERENCE: DNAB-02921
; CURRENT APPLICATION NUMBER: US/09/344,300B
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-344-300-29

Query Match 73.3%; Score 4.4; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.7e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCCGG 6
|||
Db 1 GGCCGG 6

RESULT 15
US-09-924-346-6
; Sequence 6, Application US/09924346
; Patent No. 6555674
; GENERAL INFORMATION:
; APPLICANT: Jens Tornoe
; TITLE OF INVENTION: The Jet Promoter
; FILE REFERENCE: 19313-005
; CURRENT APPLICATION NUMBER: US/09/924,346
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/224,087
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Chemically

; OTHER INFORMATION: Synthesized
US-09-924-346-6

Query Match 73.3%; Score 4.4; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.7e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCCGG 6
|||
Db 1 GGCCGG 6

RESULT 16
US-10-071-411A-61
; Sequence 61, Application US/10071411A
; Patent No. 6797475
; GENERAL INFORMATION:
; APPLICANT: Glenn Barnes
; APPLICANT: Joanne Meyer
; TITLE OF INVENTION: Detection of Polymorphisms in the Human
; TITLE OF INVENTION: 5-Lipoxygenase Gene
; FILE REFERENCE: MRI-021
; CURRENT APPLICATION NUMBER: US/10/071,411A
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/267,515
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/314,248
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-071-411A-61

Query Match 73.3%; Score 4.4; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.7e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCCGG 6
|||
Db 1 GGCCGG 6

RESULT 17
US-09-483-184A-6/c
; Sequence 6, Application US/09483184A
; Patent No. 6800750
; GENERAL INFORMATION:
; APPLICANT: DARTMOUTH COLLEGE
; APPLICANT: CRAIG, Ruth W.
; APPLICANT: BINGLE, Colin D.
; APPLICANT: WHYTE, Moira
; TITLE OF INVENTION: Mcl-1 GENE REGULATORY ELEMENTS AND A PRO-APOPTOTIC Mcl-1 VARIANT
; FILE REFERENCE: DART1110-1
; CURRENT APPLICATION NUMBER: US/09/483,184A
; CURRENT FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/166,113
; PRIOR FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide for PCR
US-09-483-184A-6

Query Match 73.3%; Score 4.4; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.7e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCCGG 6
|||
Db 6 GGCCGG 1

RESULT 18

US-08-169-950-6
; Sequence 6, Application US/08169950
; Patent No. 5366882
; GENERAL INFORMATION:
; APPLICANT: LUNNEN, KEITH D.
; APPLICANT: WILSON, GEOFFREY G.
; TITLE OF INVENTION: METHOD FOR PRODUCING THE BGLI
; TITLE OF INVENTION: RESTRICTION ENDONUCLEASE AND METHYLASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSER: CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/169,950
; FILING DATE: 17-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 43959
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-169-950-6

Query Match 66.7%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+08; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCC 4
|||
Db 1 GGCC 4

RESULT 19

US-08-169-950-6/c
; Sequence 6, Application US/08169950
; Patent No. 5366882
; GENERAL INFORMATION:
; APPLICANT: LUNNEN, KEITH D.
; APPLICANT: WILSON, GEOFFREY G.
; TITLE OF INVENTION: METHOD FOR PRODUCING THE BGLI
; TITLE OF INVENTION: RESTRICTION ENDONUCLEASE AND METHYLASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSER: CUSHMAN
; STREET: 130 WATER STREET

; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/169,950
; FILING DATE: 17-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 43959
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-169-950-6

Query Match 66.7%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+08; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCC 4
|||
Db 4 GGCC 1

RESULT 20

US-07-630-288A-14
; Sequence 14, Application US/07630288A
; Patent No. 5472840
; GENERAL INFORMATION:
; APPLICANT: Stefano, James E.
; TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
; TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Joanne M. Gieser
; STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
; CITY: Naperville
; STATE: IL
; COUNTRY: USA
; ZIP: 60563
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/630,288A
; FILING DATE: 17-DEC-1990
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/370,218
; FILING DATE: 06-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/252,243
; FILING DATE: 30-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Gieser, Joanne M.
; REGISTRATION NUMBER: 32,838

REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-14

Query Match 66.7%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCC 4
Db 1 GGCC 4

RESULT 21
US-07-630-288A-14/c
Sequence 14, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Gieser
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Gieser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-14

Query Match 66.7%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCC 4
Db 4 GGCC 1

RESULT 22
US-08-468-049-14
Sequence 14, Application US/08468049
Patent No. 5763171
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5763171val B. Galloway
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,049
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/630,288
FILING DATE: 17-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: No. 5763171val B. Galloway
REGISTRATION NUMBER: 33,595
REFERENCE/DOCKET NUMBER: CN 581903
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-468-049-14

Query Match 66.7%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCC 4
Db 1 GGCC 4

RESULT 23
US-08-468-049-14/c
Sequence 14, Application US/08468049

; Patent No. 5763171
; GENERAL INFORMATION:
; APPLICANT: Stefano, James E.
; TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
; TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5763171val B. Galloway
; STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
; CITY: Naperville
; STATE: IL
; COUNTRY: USA
; ZIP: 60563
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,049
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/630,288
; FILING DATE: 17-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/370,218
; FILING DATE: 06-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/252,243
; FILING DATE: 30-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5763171val B. Galloway
; REGISTRATION NUMBER: 33,595
; REFERENCE/DOCKET NUMBER: CN 581903
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708) 717-2443
; TELEFAX: (708) 717-2430
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
US-08-468-049-14

Query Match 66.7%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCC 4
DB 4 GGCC 1

RESULT 24
US-09-193-792-19
; Sequence 19, Application US/09193792B
; Patent No. 6180344
; GENERAL INFORMATION:
; APPLICANT: Chen, Bin
; TITLE OF INVENTION: 5(Upstream Region Sequences of the MYOD1 Gene
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: D6015
; CURRENT APPLICATION NUMBER: US/09/193,792B
; CURRENT FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 60/065,113
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 20
; SEQ ID NO 19
; LENGTH: 4
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: HpaII restriction enzyme consensus sequence
US-09-193-792-19

; LENGTH: 4
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: HpaII restriction enzyme consensus sequence
US-09-193-792-19

Query Match 66.7%; Score 4; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCGG 6
DB 1 CCGG 4

RESULT 25
US-09-193-792-19/c
; Sequence 19, Application US/09193792B
; Patent No. 6180344
; GENERAL INFORMATION:
; APPLICANT: Chen, Bin
; TITLE OF INVENTION: 5(Upstream Region Sequences of the MYOD1 Gene
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: D6015
; CURRENT APPLICATION NUMBER: US/09/193,792B
; CURRENT FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 60/065,113
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 20
; SEQ ID NO 19
; LENGTH: 4
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: HpaII restriction enzyme consensus sequence
US-09-193-792-19

Query Match 66.7%; Score 4; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 4e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCGG 6
DB 4 CCGG 1

RESULT 26
US-08-357-399-2/c
; Sequence 2, Application US/08357399
; Patent No. 5536821
; GENERAL INFORMATION:
; APPLICANT: Agrawal, Sudhir
; APPLICANT: Tang, Jin-Yan
; TITLE OF INVENTION: Site-Specific Functionalization of
; TITLE OF INVENTION: Oligodeoxynucleotides for
; TITLE OF INVENTION: No. 5536821-Radioactive Labelling
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lappin & Kusmer
; STREET: 200 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/357,399
; FILING DATE: 16-DEC-1994

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/206175
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HY2-014CPDV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-330-1300
TELEFAX: 617-330-1311
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-357-399-2

Query Match 66.7%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.2e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 GCCG 5
DB 4 GCCG 1

RESULT 27
US-08-357-666-2/c
Sequence 2, Application US/08357666
Patent No. 5541306
GENERAL INFORMATION:
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: Site-Specific Functionalization of
TITLE OF INVENTION: Oligodeoxynucleotides for
TITLE OF INVENTION: Oligodeoxynucleotides for
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lappin & Kusmer
STREET: 200 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/357,666
FILING DATE: 16-DEC-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/206175
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HY2-014CPDV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-330-1300
TELEFAX: 617-330-1311
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-357-666-2

Query Match 66.7%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.2e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 GCCG 5
DB 4 GCCG 1

RESULT 28
US-08-206-175-2/c
Sequence 2, Application US/08206175
Patent No. 5563253
GENERAL INFORMATION:
APPLICANT: Agrawal, Sudhir and
APPLICANT: Jin-Yan Tang
TITLE OF INVENTION: Site-Specific Functionalization of
TITLE OF INVENTION: Oligodeoxynucleotides for
TITLE OF INVENTION: No. 5563253-Radioactive Labelling
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lappin & Kusmer
STREET: 200 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206,175
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HY2-014 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-330-1300
TELEFAX: 617-330-1311
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-206-175-2

Query Match 66.7%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.2e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 GCCG 5
DB 4 GCCG 1

RESULT 29
US-08-795-876-19
Sequence 19, Application US/08795876
Patent No. 6403305

GENERAL INFORMATION:
APPLICANT: Gershengorn, Marvin C.
ATTORNEY/AGENT INFORMATION:
NAME: Geras-Raaka, Elizabeth
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/1280
TELEPHONE: 716-263-1636
TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-795-876-19

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,876
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: BRAMAN, SUSAN J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/1280
TELEPHONE: 716-263-1636
TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-795-876-19

Query Match 66.7%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.2e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCG 5
Db 2 GCCG 5

RESULT 30
US-08-169-950-4
Sequence 4, Application US/08169950
Patent No. 5366882
GENERAL INFORMATION:
APPLICANT: LUNNEN, KEITH D.
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, GEOFFREY G.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/1280
TELEPHONE: 716-263-1636
TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-795-876-19

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/169,950

FILING DATE: 17-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 43959
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-169-950-4

Query Match 66.7%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.7e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCC 4
Db 2 GGCC 5

Search completed: July 21, 2005, 04:29:25
Job time : 59 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:25:43 ; Search time 1348.8 Seconds
(without alignments)
169.325 Million cell updates/sec

Title: US-09-735-363A-43
Perfect score: 6
Sequence: 1 gscggg 6

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 1216

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gssi:*
9: gb_gssi2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	5	83.3	5	CN612621	CsgeEST00
C 2	5	83.3	5	CN612715	CsgeEST00
C 3	5	83.3	6	CA851141	D10E10_J1
C 4	5	83.3	6	CR787556	DXFZp469C
C 5	4	66.7	5	CF307095	HDA1--05-
C 6	4	66.7	5	CN612621	CsgeEST00
C 7	4	66.7	5	CN612715	CsgeEST00
C 8	4	66.7	6	CA850792	D06E12_E1
C 9	4	66.7	6	CA850792	D06E12_E1
C 10	4	66.7	6	CA851141	D10E10_J1
C 11	4	66.7	6	CR787556	DXFZp469C
C 12	3.4	56.7	5	CF327761	NACL--02-
C 13	3.4	56.7	5	CF339974	RCL1--06-
C 14	3.4	56.7	5	CF340386	RCL1--07-
C 15	3.4	56.7	5	CF340514	RCL1--08-
C 16	3.4	56.7	6	CF339116	RCL1--03-
C 17	3.4	56.7	6	CF340012	RCL1--06-
C 18	3.4	56.7	6	CF340239	RCL1--07-
C 19	3.4	56.7	6	CF921483	gmhrRwW3-
C 20	3	50.0	3	CA851141	DXFZp469C
C 21	3	50.0	3	CA851141	DXFZp469C
C 22	3	50.0	3	CA851141	DXFZp469C
C 23	3	50.0	3	CA851141	DXFZp469C
C 24	3	50.0	3	CF292073	14ROOT--0

C 25	3	50.0	3	CF292073	14ROOT--0
C 26	3	50.0	3	CF306332	HDA1--03-
C 27	3	50.0	3	CF306332	HDA1--03-
C 28	3	50.0	3	CF306493	HDA1--04-
C 29	3	50.0	3	CF306493	HDA1--04-
C 30	3	50.0	3	CF306655	HDA1--04-
C 31	3	50.0	3	CF306655	HDA1--04-
C 32	3	50.0	3	CF306732	HDA1--04-
C 33	3	50.0	3	CF306732	HDA1--04-
C 34	3	50.0	3	CF306759	HDA1--04-
C 35	3	50.0	3	CF306759	HDA1--04-
C 36	3	50.0	3	CF306836	HDA1--04-
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C 38	3	50.0	3	CF306855	HDA1--05-
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C 41	3	50.0	3	CF306874	HDA1--05-
C 42	3	50.0	3	CF306921	HDA1--05-
C 43	3	50.0	3	CF306921	HDA1--05-
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C 46	3	50.0	3	CF307052	HDA1--05-
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C 48	3	50.0	3	CF307058	HDA1--05-
C 49	3	50.0	3	CF307058	HDA1--05-
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C 51	3	50.0	3	CF307069	HDA1--05-
C 52	3	50.0	3	CF307073	HDA1--05-
C 53	3	50.0	3	CF307073	HDA1--05-
C 54	3	50.0	3	CF307112	HDA1--05-
C 55	3	50.0	3	CF307112	HDA1--05-
C 56	3	50.0	3	CF307117	HDA1--05-
C 57	3	50.0	3	CF307117	HDA1--05-
C 58	3	50.0	3	CF307203	HDA1--06-
C 59	3	50.0	3	CF307203	HDA1--06-
C 60	3	50.0	3	CF307223	HDA1--06-
C 61	3	50.0	3	CF307223	HDA1--06-
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C 63	3	50.0	3	CF307246	HDA1--06-
C 64	3	50.0	3	CF307290	HDA1--06-
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C 67	3	50.0	3	CF307313	HDA1--06-
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C 71	3	50.0	3	CF307404	HDA1--06-
C 72	3	50.0	3	CF307480	HDA1--06-
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C 74	3	50.0	3	CF307489	HDA1--06-
C 75	3	50.0	3	CF307489	HDA1--06-
C 76	3	50.0	3	CF307511	HDA1--06-
C 77	3	50.0	3	CF307511	HDA1--06-
C 78	3	50.0	3	CF307516	HDA1--06-
C 79	3	50.0	3	CF307516	HDA1--06-
C 80	3	50.0	3	CF307535	HDA1--06-
C 81	3	50.0	3	CF307535	HDA1--06-
C 82	3	50.0	3	CF920868	gmhrRwW3-
C 83	3	50.0	3	CF920868	gmhrRwW3-
C 84	3	50.0	3	CF921365	gmhrRwW3-
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C 86	3	50.0	3	CL423550	01S0557-0
C 87	3	50.0	3	CL423550	01S0557-0
C 88	3	50.0	4	CA853244	B06A04.8e
C 89	3	50.0	4	CA853244	B06A04.8e
C 90	3	50.0	4	CF298748	7LEAF--02
C 91	3	50.0	4	CF298748	7LEAF--02
C 92	3	50.0	4	CF306914	HDA1--05-
C 93	3	50.0	4	CF306914	HDA1--05-
C 94	3	50.0	5	CF282401	14ETL--09
C 95	3	50.0	5	CF282401	14ETL--09
C 96	3	50.0	5	CF307095	HDA1--05-
C 97	3	50.0	5	CF307095	HDA1--05-

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 99 3 50.0 5 7 CF323326 HDN--03-I
 c 100 3 50.0 5 7 CF323326

ALIGNMENTS

RESULT 1
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 LOCUS
 DEFINITION
 CsgEST00264 Culicoides sonorensis female salivary gland cDNA
 Library Culicoides sonorensis cDNA, mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 EST:
 CN612621.1 GI:47120661
 Culicoides sonorensis
 Culicoides sonorensis
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Chironomidae;
 Ceratopogonidae; Ceratopogoninae; Culicoides; Monoculicoides.
 1 (bases 1 to 5)
 Campbell,C.L., Vandyke,K., Letchworth,G.J. and Wilson,W.C.
 Expressed sequence tags from Culicoides sonorensis adult female
 salivary glands
 Unpublished (2004)
 Contact: Campbell, C.L.
 Arthropod-borne Animal Diseases Research Lab
 Agricultural Research Service
 College of Agriculture, Dept. 3354, 1000 E. University Ave.,
 Laramie, WY 82071, USA
 Tel: 307 766 3626
 Fax: 307 766 3500
 Email: camcorey@uwo.edu.

FEATURES
 source
 1..5
 Location/Qualifiers
 /organism="Culicoides sonorensis"
 /mol_type="mRNA"
 /strain="AK"
 /db_xref="taxon:179676"
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 /cell_type="epithelial"
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 /clone_lib="Culicoides sonorensis female salivary gland
 cDNA Library"

ORIGIN
 Query Match 83.3%; Score 5; DB 7; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.6e+09;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCCG 5
 |||||
 Db 5 GGCCG 1

RESULT 2
 CN612715/c
 LOCUS
 DEFINITION
 CsgEST00395 Culicoides sonorensis female salivary gland cDNA
 Library Culicoides sonorensis cDNA, mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 EST:
 CN612715.1 GI:47120755
 Culicoides sonorensis
 Culicoides sonorensis
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Chironomidae;
 Ceratopogonidae; Ceratopogoninae; Culicoides; Monoculicoides.
 1 (bases 1 to 5)
 Campbell,C.L., Vandyke,K., Letchworth,G.J. and Wilson,W.C.
 Expressed sequence tags from Culicoides sonorensis adult female

JOURNAL
 COMMENT
 salivary glands
 Unpublished (2004)
 Contact: Campbell, C.L.
 Arthropod-borne Animal Diseases Research Lab
 Agricultural Research Service
 College of Agriculture, Dept. 3354, 1000 E. University Ave.,
 Laramie, WY 82071, USA
 Tel: 307 766 3626
 Fax: 307 766 3500
 Email: camcorey@uwo.edu.
 Location/Qualifiers
 1..5
 /organism="Culicoides sonorensis"
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 /sex="female"
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 /cell_type="epithelial"
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 /clone_lib="Culicoides sonorensis female salivary gland
 cDNA Library"

ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 7.6e+09;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCCG 5
 |||||
 Db 5 GGCCG 1

RESULT 3
 CA851141/c
 LOCUS
 DEFINITION
 D10E10 J10.09.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
 cDNA clone D10E10 5', mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 EST:
 CA851141.1 GI:33387934
 Glycine max (soybean)
 Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.

REFERENCE
 1 (bases 1 to 6)
 Alkharouf,N.W., Khan,R. and Matthews,B.F.
 Analysis of expressed sequence tags from roots of resistant soybean
 infected by the soybean cyst nematode
 Unpublished (2002)
 Contact: Alkharouf, N.W.
 Soybean Genomics and Improvement Laboratory (SGIL)
 US Department of Agriculture (USDA), ARS, PSI
 Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
 USA
 Tel: 301 504 5750
 Fax: 301 504 5728
 Email: alkharoun@ba.ars.usda.gov.
 Location/Qualifiers
 1..6
 /organism="Glycine max"
 /mol_type="mRNA"
 /cultivar="Peking"
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 /clone="D10E10"
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 /dev_stage="Seedlings"
 /clone_lib="cDNA Peking library 2, 4 day SCN3"
 /note="Vector: pBluescript SK-; cDNA clones from mRNA
 extracted from Peking roots 2 and 4 days past invasion."

FEATURES
 source

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 6.3e+09;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCCG 5
 Db 6 GGCCG 2

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 LOCUS CR787556/c
 DEFINITION DKFPZ469C0243_r1_469 (synonym: pkid1) Pongo pygmaeus cDNA clone
 VERSION DKFPZ469C0243 5', mRNA sequence.
 KEYWORDS CR787556 GI:53706553
 SOURCE EST.
 ORGANISM Pongo pygmaeus (orangutan)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
 1 (bases 1 to 6)
 AUTHORS Ansorge, W.; Krieger, S.; Regiert, T.; Rittmueller, C.; Schwager, B.;
 Mewes, H.W.; Weil, B.; Amid, C.; Osanger, A.; Fobo, G.; Han, M. and
 Wiemann, S.
 TITLE Pongo pygmaeus mRNA (Ansorge, W., Krieger, S., Regiert, T., et al.)
 JOURNAL Unpublished (2004)
 COMMENT Contact: MIPS

FEATURES
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 /dev_stage="adult"
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 /clone_lib="469 (synonym: pkid1)"
 /notes="Vector: pSport1_Sfi; Site_1: SfiA; Site_2: SfiB"

ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 6.3e+09;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCCG 5
 Db 5 GGCCG 1

RESULT 5
 LOCUS CF307095/c
 DEFINITION HDAl-05-L19, g1 OshDAC1-overexpressing transgenic rice lambda phage
 cDNA library I (HDAl) Oryza sativa (japonica cultivar-group) cDNA
 clone HDAl-05-L19, mRNA sequence.
 VERSION CF307095
 KEYWORDS CF307095 GI:33678856
 SOURCE EST.
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 5)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm, B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..5
 Location/Qualifiers
 ..5
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 /mol_type="mRNA"
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 /clone_lib="OshDAC1-overexpressing transgenic rice lambda
 phage cDNA library I (HDAl)"
 /notes="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
 XhoI; Callus was treated with ABA (20um) for 1 hour. cDNA
 was inserted into lambda Uni-ZAP XR vector at 5' end with
 EcoRI and 3' end with XhoI site. mRNA was derived from
 rice Histone Deacetylase overexpression line."

ORIGIN

Query Match 66.7%; Score 4; DB 7; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.6e+09;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCG 5
 Db 5 GGCG 2

RESULT 6

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

CN612621
 CsesEST00264 Culicoides sonorensis female salivary gland cDNA
 Library Culicoides sonorensis cDNA, mRNA sequence.
 CN612621
 CN612621.1 GI:47120661
 EST.
 Culicoides sonorensis
 Culicoides sonorensis
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Chironomidae;
 Ceratopogonidae; Ceratopogoninae; Culicoides; Monoculicoides.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 5)
 Campbell, C.L., VanDyke, K., Letchworth, G.J. and Wilson, W.C.
 Expressed sequence tags from Culicoides sonorensis adult female
 salivary glands
 Unpublished (2004)
 Contact: Campbell, C.L.
 Arthropod-borne Animal Diseases Research Lab
 Agricultural Research Service
 College of Agriculture, Dept. 3354, 1000 E. University Ave.,
 Laramie, WY 82071, USA
 Tel: 307 766 3626
 Fax: 307 766 3500
 Email: camcore@uwyo.edu.
 Location/Qualifiers
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 /db_xref="taxon:179676"

FEATURES

source

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cDNA Library"

ORIGIN
Query Match      66.7%; Score 4; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.6e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCC 4
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Db 2 GGCC 5

RESULT 7
CN612715
LOCUS
DEFINITION      CsgEST00395 Culicoides sonorensis female salivary gland cDNA
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Culicoides sonorensis
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Chironomidae;
Ceratopogonidae; Ceratopogoninae; Culicoides; Monoculicoides.
1 (bases 1 to 5)
Campbell,C.L., VanDyke,K., Letchworth,G.J. and Wilson,W.C.
Expressed sequence tags from Culicoides sonorensis adult female
salivary glands
Unpublished (2004)
Contact: Campbell, C.L.
Arthropod-borne Animal Diseases Research Lab
Agricultural Research Service
College of Agriculture, Dept. 3354, 1000 E. University Ave.,
Laramie, WY 82071, USA
Tel: 307 766 3626
Fax: 307 766 3500
Email: camcore@uwyo.edu.

FEATURES
source
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/dev_stage="adult, 2-4 day-old"
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cDNA Library"

ORIGIN
Query Match      66.7%; Score 4; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.6e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCC 4
    ||||
Db 2 GGCC 5

RESULT 8
CA850792
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DEFINITION      D06E12_E12_10_ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Glycine max (soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 6)
Alkharouf,N.W., Khan,R. and Matthews,B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.

FEATURES
source
1..6
/organism="Glycine max"
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/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D06E12"
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/clone_lib="cDNA Peking library 2, 4 day SCN3"
/notes="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."

ORIGIN
Query Match      66.7%; Score 4; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCGG 6
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Db 1 CCGG 4

RESULT 9
CA850792/c
LOCUS
DEFINITION      D06E12_E12_10_ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
ACCESSION      CA850792
VERSION
KEYWORDS
SOURCE
ORGANISM
Glycine max (soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 6)
Alkharouf,N.W., Khan,R. and Matthews,B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.

FEATURES
source
1..6
/organism="Glycine max"

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ORIGIN		/mol_type="mRNA" /cultivar="Peking" /db_xref="taxon:3847" /clone="D06E12" /tissue_type="Roots" /dev_stage="Seedlings" /clone_lib="cDNA Peking library 2, 4 day SCN3" /note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from Peking roots 2 and 4 days past invasion."	
Query Match		66.7%; Score 4; DB 6; Length 6;	
Best Local Similarity		100.0%; Pred. No. 6.3e+09;	
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	3 CCGG 6		
DB	4 CCGG 1		
RESULT 10			
CA851141			
LOCUS			
DEFINITION			
CA851141 6 bp mRNA linear EST 01-AUG-2003			
cDNA clone D10E10 5', mRNA sequence.			
CA851141			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
Glycine max (soybean)			
Glycine max			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.			
REFERENCE			
1 (bases 1 to 6)			
Alkharouf, N.W., Khan, R. and Matthews, B.F.			
AUTHORS			
TITLE			
Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode			
JOURNAL			
COMMENT			
Unpublished (2002)			
Contact: Alkharouf, N.W.			
Soybean Genomics and Improvement Laboratory (SGIL)			
US Department of Agriculture (USDA), ARS, PSI			
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350, USA			
Tel: 301 504 5750			
Fax: 301 504 5728			
Email: alkharouf@ba.ars.usda.gov.			
Location/Qualifiers			
1. 6			
FEATURES			
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/organism="Glycine max"			
/mol_type="mRNA"			
/cultivar="Peking"			
/db_xref="taxon:3847"			
/clone="D10E10"			
/tissue_type="Roots"			
/dev_stage="Seedlings"			
/clone_lib="cDNA Peking library 2, 4 day SCN3"			
/note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from Peking roots 2 and 4 days past invasion."			
ORIGIN			
Query Match			
Best Local Similarity			
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 GGCC 4		
DB	3 GGCC 6		
RESULT 11			
CR787556			
LOCUS			
6 bp mRNA linear EST 01-OCT-2004			

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FEATURES
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        /mol_type="mrna"
        /cultivar="Nackdong"
        /db_xref="taxon:39947"
        /clone="NACL--02-G02"
        /tissue_type="callus"
        /dev_stage="proliferated callus on 2N6 media for 30 days"
        /lab_host="E.coli DH10B"
        /clone_lib="Rice callus plasmid cDNA library (NACL)"
        /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

ORIGIN
  Query Match      56.7%; Score 3.4; DB 7; Length 5;
  Best Local Similarity 80.0%; Pred. No. 7.6e+09;
  Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCGCG 5
Db 5 GCGCG 1

RESULT 13
LOCUS CF339974
DEFINITION RCL1--06-118.g1 Regenerated callus lambda phage cDNA library (RCL1)
Oryza sativa (japonica cultivar-group) cDNA clone RCL1--06-118, mRNA sequence.
ACCESSION CF339974
VERSION CF339974.1 GI:33828316
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE 1 (bases 1 to 5)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
  source
    1..5
      /organism="Oryza sativa (japonica cultivar-group)"
      /mol_type="mrna"
      /cultivar="Nackdong"
      /db_xref="taxon:39947"
      /clone="RCL1--07-N21"
      /tissue_type="callus"
      /dev_stage="proliferated callus on 2N6 media for 30 days"
      /lab_host="E.coli SOLR"
      /clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
      /note="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

ORIGIN
  Query Match      56.7%; Score 3.4; DB 7; Length 5;
  Best Local Similarity 80.0%; Pred. No. 7.6e+09;
  Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGCG 6
Db 1 GCTGG 5

RESULT 14
LOCUS CF340386
DEFINITION RCL1--07-N21.g1 Regenerated callus lambda phage cDNA library (RCL1)
Oryza sativa (japonica cultivar-group) cDNA clone RCL1--07-N21, mRNA sequence.
ACCESSION CF340386
VERSION CF340386.1 GI:33829128
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE 1 (bases 1 to 5)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
  source
    1..5
      /organism="Oryza sativa (japonica cultivar-group)"
      /mol_type="mrna"
      /cultivar="Nackdong"
      /db_xref="taxon:39947"
      /clone="RCL1--07-N21"
      /tissue_type="callus"
      /dev_stage="proliferated callus on 2N6 media for 30 days"
      /lab_host="E.coli SOLR"
      /clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
      /note="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

ORIGIN
  Query Match      56.7%; Score 3.4; DB 7; Length 5;
  Best Local Similarity 80.0%; Pred. No. 7.6e+09;
  Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGCG 6
Db 1 GCTGG 5

RESULT 15
LOCUS CF340514
DEFINITION RCL1--08-E10.g1 Regenerated callus lambda phage cDNA library (RCL1)
Oryza sativa (japonica cultivar-group) cDNA clone RCL1--08-E10, mRNA sequence.
ACCESSION CF340514
VERSION CF340514.1 GI:33829381
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;


```

```

REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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1..5
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="RCL1--08-E10"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library
(RCL1)"
/notes="Vector: pBluescript SK(+); Site_1: SstI; Site_2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with SstI and 3' end with XhoI site. Callus was
induced on 2N6 media for 30 days and cultured for 36hrs on
regenerated media"

ORIGIN
Query Match      56.7%; Score 3.4; DB 7; Length 5;
Best Local Similarity 80.0%; Pred. No. 7.6e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GCCGG 6
      |||
Db      1 GCTGG 5

RESULT 16
LOCUS      CF339116
DEFINITION      CF339116.1 GI:33826619
Oryza sativa (japonica cultivar-group) cDNA clone RCL1--03-N11,
mRNA sequence.
ACCESSION      CF339116
VERSION      CF339116.1 GI:33826619
KEYWORDS      EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM      Oryza sativa (japonica cultivar-group)
              Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE      1 (bases 1 to 5)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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1..6
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="RCL1--03-N11"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library
(RCL1)"
/notes="Vector: pBluescript SK(+); Site_1: SstI; Site_2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with SstI and 3' end with XhoI site. Callus was
induced on 2N6 media for 30 days and cultured for 36hrs on
regenerated media"

ORIGIN
Query Match      56.7%; Score 3.4; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GCCGG 6
      |||
Db      2 GCTGG 6

RESULT 17
LOCUS      CF340012
DEFINITION      CF340012.1 GI:33828387
Oryza sativa (japonica cultivar-group) cDNA clone RCL1--06-K19,
mRNA sequence.
ACCESSION      CF340012
VERSION      CF340012.1 GI:33828387
KEYWORDS      EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM      Oryza sativa (japonica cultivar-group)
              Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE      1 (bases 1 to 6)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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1..6
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="RCL1--06-K19"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library
(RCL1)"
/notes="Vector: pBluescript SK(+); Site_1: SstI; Site_2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with SstI and 3' end with XhoI site. Callus was
induced on 2N6 media for 30 days and cultured for 36hrs on
regenerated media"

ORIGIN
Query Match      56.7%; Score 3.4; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GCCGG 6
      |||

```

Db 2 GCTGG 6

RESULT 18
CF340239
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone RCL1--07-G09, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 6)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1. .6
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="RCL1--07-G09"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
/note="Vector: pBluescript SK(+); Site1: SstI; Site2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

ORIGIN
Query Match 56.7%; Score 3.4; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 GCCGG 6
|||
Db 2 GCTGG 6

RESULT 19
CF921483
LOCUS
DEFINITION
GmhrRw3-09 H07_1_049 Soybean root hair subtracted cDNA library
GmhrRw3 Glycine max cDNA, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 6)
Scheffler,B.E., Huang,S., Liu,X., Nguyen,H., Duke,M. and Stacey,G.

Expressed sequence tags from soybean root hair subtractive cDNA library
Unpublished (2003)
Contact: Gary Stacey
University of Missouri
108 Watera Hall, Columbia, MO 65211, USA
Tel: 573-884-4752
Fax: 573-882-0588
Email: staceyg@missouri.edu
Single pass sequence
Seq primer: T7

FEATURES
Location/Qualifiers
1. .6
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
/tissue_type="root hairs"
/clone_lib="Soybean root hair subtracted cDNA library gmhrRw3"
/note="Organ: root hairs; Vector: pCR2-1 Topo; cDNA clones generated from soybean root hair tissue treated with Bradyrhizobium japonicum for 3 hours."

ORIGIN
Query Match 56.7%; Score 3.4; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 GCCGG 6
|||
Db 1 GCGGG 5

RESULT 20
BX266151
LOCUS
DEFINITION
BX266151 AGENAE Gallus gallus multi-tissues normalized and once-subtracted cDNA library (gcsl) Gallus gallus cDNA clone gcsl0011c.i.02 3prim, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Gallus gallus (chicken)
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 3)
Herault,F., Le Meuth-Metzinger,V., Desert,C., Retout,E., Piumi,F., Klopp,C. and Douaire,M.
Construction and primary characterization of chicken normalized multi-tissue cDNA libraries
Unpublished (2003)
On Feb 27, 2003 this sequence version replaced gi:28588749.
Contact: Douaire M
INRA, UMR INRA-ENSAR Genetique Animale
65, rue de Saint-Brieuc, RENNES cedex, 35042, FRANCE
Tel: +33 (0) 2.23.48.54.63
Fax: +33 (0) 2.23.48.54.70
Email: Madeleine.Douaire@roazhon.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us at signasupport@jouy.inra.fr to obtain the chromatogram of this sequence.
Plate: 0011 row: i column: 2
Seq primer: M13F.

FEATURES
Location/Qualifiers
1. .3
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="gcsl0011c.i.02"
/tissue_type="multi-tissues"

/dev_stage="from embryos to adults"

/lab_host="DH108"
/clone_lib="AGENAE Gallus gallus multi-tissues normalized
and once-subtracted cDNA library (gcal)"
/notes="Vector: pT7T3D-pac; tissues: adipose tissue, brain,
kidney, liver, multi-tissues, muscle, ovary, testis, bone
marrow, caecum, duodenum, embryos, fabricius gland,
granulosa, hypothalamus, ileon, jejunum, oviduct,
pancreas, skin, spleen, thymus, utero-vaginal gland,
pituitary gland, hematopoietic progenitor cells, small
follicle. Clone distribution : AGENAE Resource centre.
Francois PIUMI, Francois.Piumi.inra.fr, INRA, CEA
Radiobiologie et Etude du genome (LREG), Domaine de
Vilvert, 78352, Jouy-en-Josas cedex, FRANCE"

ORIGIN

Query Match 50.0%; Score 3; DB 5; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCC 4
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Db 1 GCC 3

RESULT 21

BX266151/c

LOCUS

DEFINITION

BX266151 AGENAE Gallus gallus multi-tissues normalized
once-subtracted cDNA library (gcal) EST 26-MAY-2004

gcal0011c.i.02 3prim, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

1 (bases 1 to 3)

Herault,F., Le Meuth-Metzinger,V., Desert,C., Retout,E., Piumi,F.,

Klopp,C. and Douaire M.

Construction and primary characterization of chicken normalized

multi-tissue cDNA libraries

Unpublished (2003)

On Feb 27, 2003 this sequence version replaced gi:28588749.

Contact: Douaire M

INRA, UMR INRA-ENSAR Genetique Animale

65, rue de Saint-Brieuc, RENNES cedex, 35042, FRANCE

Tel: +33 (0) 2.23.48.54.63

Fax: +33 (0) 2.23.48.54.70

Email: Madeleine.Douaire@roazhon.inra.fr

Sequence cleaned of vector, adaptor and repetitions. Contact us

at sigenasupport@jouy.inra.fr to obtain the chromatogram of this

sequence.

Plate: 0011 row: i column: 2

Seq primer: M13F.

Location/Qualifiers

1. .3

/organism="Gallus gallus"

/mol_type="mRNA"

/db_xref="taxon:9031"

/clone="gcal0011c.i.02"

/tissue_type="multi-tissues"

/dev_stage="from embryos to adults"

/lab_host="DH108"

/clone_lib="AGENAE Gallus gallus multi-tissues normalized

and once-subtracted cDNA library (gcal)"

/notes="Vector: pT7T3D-pac; tissues: adipose tissue, brain,

kidney, liver, multi-tissues, muscle, ovary, testis, bone

marrow, caecum, duodenum, embryos, fabricius gland,

granulosa, hypothalamus, ileon, jejunum, oviduct,

pancreas, skin, spleen, thymus, utero-vaginal gland,

pituitary gland, hematopoietic progenitor cells, small

follicle. Clone distribution : AGENAE Resource centre.

Francois PIUMI, Francois.Piumi.inra.fr, INRA, CEA

Radiobiologie et Etude du genome (LREG), Domaine de

Vilvert, 78352, Jouy-en-Josas cedex, FRANCE"

ORIGIN

Query Match 50.0%; Score 3; DB 5; Length 3;

Best Local Similarity 100.0%; Pred. No. 1.3e+10;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCC 3

|||

Db 3 GCC 1

Query Match 50.0%; Score 3; DB 5; Length 3;

Best Local Similarity 100.0%; Pred. No. 1.3e+10;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCC 3

|||

Db 3 GCC 1

Query Match 50.0%; Score 3; DB 5; Length 3;

Best Local Similarity 100.0%; Pred. No. 1.3e+10;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCC 3

|||

Db 3 GCC 1

Query Match 50.0%; Score 3; DB 5; Length 3;

Best Local Similarity 100.0%; Pred. No. 1.3e+10;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCC 3

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Db 3 GCC 1

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Best Local Similarity 100.0%; Pred. No. 1.3e+10;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCC 3

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Db 3 GCC 1

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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3 GCC 1

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Best Local Similarity 100.0%; Pred. No. 1.3e+10;

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Best Local Similarity 100.0%; Pred. No. 1.3e+10;

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QY 1 GCC 3

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QY 1 GCC 3

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QY 3 CCG 5
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Db 1 CCG 3

RESULT 23
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LOCUS BX267257 AGENAE Gallus gallus multi-tissues normalized and EST 26-MAY-2004
DEFINITION once-subtracted cDNA library (gccl) Gallus gallus cDNA clone
          gcal0011c.a.24 3prim, mRNA sequence.
ACCESSION BX267257
VERSION 1
KEYWORDS 1
SOURCE 1
ORGANISM Gallus gallus (chicken)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 3)
AUTHORS Herault,F., Le Meuth-Metzinger,V., Desert,C., Retout,E., Piumi,F.,
Klopp,C. and Douaire,M.
TITLE Construction and primary characterization of chicken normalized
multi-tissue cDNA libraries
JOURNAL Unpublished (2003)
COMMENT On Feb 27, 2003 this sequence version replaced gi:28589855.
Contact: Douaire M
INRA, UMR INRA-ENSAR Genetique Animale
65, rue de Saint-Brieuc, RENNES cedex, 35042, FRANCE
Tel: +33 (0) 2.23.48.54.63
Fax: +33 (0) 2.23.48.54.70
Email: Madeleine.Douaire@roazhon.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at signasupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0011 row: a column: 24
Seq primer: M13F.
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              /note="Vector: pT7T3D-pac; tissues: adipose tissue, brain,
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              granulosa, hypothalamus, ileon, jejunum, oviduct,
              pancreas, skin, spleen, thymus, utero-vaginal gland,
              pituitary gland, hematopoietic progenitor cells, small
              follicle. Clone distribution : AGENAE Resource centre.
              Francois PIUMI, Francois.Piumi@roazhon.inra.fr, INRA, CEA
              Radiobiologie et Etude du genome (LREG), Domaine de
              Vilvert, 78352, Jouy-en-Josas cedex, FRANCE"

ORIGIN
Query Match 50.0%; Score 3; DB 5; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCG 6
    |||
Db 3 CCG 1

RESULT 24
CF292073
LOCUS CF292073 AGENAE Gallus gallus multi-tissues normalized and EST 14-AUG-2003
DEFINITION once-subtracted cDNA library (gccl) Gallus gallus cDNA clone
          14ROOT--02-M03 3bp, mRNA sequence.
ACCESSION CF292073
VERSION 1
KEYWORDS 1
SOURCE 1
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
          Location/Qualifiers
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              RT-PCR."

ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCC 4
    |||
Db 1 GCC 3

RESULT 25
CF292073/c
LOCUS CF292073 AGENAE Gallus gallus multi-tissues normalized and EST 14-AUG-2003
DEFINITION once-subtracted cDNA library (gccl) Gallus gallus cDNA clone
          14ROOT--02-M03 3bp, mRNA sequence.
ACCESSION CF292073
VERSION 1
KEYWORDS 1
SOURCE 1
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193

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```

Fax: 82 31 321 6355
Email: bhnamhggbio.com, bhnamh@bio.myongji.ac.kr.

FEATURES
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1. .3
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGC 3
Db 3 GGC 1

RESULT 26
CF306332 3 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION
HDAL--03-H16.g1 OSHDAC1-overexpressing transgenic rice lambda phage
cDNA library I (HDAL) Oryza sativa (japonica cultivar-group) cDNA
clone HDAL--03-H16, mRNA sequence.
CF306332
CF306332.1 GI:33678093
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 3)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnamhggbio.com, bhnamh@bio.myongji.ac.kr.

FEATURES
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phage cDNA library I (HDAL)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
was inserted into lambda Uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."

ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGC 4
Db 3 GGC 1

RESULT 28
CF306493 3 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION
HDAL--04-A07.g1 OSHDAC1-overexpressing transgenic rice lambda phage
cDNA library I (HDAL) Oryza sativa (japonica cultivar-group) cDNA
clone HDAL--04-A07, mRNA sequence.
CF306493
CF306493.1 GI:33678254
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 3)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnamhggbio.com, bhnamh@bio.myongji.ac.kr.

FEATURES
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phage cDNA library I (HDAL)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
was inserted into lambda Uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."

ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 3;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 3)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

Location/Qualifiers
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/cultivar="Nackdong"
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phage CDNA library I (HDAL)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
was inserted into lambda Uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."

FEATURES

source

Query Match 50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGC 3

DB 1 GGC 3

RESULT 29

LOCUS

DEFINITION HDAL--04-A07.g1 OshDAC1-overexpressing transgenic rice lambda phage CDNA library I (HDAL) Oryza sativa (japonica cultivar-group) cDNA clone HDAL--04-A07, mRNA sequence.
ACCESSION CF306493
VERSION CF306493.1 GI:33678254
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

ORIGIN

Query Match 50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGC 3

DB 1 GGC 3

RESULT 29

LOCUS

DEFINITION HDAL--04-A07.g1 OshDAC1-overexpressing transgenic rice lambda phage CDNA library I (HDAL) Oryza sativa (japonica cultivar-group) cDNA clone HDAL--04-A07, mRNA sequence.
ACCESSION CF306493
VERSION CF306493.1 GI:33678254
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

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XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
was inserted into lambda Uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."

ORIGIN

Query Match 50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCC 4

DB 3 GCC 1

RESULT 30

LOCUS

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ACCESSION CF306655
VERSION CF306655.1 GI:33678416
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
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REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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was inserted into lambda Uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."

ORIGIN

Query Match 50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGC 3
Db 1 GGC 3

Search completed: July 21, 2005, 01:54:37
Job time : 1349.8 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 21:46:09 ; Search time 187.4 Seconds
(without alignments)
189.533 Million cell updates/sec

Title: US-09-735-363A-43

Perfect score: 6

Sequence: 1 ggcggg 6

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 1582

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : N_Geneseq_16Dec04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	83.3	6	12	ADJ35370 Stabilisi
2	5	83.3	6	12	ADJ35370 Stabilisi
3	5	83.3	6	12	ADJ35397 Stabilisi
4	5	83.3	6	12	ADJ35516 Stabilisi
5	5	83.3	6	12	ADJ35680 Immunosti
6	5	83.3	6	12	ADN96880 Immunosti
7	5	83.3	6	12	ADN96880 Immunosti
8	4.6	76.7	6	13	ADN96880 Cpg oligo
9	4.6	76.7	6	13	ADN96880 Human nic
10	4.6	76.7	6	13	ADN96880 Human nic
11	4.6	76.7	6	13	ADN96880 Human nic
12	4.4	73.3	6	4	AAF91686 Breast-ca
13	4.4	73.3	6	6	ABK87321 Mammalian
14	4.4	73.3	6	6	ABK87320 Mammalian
15	4.4	73.3	6	12	ADJ35665 Stabilisi
16	4	66.7	6	1	AAN60771 Restricti
17	4	66.7	6	1	AAN60771 Restricti
18	4	66.7	6	2	AAQ27868 Cfr91 rec
19	4	66.7	6	2	AAQ27868 Cfr91 rec
20	4	66.7	6	2	AAT80319 Oligo HCV

C	21	4	66.7	6	2	AAT80319	Oligo HCV
C	22	4	66.7	6	2	AAT77251	Immunosti
C	23	4	66.7	6	2	AAT77251	Immunosti
C	24	4	66.7	6	2	AXA21981	Hexamer O
C	25	4	66.7	6	2	AXA21981	Hexamer O
C	26	4	66.7	6	6	ABG565903	Inhibitor
C	27	4	66.7	6	6	ABG565903	Inhibitor
C	28	4	66.7	6	6	ABG565903	Inhibitor
C	29	4	66.7	6	8	ACC69109	Cucumber
C	30	4	66.7	6	8	ACC69109	Cucumber
C	31	4	66.7	6	10	ADN38330	Immune mo
C	32	4	66.7	6	10	ADN38330	Immune mo
C	33	4	66.7	6	10	ADN38329	Immune mo
C	34	4	66.7	6	10	ADN38329	Immune mo
C	35	4	66.7	6	10	ADN38279	Immune mo
C	36	4	66.7	6	12	ADJ35778	Stabilisi
C	37	4	66.7	6	12	ADJ35778	Stabilisi
C	38	4	66.7	6	12	ADJ35966	Stabilisi
C	39	4	66.7	6	12	ADJ35397	Stabilisi
C	40	4	66.7	6	12	ADJ35500	Stabilisi
C	41	4	66.7	6	12	ADJ35812	Stabilisi
C	42	4	66.7	6	12	ADJ35355	Stabilisi
C	43	4	66.7	6	12	ADJ35385	Stabilisi
C	44	4	66.7	6	12	ADJ35463	Stabilisi
C	45	4	66.7	6	12	ADJ35516	Stabilisi
C	46	4	66.7	6	12	ADJ35729	Stabilisi
C	47	4	66.7	6	12	ADJ35514	Stabilisi
C	48	4	66.7	6	12	ADJ35514	Stabilisi
C	49	4	66.7	6	12	ADK14341	Candida G
C	50	4	66.7	6	12	ADK14341	Candida G
C	51	4	66.7	6	12	ADN96876	Immunosti
C	52	4	66.7	6	12	ADN96876	Immunosti
C	53	4	66.7	6	12	ADN96876	Immunosti
C	54	4	66.7	6	13	ADR32501	Human nic
C	55	4	66.7	6	13	ADR32501	Human nic
C	56	4	66.7	6	13	ADR32492	Human nic
C	57	4	66.7	6	13	ADR32492	Human nic
C	58	4	66.7	6	13	ADN33275	E. coli 2
C	59	4	66.7	6	13	ADN33284	E. coli 2
C	60	3.6	60.0	6	2	AAQ85606	T-DNA Vir
C	61	3.6	60.0	6	2	AAQ85606	T-DNA Vir
C	62	3.6	60.0	6	13	ADR35700	Human nic
C	63	3.6	60.0	6	13	ADR35700	Human nic
C	64	3.6	60.0	6	13	ADR35724	Human nic
C	65	3.6	60.0	6	13	ADR35724	Human nic
C	66	3.6	60.0	6	13	ADR34424	Human nic
C	67	3.6	60.0	6	13	ADR35703	Human nic
C	68	3.6	60.0	6	13	ADR35703	Human nic
C	69	3.6	60.0	6	13	ADR34422	Human nic
C	70	3.6	60.0	6	13	ADR35722	Human nic
C	71	3.6	60.0	6	13	ADR35722	Human nic
C	72	3.6	60.0	6	13	ADR35702	Human nic
C	73	3.6	60.0	6	13	ADR35702	Human nic
C	74	3.6	60.0	6	13	ADR35723	Human nic
C	75	3.6	60.0	6	13	ADR35723	Human nic
C	76	3.6	60.0	6	13	ADR35721	Human nic
C	77	3.6	60.0	6	13	ADR35721	Human nic
C	78	3.6	60.0	6	13	ADR34423	Human nic
C	79	3.6	60.0	6	13	ADR35701	Human nic
C	80	3.6	60.0	6	13	ADR35701	Human nic
C	81	3.6	60.0	6	13	ADR34421	Human nic
C	82	3.4	56.7	5	3	AAA56981	Human col
C	83	3.4	56.7	5	8	ABT12403	Orestes s
C	84	3.4	56.7	5	8	ABZ75669	Helicase-
C	85	3.4	56.7	5	8	ABZ75665	Helicase-
C	86	3.4	56.7	5	8	ABZ75667	Helicase-
C	87	3.4	56.7	5	8	ABZ75663	Helicase-
C	88	3.4	56.7	5	10	ACD91697	Human col
C	89	3.4	56.7	6	2	AAQ53911	Portion O
C	90	3.4	56.7	6	2	AAT80318	Oligo HCV
C	91	3.4	56.7	6	4	AAQ56240	PCR prime
C	92	3.4	56.7	6	6	ABG565902	Inhibitor
C	93	3.4	56.7	6	6	ABK88579	Hepatitis

```
94 3.4 56.7 6 8 ABZ75668 Helicase-
c 95 3.4 56.7 6 10 ADE38284 Immune mo
c 96 3.4 56.7 6 10 ADE38283 Immune mo
c 97 3.4 56.7 6 12 ADJ35778 Stabilisi
c 98 3.4 56.7 6 12 ADJ35694 Stabilisi
c 99 3.4 56.7 6 12 ADJ35808 Stabilisi
c 100 3.4 56.7 6 12 ADJ35483 Stabilisi

ALIGNMENTS

RESULT 1
ADJ35370
ID ADJ35370 standard; DNA; 6 BP.
XX
AC ADJ35370;
XX
DT 22-APR-2004 (first entry)
XX
DE Stabilising anti-repression, STAR, element dyad sequence #36.
XX
KW STAR affiliated proteinaceous molecule; post translational modification;
KW stabilising anti-repression; STAR; STAR element; ds; dyad.
XX
OS Unidentified.
XX
PN WO2003106674-A2.
XX
PD 24-DEC-2003.
XX
PF 30-MAY-2003; 2003WO-NL000410.
XX
PR 14-JUN-2002; 2002EP-00077344.
XX
PA (CHRO-) CHROMAGENICS BV.
XX
PI Otte AP, Kruckeberg AL, Satijn DPE;
XX
DR WPI; 2004-082195/08.
XX
PT Producing proteinaceous molecules in cells by selecting a cell, providing
PT a nucleic acid encoding a proteinaceous molecule with an Stabilizing Anti
PT -Repression sequence and expressing proteinaceous molecule.
XX
PS Disclosure; Page 95; 177pp; English.
XX
CC The invention relates to a method of producing a proteinaceous molecule
CC (I) in a cell comprising selecting a cell for its suitability for
CC producing (II), providing a nucleic acid encoding (I) with a nucleic acid
CC comprising a Stabilising Anti-Repression (STAR) sequence, expressing the
CC resulting nucleic acid in the cell and collecting (I). The method is
CC useful for producing (I). A cell line (II) provided with a nucleic acid
CC comprising a STAR sequence is useful for producing (I). (II) Enables
CC production of affiliated proteinaceous molecule, as cell carries out
CC proper post-translational modifications of produced proteins. The present
CC sequence represents a stabilising anti-repression, STAR, element primer
CC dyad sequence.
XX
SQ Sequence 6 BP; 0 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
Query Match 83.3%; Score 5; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.8e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GCCGG 6
Db 6 GCCGG 2
RESULT 3
ADJ35397/c
ID ADJ35397 standard; DNA; 6 BP.
XX
AC ADJ35397;
XX
DT 22-APR-2004 (first entry)
XX
DE Stabilising anti-repression, STAR, element dyad sequence #63.
XX
KW STAR affiliated proteinaceous molecule; post translational modification;
KW stabilising anti-repression; STAR; STAR element; ds; dyad.
XX
OS Unidentified.
XX
PN WO2003106674-A2.
XX
PD 24-DEC-2003.
Query Match 83.3%; Score 5; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.8e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GCCGG 6
Db 1 GCCGG 5
RESULT 2
ADJ35370/c
ID ADJ35370 standard; DNA; 6 BP.
```

XX 30-MAY-2003; 2003WO-NL000410.
 XX 14-JUN-2002; 2002EP-00077344.
 XX (CHRO-) CHROMAGENICS BV.
 XX Otte AP, Kruckeberg AL, Satijn DPE;
 XX WPI; 2004-082195/08.
 DR Producing proteinaceous molecules in cells by selecting a cell, providing
 PT a nucleic acid encoding a proteinaceous molecule with an Stabilizing Anti
 PT -Repression sequence and expressing proteinaceous molecule.
 XX
 PS Disclosure; Page 96; 177pp; English.
 CC The invention relates to a method of producing a proteinaceous molecule
 CC (I) in a cell comprising selecting a cell for its suitability for
 CC producing (I), providing a nucleic acid encoding (I) with a nucleic acid
 CC comprising a Stabilising Anti-Repression (STAR) sequence, expressing the
 CC resulting nucleic acid in the cell and collecting (I). The method is
 CC useful for producing (I). A cell line (II) provided with a nucleic acid
 CC comprising a STAR sequence is useful for producing (I). (II) Enables
 CC production of affiliated proteinaceous molecule, as cell carries out
 CC proper post-translational modifications of produced proteins. The present
 CC sequence represents a stabilising anti-repression, STAR, element primer
 CC dyad sequence.
 XX
 SQ Sequence 6 BP; 1 A; 3 C; 2 G; 0 T; 0 U; 0 Other;
 Query Match 83.3%; Score 5; DB 12; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.8e+08;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 OY 2 GCCGG 6
 DB 5 GCCGG 1
 RESULT 4
 ID ADJ35516/C
 AC ADJ35516;
 XX 22-APR-2004 (first entry)
 XX Stabilising anti-repression, STAR, element dyad sequence #182.
 DE STAR affiliated proteinaceous molecule; post translational modification;
 KW stabilising anti-repression; STAR; STAR element; ds; dyad.
 XX Unidentified.
 OS
 XX WO2003106674-A2.
 PN 24-DEC-2003.
 XX 30-MAY-2003; 2003WO-NL000410.
 XX 14-JUN-2002; 2002EP-00077344.
 XX (CHRO-) CHROMAGENICS BV.
 XX Otte AP, Kruckeberg AL, Satijn DPE;
 XX WPI; 2004-082195/08.
 DR Producing proteinaceous molecules in cells by selecting a cell, providing
 PT a nucleic acid encoding a proteinaceous molecule with an Stabilising Anti
 PT -Repression sequence and expressing proteinaceous molecule.
 XX

PS Disclosure; Page 98; 177pp; English.
 XX The invention relates to a method of producing a proteinaceous molecule
 CC (I) in a cell comprising selecting a cell for its suitability for
 CC producing (I), providing a nucleic acid encoding (I) with a nucleic acid
 CC comprising a Stabilising Anti-Repression (STAR) sequence, expressing the
 CC resulting nucleic acid in the cell and collecting (I). The method is
 CC useful for producing (I). A cell line (II) provided with a nucleic acid
 CC comprising a STAR sequence is useful for producing (I). (II) Enables
 CC production of affiliated proteinaceous molecule, as cell carries out
 CC proper post-translational modifications of produced proteins. The present
 CC sequence represents a stabilising anti-repression, STAR, element primer
 CC dyad sequence.
 XX
 SQ Sequence 6 BP; 0 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 83.3%; Score 5; DB 12; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.8e+08;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 GCCGG 6
 DB 5 GCCGG 1
 RESULT 5
 ADN96880
 ID ADN96880 standard; DNA; 6 BP.
 AC ADN96880;
 XX 26-AUG-2004 (first entry)
 DE Immunostimulatory CpG oligonucleotide seqid 14.
 XX
 KW virucide; anti-HIV; antibacterial; fungicide; cerebroprotective;
 KW tuberculostatic; anti-inflammatory; hepatotropic; cytostatic;
 KW dermatological; bacterial growth inhibitor; immunostimulator;
 KW immune response; immunostimulatory; opportunistic infection;
 KW lentivirus infection; human immunodeficiency virus infection; AIDS;
 KW Leishmania infection; bacterial infection; fungal infection;
 KW viral infection; protozoan infection; prion disease; nucleoplasm;
 KW salmonellosis; syphilis; neurosyphilis; tuberculosis;
 KW bacillary angiomatosis; aspergillosis; candidiasis; coccidioidomycosis;
 KW cryptococcal meningitis; hepatitis B; histoplasmosis; cryptosporidiosis;
 KW isosporiasis; microsporidiosis; pneumocystis carinii pneumonia;
 KW toxoplasmosis; cytomegalovirus; hepatitis; herpes simplex; herpes zoster;
 KW human papillomavirus; molluscum contagiosum; oral hairy leukoplakia;
 KW progressive multifocal leukoencephalopathy; neoplasm; Kaposi's sarcoma;
 KW systemic non-Hodgkin's lymphoma; primary central nervous system lymphoma;
 KW HSV; genital herpes; HZV; shingles; genital wart; cervical cancer;
 KW immunostimulatory CpG oligonucleotide; ss.
 XX
 OS Synthetic.
 XX US2004105872-A1.
 PN 03-JUN-2004.
 XX 17-SEP-2003; 2003US-00666022.
 XX 18-SEP-2002; 2002US-0411944P.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Klimman DM, Verthelyi D;
 XX WPI; 2004-419442/39.
 XX Increasing an immune response to an opportunistic infection e.g.
 PT bacterial infections in an immunocompromised subject involves
 PT administering immunostimulatory D oligodeoxynucleotide or an
 PT immunostimulatory K oligodeoxynucleotide.

XX Claim 21; SEQ ID NO 14; 64pp; English.

PS The invention describes a method of increasing an immune response to an

XX opportunistic infection in an immunocompromised subject involves

XX administering an immunostimulatory D oligodeoxynucleotide or an

XX immunostimulatory K oligodeoxynucleotide, where an antigenic epitope of a

XX polypeptide is not administered to the subject. The method is useful for

XX increasing an immune response to an opportunistic infection e.g.

XX infection with a lentivirus such as human immunodeficiency virus

XX (including HIV-1, HIV-2) e.g. AIDS; infection with Leishmania; bacterial

XX infections; fungal infections; viral infections; protozoan infections;

XX prion disease; and nucleoplasm in an immunocompromised subject or a

XX subject infected with a lentivirus. The bacterial infections include

XX salmonellosis, syphilis and neurosyphilis, tuberculosis and bacillary

XX angiomatosis, the fungal infections include aspergillosis, candidiasis,

XX coccidioidomycosis, cryptococcal meningitis, hepatitis B, and

XX histoplasmosis, the protozoal infections include cryptosporidiosis,

XX isosporiasis, microsporidiosis, pneumocystis carinii pneumonia and

XX toxoplasmosis, viral infections include cytomegalovirus, hepatitis,

XX herpes simplex, herpes zoster, human papilloma virus, molluscum

XX contagiosum, oral hairy leukoplakia and progressive multifocal

XX leukoencephalopathy and neoplasms include Kaposi's sarcoma, systemic non-

XX Hodgkin's lymphoma and primary central nervous system lymphoma. The

XX herpes simplex includes HSV, genital herpes. The herpes zoster includes

XX HHV and shingles. The human papilloma virus includes HPV, genital warts

XX and cervical cancer. The method stimulates immune responses to any

XX opportunistic infection in immunocompromised subjects. This sequence

XX represents an immunostimulatory CpG oligonucleotide sequence used to

XX increase immune response in the method of the invention.

XX Sequence 6 BP; 0 A; 3 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 83.3%; Score 5; DB 12; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.8e+08;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6

DB 1 GCCGG 5

RESULT 6

ADN96880/c

ID ADN96880 standard; DNA; 6 BP.

XX ADN96880;

XX 26-AUG-2004 (first entry)

XX Immunostimulatory CpG oligonucleotide seqid 14.

XX virucide; anti-HIV; antibacterial; fungicide; cerebroprotective;

XX tuberculostatic; anti-inflammatory; hepatotropic; cytostatic;

XX dermatological; bacterial growth inhibitor; immunostimulatory;

XX immune response; immunostimulatory; opportunistic infection;

XX lentivirus infection; human immunodeficiency virus infection; AIDS;

XX Leishmania infection; bacterial infection; fungal infection;

XX viral infection; protozoan infection; prion disease; nucleoplasm;

XX salmonellosis; syphilis; neurosyphilis; tuberculosis;

XX bacillary angiomatosis; aspergillosis; candidiasis; coccidioidomycosis;

XX cryptosporidiosis; hepatitis B; histoplasmosis; cryptosporidiosis;

XX toxoplasmosis; microsporidiosis; pneumocystis carinii pneumonia;

XX human papillomavirus; molluscum contagiosum; oral hairy leukoplakia;

XX progressive multifocal leukoencephalopathy; neoplasm; Kaposi's sarcoma;

XX systemic non-Hodgkin's lymphoma; primary central nervous system lymphoma;

XX HSV; genital herpes; HHV; shingles; genital wart; cervical cancer;

XX immunostimulatory CpG oligonucleotide; ss.

XX Synthetic.

OS US2004105872-A1.

XX

PN

XX 03-JUN-2004.

XX 17-SEP-2003; 2003US-00666022.

XX 18-SEP-2002; 2002US-0411944P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Klinman DM, Verthelyi D;

XX WPI; 2004-419442/39.

DR Increasing an immune response to an opportunistic infection e.g.

XX bacterial infections in an immunocompromised subject involves

XX administering immunostimulatory D oligodeoxynucleotide or an

XX immunostimulatory K oligodeoxynucleotide.

XX Claim 21; SEQ ID NO 14; 64pp; English.

XX The invention describes a method of increasing an immune response to an

XX opportunistic infection in an immunocompromised subject involves

XX administering an immunostimulatory D oligodeoxynucleotide or an

XX immunostimulatory K oligodeoxynucleotide, where an antigenic epitope of a

XX polypeptide is not administered to the subject. The method is useful for

XX increasing an immune response to an opportunistic infection e.g.

XX infection with a lentivirus such as human immunodeficiency virus

XX (including HIV-1, HIV-2) e.g. AIDS; infection with Leishmania; bacterial

XX infections; fungal infections; viral infections; protozoan infections;

XX prion disease; and nucleoplasm in an immunocompromised subject or a

XX subject infected with a lentivirus. The bacterial infections include

XX salmonellosis, syphilis and neurosyphilis, tuberculosis and bacillary

XX angiomatosis, the fungal infections include aspergillosis, candidiasis,

XX coccidioidomycosis, cryptococcal meningitis, hepatitis B, and

XX histoplasmosis, the protozoal infections include cryptosporidiosis,

XX isosporiasis, microsporidiosis, pneumocystis carinii pneumonia and

XX toxoplasmosis, viral infections include cytomegalovirus, hepatitis,

XX herpes simplex, herpes zoster, human papilloma virus, molluscum

XX contagiosum, oral hairy leukoplakia and progressive multifocal

XX leukoencephalopathy and neoplasms include Kaposi's sarcoma, systemic non-

XX Hodgkin's lymphoma and primary central nervous system lymphoma. The

XX herpes simplex includes HSV, genital herpes. The herpes zoster includes

XX HHV and shingles. The human papilloma virus includes HPV, genital warts

XX and cervical cancer. The method stimulates immune responses to any

XX opportunistic infection in immunocompromised subjects. This sequence

XX represents an immunostimulatory CpG oligonucleotide sequence used to

XX increase immune response in the method of the invention.

XX Sequence 6 BP; 0 A; 3 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 83.3%; Score 5; DB 12; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.8e+08;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCGG 6

DB 6 GCCGG 2

RESULT 7

ADN04836

ID ADN04836 standard; DNA; 6 BP.

XX ADN04836;

XX 26-AUG-2004 (first entry)

XX CpG oligonucleotide #109 tested for immunostimulatory activity.

XX Unmethylated CpG dinucleotide; immune response; T helper cell; Th;

XX immune activation; cytokine production; NK; B cell proliferation;

XX natural killer cell lytic activity; NK; B cell proliferation;

XX asthmatic disorder; autoimmune disorder; CpG associated disorder;

KW systemic lupus erythematosus; sepsis; inflammatory bowel disease;
 KW psoriasis; gingivitis; arthritis; Crohn's disease; Grave's disease;
 KW cancer; viral; fungal; bacterial; parasitic; antinflammatory;
 KW dermatological; immunosuppressive; antibacterial; antipsoriatic;
 KW antiarthritic; antithyroid; cytostatic; virucide; fungicide;
 KW antiparasitic; ss.
 XX
 OS Synthetic.
 XX
 XX US2004106568-A1.
 XX
 XX 03-JUN-2004.
 XX
 XX 25-JUL-2003; 2003US-00627331.
 XX
 XX 15-JUL-1994; 94US-00276358.
 PR 07-FEB-1995; 95US-00386063.
 PR 30-OCT-1996; 96US-00738652.
 PR 30-OCT-1997; 97US-00960774.
 PR 31-JUL-2000; 2000US-00630319.
 PR 02-JUL-2002; 2002US-00187489.
 XX
 XX (IOWA) UNIV IOWA RES FOUND.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (COLE-) COLEY PHARM GROUP INC.
 XX
 PI Krieg AM, Klinman D, Steinberg AD;
 XX
 DR WPI; 2004-419485/39.
 XX
 XX New nucleic acid sequence containing unmethylated cytosine-guanine (CpG)
 PT dinucleotide, useful for modulating immune response, e.g. stimulating Th1
 PT pattern of immune activation, cytokine production, or B cell
 PT proliferation.
 XX
 XX Disclosure; SEQ ID NO 109; 72pp; English.
 XX
 CC The present invention relates to oligonucleotide sequences containing at
 CC least one unmethylated CpG dinucleotide that are able of modulating an
 CC immune response such as stimulating T helper cell (Th) pattern of immune
 CC activation, cytokine production, natural killer cell (NK) lytic activity,
 CC and B cell proliferation in a subject, preferably human. The
 CC immunostimulatory oligonucleotides of the invention are useful for
 CC treating aschmatic disorders, autoimmune or other CpG associated
 CC disorders (e.g. systemic lupus erythematosus, sepsis, inflammatory bowel
 CC disease, psoriasis, gingivitis, arthritis, Crohn's disease, Grave's
 CC disease), cancer, and viral, fungal, bacterial, and parasitic diseases.
 CC The present sequence represents an unmethylated CpG dinucleotide
 CC oligonucleotide that is tested for its ability to modulate an immune
 CC response.
 XX
 XX Sequence 6 BP; 0 A; 2 C; 3 G; 1 T; 0 U; 0 Other;
 SQ
 Query Match 83.3%; Score 5; DB 12; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.8e+08;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GCCGG 6
 Db 1 GCCGG 5
 |||||
 RESULT 8
 ADR34424
 ID ADR34424 standard; DNA; 6 BP.
 XX
 AC ADR34424;
 XX
 XX 04-NOV-2004 (first entry)
 DT
 XX Human nicking agent DNA containing BstNBI restriction site #844.
 DE
 XX ss; nicking agent; assay panel; diagnosis; expression pattern;
 KW

KW DNA fingerprinting; nosocomial infection; microbiological assay;
 KW bacterial contamination; genome mapping; bioremediation.
 XX
 OS Homo sapiens.
 XX
 PN WO2004067765-A2.
 XX
 PD 12-AUG-2004.
 XX
 XX 29-JAN-2004; 2004WO-US002720.
 PF
 XX 29-JAN-2003; 2003US-0443811P.
 PR
 XX (KECK-) KECK GRADUATE INST.
 PA
 XX Van Ness J, Galas DJ, Van Ness LK;
 PI
 XX WPI; 2004-581010/56.
 DR
 XX Identifying nucleic acid sample source, useful for identifying bacterial
 PT strains involved in nosocomial infections, comprises treating the nucleic
 PT acid sample with components comprising a nicking agent under nicking
 PT conditions.
 XX
 XX Example 3; Page 105-219; 238pp; English.
 PS
 XX The invention relates to a method of treating a nucleic acid sample with
 CC components under nicking conditions, where the components comprise a
 CC nicking agent, and the conditions cause the nicking agent to nick the
 CC nucleic acid sample to thus produce a family of initiating
 CC oligonucleotide fragments, and subjecting one or more members of the
 CC family of initiating oligonucleotide fragments to a characterization
 CC process to thus provide results. The method is useful for creating an
 CC assay panel of diagnostic oligonucleotides that can identify any organism
 CC or individual. The method is useful for characterizing other DNA
 CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
 CC The method, kit or composition is useful for identifying the source
 CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
 CC non-human animal or human. The method is particularly useful for rapidly
 CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
 CC subspecies, and especially strains or individuals of the subspecies. It
 CC is especially useful for identifying different bacterial strains involved
 CC in e.g., nosocomial infections. Furthermore, the method is useful for
 CC diagnosing bacterial disease in plants and humans, monitoring for
 CC bacterial content and/or contamination in the environment, monitoring
 CC food for bacterial contamination, monitoring manufacturing processes for
 CC bacterial contamination, monitoring quality assurance/quality control of
 CC laboratory tests involving microbiological assays, tracing bacterial
 CC contamination and/or outbreaks of bacterial infections, genome mapping,
 CC monitoring bioremediation sites, and for monitoring agricultural sites
 CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-
 CC ADR37496 correspond to target nucleic acids containing an NBstNBI
 CC restriction site and used in the method of the invention.
 XX
 XX Sequence 6 BP; 0 A; 2 C; 2 G; 1 T; 0 U; 1 Other;
 SQ
 Query Match 76.7%; Score 4.6; DB 13; Length 6;
 Best Local Similarity 80.0%; Pred. No. 9.8e+08;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GCCGG 6
 Db 2 GCCGG 6
 |||||
 RESULT 9
 ADR34422
 ID ADR34422 standard; DNA; 6 BP.
 XX
 AC ADR34422;
 XX
 XX 04-NOV-2004 (first entry)
 DT
 XX

DE Human nicking agent DNA containing BstNBI restriction site #842.
XX
XX ss; nicking agent; assay panel; diagnosis; expression pattern;
KW DNA fingerprinting; nosocomial infection; microbiological assay;
KW bacterial contamination; genome mapping; bioremediation.
XX
XX Homo sapiens.
PN WO2004067765-A2.
XX
XX 12-AUG-2004.
PD
XX 29-JAN-2004; 2004WO-US002720.
PF
XX 29-JAN-2003; 2003US-0443811P.
PR
XX (KECK-) KECK GRADUATE INST.
PA
XX Van Ness J, Galas DJ, Van Ness LK;
PI WPI; 2004-581010/56.
XX
XX Identifying nucleic acid sample source, useful for identifying bacterial
PT strains involved in nosocomial infections, comprises treating the nucleic
PT acid sample with components comprising a nicking agent under nicking
PT conditions.
XX
XX Example 3; Page 105-219; 238pp; English.
PS
XX The invention relates to a method of treating a nucleic acid sample with
CC components under nicking conditions, where the components comprise a
CC nicking agent, and the conditions cause the nicking agent to nick the
CC nucleic acid sample to thus produce a family of initiating
CC oligonucleotide fragments, and subjecting one or more members of the
CC family of initiating oligonucleotide fragments to a characterization
CC process to thus provide results. The method is useful for creating an
CC assay panel of diagnostic oligonucleotides that can identify any organism
CC or individual. The method is useful for characterizing other DNA
CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC The method, kit or composition is useful for identifying the source
CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC non-human animal or human. The method is particularly useful for rapidly
CC fingerprinting DNA to identifying prokaryotic and eukaryotic species.
CC It is especially useful for identifying different bacterial strains involved
CC in e.g., nosocomial infections. Furthermore, the method is useful for
CC diagnosing bacterial disease in plants and humans, monitoring for
CC bacterial content and/or contamination in the environment, monitoring
CC food for bacterial contamination, monitoring quality assurance/quality control of
CC laboratory tests involving microbiological assays, tracing bacterial
CC contamination and/or outbreaks of bacterial infections, genome mapping,
CC monitoring bioremediation sites, and for monitoring agricultural sites
CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-
CC ADR37496 correspond to target nucleic acids containing an NBstNBI
CC restriction site and used in the method of the invention.
XX
XX Sequence 6 BP; 0 A; 2 C; 2 G; 1 T; 0 U; 1 Other;
SQ
Query Match 76.7%; Score 4.6; DB 13; Length 6;
Best Local Similarity 80.0%; Pred. No. 9.8e+08;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 GCCGG 6
DB 2 GCCSG 6
|||:|
|||:|
RESULT 10
ADR34423
ID ADR34423 standard; DNA; 6 BP.
XX
XX AC ADR34423;

XX
DT 04-NOV-2004 (first entry)
DE Human nicking agent DNA containing BstNBI restriction site #843.
XX
XX ss; nicking agent; assay panel; diagnosis; expression pattern;
KW DNA fingerprinting; nosocomial infection; microbiological assay;
KW bacterial contamination; genome mapping; bioremediation.
XX
XX Homo sapiens.
OS
XX WO2004067765-A2.
PN
XX 12-AUG-2004.
PD
XX 29-JAN-2004; 2004WO-US002720.
PF
XX 29-JAN-2003; 2003US-0443811P.
PR
XX (KECK-) KECK GRADUATE INST.
PA
XX Van Ness J, Galas DJ, Van Ness LK;
PI WPI; 2004-581010/56.
XX
XX Identifying nucleic acid sample source, useful for identifying bacterial
PT strains involved in nosocomial infections, comprises treating the nucleic
PT acid sample with components comprising a nicking agent under nicking
PT conditions.
XX
XX Example 3; Page 105-219; 238pp; English.
PS
XX The invention relates to a method of treating a nucleic acid sample with
CC components under nicking conditions, where the components comprise a
CC nicking agent, and the conditions cause the nicking agent to nick the
CC nucleic acid sample to thus produce a family of initiating
CC oligonucleotide fragments, and subjecting one or more members of the
CC family of initiating oligonucleotide fragments to a characterization
CC process to thus provide results. The method is useful for creating an
CC assay panel of diagnostic oligonucleotides that can identify any organism
CC or individual. The method is useful for characterizing other DNA
CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC The method, kit or composition is useful for identifying the source
CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC non-human animal or human. The method is particularly useful for rapidly
CC fingerprinting DNA to identifying prokaryotic and eukaryotic species.
CC It is especially useful for identifying different bacterial strains involved
CC in e.g., nosocomial infections. Furthermore, the method is useful for
CC diagnosing bacterial disease in plants and humans, monitoring for
CC bacterial content and/or contamination in the environment, monitoring
CC food for bacterial contamination, monitoring quality assurance/quality control of
CC laboratory tests involving microbiological assays, tracing bacterial
CC contamination and/or outbreaks of bacterial infections, genome mapping,
CC monitoring bioremediation sites, and for monitoring agricultural sites
CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-
CC ADR37496 correspond to target nucleic acids containing an NBstNBI
CC restriction site and used in the method of the invention.
XX
XX Sequence 6 BP; 0 A; 2 C; 2 G; 1 T; 0 U; 1 Other;
SQ
Query Match 76.7%; Score 4.6; DB 13; Length 6;
Best Local Similarity 80.0%; Pred. No. 9.8e+08;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 GCCGG 6
DB 2 GCCSG 6
|||:|
|||:|
RESULT 11
ADR34421

ID ADR34421 standard; DNA; 6 BP.
 AC ADR34421;
 XX
 DT 04-NOV-2004 (first entry)
 XX
 DE Human nicking agent DNA containing BstNBI restriction site #841.
 XX
 KW ss; nicking agent; assay panel; diagnosis; expression pattern;
 KW DNA fingerprinting; nosocomial infection; microbiological assay;
 KW bacterial contamination; genome mapping; bioremediation.
 XX
 OS Homo sapiens.
 XX
 PN WO2004067765-A2.
 XX
 XX 12-AUG-2004.
 XX
 XX 29-JAN-2004; 2004WO-US002720.
 XX
 XX 29-JAN-2003; 2003US-0443811P.
 PR (KECK-) KECK GRADUATE INST.
 XX
 PA Van Ness J, Galas DJ, Van Ness LK;
 XX
 PI WPI; 2004-591010/56.
 XX
 DR Identifying nucleic acid sample source, useful for identifying bacterial
 XX strains involved in nosocomial infections, comprises treating the nucleic
 PT acid sample with components comprising a nicking agent under nicking
 PT conditions.
 XX
 PS Example 3; Page 105-219; 238pp; English.
 XX
 CC The invention relates to a method of treating a nucleic acid sample with
 CC components under nicking conditions, where the components comprise a
 CC nicking agent, and the conditions cause the nicking agent to nick the
 CC nucleic acid sample to thus produce a family of initiating
 CC oligonucleotide fragments, and subjecting one or more members of the
 CC family of initiating oligonucleotide fragments to a characterization
 CC process to thus provide results. The method is useful for creating an
 CC assay panel of diagnostic oligonucleotides that can identify any organism
 CC or individual. The method is useful for characterizing other DNA
 CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
 CC The method, kit or composition is useful for identifying the source
 CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
 CC non-human animal or human. The method is particularly useful for rapidly
 CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
 CC subspecies, and especially strains or individuals of the subspecies. It
 CC is especially useful for identifying different bacterial strains involved
 CC in e.g., nosocomial infections. Furthermore, the method is useful for
 CC diagnosing bacterial disease in plants and humans, monitoring for
 CC bacterial content and/or contamination in the environment, monitoring
 CC food for bacterial contamination, monitoring quality assurance processes for
 CC bacterial contamination, monitoring quality assurance/control of
 CC laboratory tests involving microbiological assays, tracing bacterial
 CC contamination and/or outbreaks of bacterial infections, genome mapping,
 CC monitoring bioremediation sites, and for monitoring agricultural sites
 CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-
 CC ADR37496 correspond to target nucleic acids containing an NBstNBI
 XX restriction site and used in the method of the invention.
 XX
 SQ Sequence 6 BP; 0 A; 2 C; 2 G; 1 T; 0 U; 1 Other;
 XX
 Query Match 76.7%; Score 4.6; DB 13; Length 6;
 Best Local Similarity 80.0%; Pred. No. 9.8e+08;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GCGCG 6
 |||||
 Db 2 GCGCG 6
 ADR34421 standard; DNA; 6 BP.
 AC ADR34421;
 XX
 DT 04-NOV-2004 (first entry)
 XX
 DE Human nicking agent DNA containing BstNBI restriction site #841.
 XX
 KW ss; nicking agent; assay panel; diagnosis; expression pattern;
 KW DNA fingerprinting; nosocomial infection; microbiological assay;
 KW bacterial contamination; genome mapping; bioremediation.
 XX
 OS Homo sapiens.
 XX
 PN WO2004067765-A2.
 XX
 XX 12-AUG-2004.
 XX
 XX 29-JAN-2004; 2004WO-US002720.
 XX
 XX 29-JAN-2003; 2003US-0443811P.
 PR (KECK-) KECK GRADUATE INST.
 XX
 PA Van Ness J, Galas DJ, Van Ness LK;
 XX
 PI WPI; 2004-591010/56.
 XX
 DR Identifying nucleic acid sample source, useful for identifying bacterial
 XX strains involved in nosocomial infections, comprises treating the nucleic
 PT acid sample with components comprising a nicking agent under nicking
 PT conditions.
 XX
 PS Example 3; Page 105-219; 238pp; English.
 XX
 CC The invention relates to a method of treating a nucleic acid sample with
 CC components under nicking conditions, where the components comprise a
 CC nicking agent, and the conditions cause the nicking agent to nick the
 CC nucleic acid sample to thus produce a family of initiating
 CC oligonucleotide fragments, and subjecting one or more members of the
 CC family of initiating oligonucleotide fragments to a characterization
 CC process to thus provide results. The method is useful for creating an
 CC assay panel of diagnostic oligonucleotides that can identify any organism
 CC or individual. The method is useful for characterizing other DNA
 CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
 CC The method, kit or composition is useful for identifying the source
 CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
 CC non-human animal or human. The method is particularly useful for rapidly
 CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
 CC subspecies, and especially strains or individuals of the subspecies. It
 CC is especially useful for identifying different bacterial strains involved
 CC in e.g., nosocomial infections. Furthermore, the method is useful for
 CC diagnosing bacterial disease in plants and humans, monitoring for
 CC bacterial content and/or contamination in the environment, monitoring
 CC food for bacterial contamination, monitoring quality assurance processes for
 CC bacterial contamination, monitoring quality assurance/control of
 CC laboratory tests involving microbiological assays, tracing bacterial
 CC contamination and/or outbreaks of bacterial infections, genome mapping,
 CC monitoring bioremediation sites, and for monitoring agricultural sites
 CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-
 CC ADR37496 correspond to target nucleic acids containing an NBstNBI
 XX restriction site and used in the method of the invention.
 XX
 SQ Sequence 6 BP; 0 A; 2 C; 2 G; 1 T; 0 U; 1 Other;
 XX
 Query Match 76.7%; Score 4.6; DB 13; Length 6;
 Best Local Similarity 80.0%; Pred. No. 9.8e+08;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GCGCG 6
 |||||
 Db 2 GCGCG 6

RESULT 12
 AAF91686/c
 ID AAF91686 standard; DNA; 6 BP.
 XX
 AC AAF91686;
 XX
 DT 10-MAY-2001 (first entry)
 XX
 DE Breast-cancer associated protein isoform BPI-42 preferred probe #10.
 KW Human; breast cancer; breast cancer associated protein isoform; BPI;
 KW breast cancer associated feature; BF; diagnosis; cytostatic; probe; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200113117-A2.
 XX
 XX 22-FEB-2001.
 XX
 XX 14-AUG-2000; 2000WO-GB003143.
 PF 13-AUG-1999; 99GB-00019258.
 PR 30-MAR-2000; 2000GB-00007754.
 XX
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 PA
 XX Herath HMAC;
 PI
 XX WPI; 2001-211252/21.
 DR
 XX Screening, diagnosis or prognosis of breast cancer, by analyzing a sample
 PT of serum or plasma by two dimensional electrophoresis to detect the
 PT presence or level of a breast cancer-associated feature.
 XX
 PS Claim 152; Page 42; 146pp; English.
 XX
 CC The present invention describes a method for the screening, diagnosis or
 CC prognosis of breast cancer (BC), determining the stage or severity of BC,
 CC and monitoring the effect of therapy administered to a subject having BC,
 CC comprising analysing a sample of body fluid by two dimensional
 CC electrophoresis to generate a two-dimensional array of features,
 CC comprising a chosen feature whose relative abundance correlates with BC
 CC or predicts the onset of BC; and (b) comparing the abundance of each
 CC chosen feature in the sample with the abundance of that chosen feature in
 CC the body fluid from one or more persons free from BC, or with a
 CC previously determined reference range for that feature in subjects free
 CC from BC, or with the abundance of an expression reference feature (ERF)
 CC in the test sample. The method is useful for screening, diagnosis or
 CC prognosis of breast cancer, determining the stage or severity of BC,
 CC monitoring the effect of therapy administered to a subject having BC, and
 CC for identifying a subject at risk of developing BC. AAB87186 to AAB87340
 CC represents breast cancer associated protein isoform (BPI) peptide
 CC sequences, and AAF91643 to AAF91848 represent BPI probes used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 6 BP; 0 A; 5 C; 1 G; 0 T; 0 U; 0 Other;
 XX
 Query Match 73.3%; Score 4.4; DB 4; Length 6;
 Best Local Similarity 83.3%; Pred. No. 9.8e+08;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GCGCG 6
 |||||
 Db 6 GCGCG 1

RESULT 13
 ABR87321/c

XX 06-JUN-1995; 95US-00471968.
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA (HYBR-) HYBRIDON INC.
XX Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
PI Roberts PC, Walther DM, Wolfe JL;
XX WPI; 1997-043122/04.
DR Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
carcinoma.
XX Claim 1; Page 18; 100pp; English.
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides
CC which are complementary to a portion of the 5' untranslated region (UTR)
CC of hepatitis C virus (HCV). These sequences may be used in a
CC pharmaceutical composition for the control or prevention of HCV
CC infection. They may be used to inhibit replication or expression of HCV
CC or for detecting the presence of HCV in a sample. They may be used to
CC inhibit HCV replication in a cell and are therefore useful in the
CC treatment of HCV infections such as chronic and acute hepatitis and
CC hepatocarcinoma
XX Sequence 6 BP; 1 A; 3 C; 2 G; 0 T; 0 U; 0 Other;
SQ Query Match 66.7%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.8e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 CCGG 6
DB ||||
3 CCGG 6
RESULT 21
AAT80319/C
ID AAT80319 standard; DNA; 6 BP.
XX AAT80319;
AC AAT80319;
XX 16-OCT-1997 (first entry)
DT Oligo HCV-215, targetted to HCV mRNA position +235 to +240.
DE Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
KW inhibition; replication; expression; detection; chronic hepatitis;
KW acute hepatitis; hepatocarcinoma; ss.
XX Synthetic.
OS Synthetic.
FH Key Location/Qualifiers
FT modified_base 1..6
FT /*tag= a
FT /note= "Comprises phosphorothioate linkages"
XX W09639500-A2.
PN W09639500-A2.
XX 12-DEC-1996.
PD 12-DEC-1996.
XX 04-JUN-1996; 96WO-EP002427.
PF 04-JUN-1996; 96WO-EP002427.
XX 06-JUN-1995; 95US-00471968.
PR (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA (HYBR-) HYBRIDON INC.
XX Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
PI Roberts PC, Walther DM, Wolfe JL;
XX

DR WPI; 1997-043122/04.
XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
carcinoma.
XX Claim 1; Page 18; 100pp; English.
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides
CC which are complementary to a portion of the 5' untranslated region (UTR)
CC of hepatitis C virus (HCV). These sequences may be used in a
CC pharmaceutical composition for the control or prevention of HCV
CC infection. They may be used to inhibit replication or expression of HCV
CC or for detecting the presence of HCV in a sample. They may be used to
CC inhibit HCV replication in a cell and are therefore useful in the
CC treatment of HCV infections such as chronic and acute hepatitis and
CC hepatocarcinoma
XX Sequence 6 BP; 1 A; 3 C; 2 G; 0 T; 0 U; 0 Other;
SQ Query Match 66.7%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.8e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 CCGG 6
DB ||||
3 CCGG 6
RESULT 22
AAT77251
ID AAT77251 standard; DNA; 6 BP.
XX AAT77251;
AC AAT77251;
XX 18-MAR-1998 (first entry)
DT 18-MAR-1998 (first entry)
DE Immunostimulatory polynucleotide 10.
XX Immunostimulatory polynucleotide; ISP; palindrome; vaccine;
KW immune response; antigen; naked gene expression vector; Ig; antibody;
KW immunotherapy; ss.
XX Synthetic.
OS Synthetic.
XX W09728259-A1.
PN W09728259-A1.
XX 07-AUG-1997.
PD 07-AUG-1997.
XX 28-JAN-1997; 97WO-US001277.
PF 28-JAN-1997; 97WO-US001277.
XX 30-JAN-1996; 96US-00593554.
PR 30-JAN-1996; 96US-00593554.
XX (REGC) UNIV CALIFORNIA.
PA (REGC) UNIV CALIFORNIA.
XX Carson DA, Raz E;
PI Carson DA, Raz E;
XX WPI; 1997-402613/37.
DR WPI; 1997-402613/37.
XX Recombinant vector containing immunostimulatory palindromic
PT polynucleotide - useful for selectively enhancing the Th1 immune response
PT in a host, whilst reducing the risk of anaphylaxis.
XX Claim 16; Page 15; 102pp; English.
XX This sequence represents a non-coding immunostimulatory polynucleotide
CC (ISP) comprised of at least one strand of a palindrome, which includes at
CC least one dinucleotide consisting of adjacent, unmethylated cytosine and
CC guanine residues. ISP's could be used in vaccination methods for
CC enhancing the immune response of a host to an antigen. Administration of
CC naked gene expression vectors which encode antigens or their
CC immunostimulatory fragments suppresses IgE antibody production reducing
CC the risk of anaphylaxis posed by conventional immunotherapy

PR 19-MAY-1997; 97US-0047121P.
 XX (MERI) MERCK & CO INC.
 XX Caulfield MJ;
 XX WPI; 1999-131687/11.
 XX
 PT New oligonucleotide vaccine adjuvants that generate cell
 PT mediated/antibody responses in animals - useful in the vaccination of
 PT animals.
 XX
 XX Claim 1; Page 37; 42pp; English.
 XX
 CC The invention relates to an oligonucleotide vaccine adjuvant for
 CC generating a cell mediated/antibody response in an animal, comprising one
 CC of the sequences shown in AAX21979-X21981. The oligonucleotide adjuvant
 CC forms a method of vaccinating animals. The antigen can be any derivative
 CC of hepatitis B, hepatitis C virus, hepatocellular carcinoma antigens
 CC induced by hepatitis B virus, rotavirus, HIV proteins, varicella, and
 CC antigens derived from bacteria or humans/animals. The oligonucleotide
 CC adjuvants provide a method of eliciting a cytotoxic T lymphocyte (CTL)
 CC response to an antigen presented in a vaccine. CTLs are known to kill
 CC viral or bacterial infected cells
 XX
 XX Sequence 6 BP; 1 A; 2 C; 2 G; 1 T; 0 U; 0 Other;
 SQ
 Query Match 66.7%; Score 4; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.8e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 CCGG 6
 DB ||||
 5 CCGG 2

RESULT 26
 AAF91710/c
 ID AAF91710 standard; DNA; 6 BP.
 XX
 AC AAF91710;
 DT 10-MAY-2001 (first entry)
 XX
 XX Breast-cancer associated protein isoform BPI-42 degenerate probe #10.
 DE
 XX Human; breast cancer; breast cancer associated protein isoform; BPI;
 KW breast cancer associated feature; BF; diagnosis; cytostatic; probe; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200113117-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 14-AUG-2000; 2000WO-GB003143.
 XX
 PR 13-AUG-1999; 99GB-00019258.
 XX
 PR 30-MAR-2000; 2000GB-00007754.
 XX
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX
 PI Herath HMAc;
 XX
 XX WPI; 2001-211252/21.
 DR
 XX
 PT Screening, diagnosis or prognosis of breast cancer, by analyzing a sample
 PT of serum or plasma by two dimensional electrophoresis to detect the
 PT presence or level of a breast cancer-associated feature.
 XX
 PS Claim 144; Page 42; 146pp; English.
 XX
 CC The present invention describes a method for the screening, diagnosis or

CC prognosis of breast cancer (BC), determining the stage or severity of BC,
 CC and monitoring the effect of therapy administered to a subject having BC,
 CC comprising analysing a sample of body fluid by two dimensional
 CC electrophoresis to generate a two-dimensional array of features,
 CC comprising a chosen feature whose abundance correlates with BC or
 CC predicts the onset or course of BC. The method (I) involves: (a)
 CC analysing a sample of body fluid from the subject by two-dimensional
 CC electrophoresis to generate a two-dimensional array of features,
 CC comprising a chosen feature whose relative abundance correlates with BC
 CC or predicts the onset of BC; and (b) comparing the abundance of each
 CC chosen feature in the sample with the abundance of that chosen feature in
 CC the body fluid from one or more persons free from BC, or with a
 CC previously determined reference range for that feature in subjects free
 CC from BC, or with the abundance of an expression reference feature (ERF)
 CC in the test sample. The method is useful for screening, diagnosis or
 CC prognosis of breast cancer, determining the stage or severity of BC,
 CC monitoring the effect of therapy administered to a subject having BC, and
 CC for identifying a subject at risk of developing BC. AAB87186 to AAB87340
 CC represents breast cancer associated protein isoform (BPI) peptide
 CC sequences, and AAF91643 to AAF91848 represent BPI probes used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 6 BP; 0 A; 3 C; 1 G; 0 T; 0 U; 2 Other;
 Query Match 66.7%; Score 4; DB 4; Length 6;
 Best Local Similarity 80.0%; Pred. No. 9.8e+08;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 GCCGG 6
 DB ||||
 5 GCNGG 1

RESULT 27
 ABS65903
 ID ABS65903 standard; DNA; 6 BP.
 XX
 AC ABS65903;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Inhibitory oligonucleotide specific for hepatitis C virus #109.
 XX
 KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;
 KW non-B hepatitis; acute hepatitis; chronic hepatitis;
 KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;
 KW gene therapy; ss.
 XX
 OS Synthetic.
 XX
 PN US2002081577-A1.
 XX
 PD 27-JUN-2002.
 XX
 PF 02-JUL-1997; 97US-00887505.
 XX
 PR 06-JUN-1995; 95US-00471968.
 PR 02-JUL-1996; 96US-0021104P.
 XX
 PA (KILK/) KILKUSKIE R L.
 PA (FRAN/) FRANK B L.
 PA (GOOD/) GOODCHILD J.
 PA (WOLF/) WOLFE J L.
 PA (ROBE/) ROBERTS P C.
 PA (HAML/) HAMLIN H A.
 PA (ROBE/) ROBERTS N A.
 PA (WALT/) WALTHER D M.
 XX
 XX Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;
 PI Hamlin HA, Roberts NA, Walther DW;
 XX WPI; 2002-537132/57.
 DR
 XX

CC in one reaction vessel. (M) is useful for determining a developmental or
 CC physiological stage of an organism (especially a plant). (M) is
 CC particularly useful for expression profiling for use in testing plant
 CC quality of horticultural and agricultural products. With quality loss,
 CC e.g. stress-induced senescence, oxidative damage or desiccation, the
 CC plant tissues will go through various physiological stages, in which
 CC different genes are switched on or off. The level of expression of these
 CC marker genes reflects the physiological stage and therefore the condition
 CC and quality of the plant and/or product. Quality of fresh products is
 CC generally judged on subjective criteria that usually involves visual
 CC examination. The present invention provides a way of taking objective
 CC quantitative measurements using biotechnology: there is a direct relation
 CC between the pattern of gene expression at the RNA and protein level, and
 CC the physiological status of a cell. The present sequence represents a
 CC cucumber BGL target sequence, which is used in an example from the
 CC present invention
 XX
 SQ Sequence 6 BP; 2 A; 2 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.8e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCC 4
 ||||
 Db 3 GGCC 6

RESULT 30
 ACC69109/C
 ID ACC69109 standard; DNA; 6 BP.
 XX
 AC ACC69109;
 XX
 DT 10-JUL-2003 (first entry)
 XX
 DE Cucumber BGL related target sequence SEQ ID NO:16.

XX Cucumber; expression profiling; DNA sequencing; plant; developmental;
 KW physiological; horticultural; agricultural; target; ss.

XX Cucumis sp.
 OS Synthetic.

XX EP1295950-A1.

PN 26-MAR-2003.

XX 25-SEP-2001; 2001EP-00203617.

XX 25-SEP-2001; 2001EP-00203617.

XX (GTDI-) GT DIAGNOSTICS BV.

XX Langeveld SA, Van Der Kop DAM, De Boer AD;

XX WPI; 2003-383798/37.

XX Determining developmental/physiological stage of organism (especially in
 PT plants); comprises determining expression of first and second genes by
 PT hybridizing nucleic acid templates derived from the genes with specific
 PT primers.

XX Example; Fig 1A; 27pp; English.

XX The present invention describes a method (M) for determining a
 CC developmental or physiological stage of an organism by determining
 CC expression of a first and second gene (I)-(II), respectively, or gene
 CC fragment. (M) comprises: (a) providing first and second nucleic acid
 CC templates (T1)-(T2) derived from (I) and (II), respectively; (b)
 CC hybridizing first and second primers (P1)-(P2) to (T1) and (T2),
 CC respectively; and (c) determining binding of the primers to the templates
 CC in one reaction vessel. (M) is useful for determining a developmental or

CC physiological stage of an organism (especially a plant). (M) is
 CC particularly useful for expression profiling for use in testing plant
 CC quality of horticultural and agricultural products. With quality loss,
 CC e.g. stress-induced senescence, oxidative damage or desiccation, the
 CC plant tissues will go through various physiological stages, in which
 CC different genes are switched on or off. The level of expression of these
 CC marker genes reflects the physiological stage and therefore the condition
 CC and quality of the plant and/or product. Quality of fresh products is
 CC generally judged on subjective criteria that usually involves visual
 CC examination. The present invention provides a way of taking objective
 CC quantitative measurements using biotechnology: there is a direct relation
 CC between the pattern of gene expression at the RNA and protein level, and
 CC the physiological status of a cell. The present sequence represents a
 CC cucumber BGL target sequence, which is used in an example from the
 CC present invention
 XX
 SQ Sequence 6 BP; 2 A; 2 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.8e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCC 4
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 Db 6 GGCC 3

Search completed: July 20, 2005, 22:59:07
 Job time : 189.4 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 21:47:48 ; Search time 738.2 Seconds
(without alignments)
393.838 Million cell updates/sec

Title: US-09-735-363A-43
Perfect score: 6
Sequence: 1 ggcggg 6

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 4754

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_hgt.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sta.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	100.0	6	6	AX175279 Sequence
2	5	83.3	5	6	AX359007 Sequence
3	5	83.3	6	6	BD194759 Homogeneo
C 4	5	83.3	6	6	BD194759 Homogeneo
5	5	83.3	6	6	BD244954 Targeted
C 6	5	83.3	6	6	BD244954 Targeted
7	5	83.3	6	6	BD244964 Targeted
C 8	5	83.3	6	6	BD244964 Targeted
C 9	5	83.3	6	6	CQ755690 Sequence
10	5	83.3	6	6	CQ755696 Sequence
C 11	5	83.3	6	6	CQ755696 Sequence
C 12	5	83.3	6	6	CQ755711 Sequence
13	5	83.3	6	6	CQ755712 Sequence
C 14	5	83.3	6	6	CQ755722 Sequence
C 15	5	83.3	6	6	CQ755767 Sequence
C 16	5	83.3	6	6	CQ755774 Sequence
C 17	5	83.3	6	6	CQ755824 Sequence
18	5	83.3	6	6	CQ755877 Sequence
C 19	5	83.3	6	6	CQ755877 Sequence

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c 93      4 66.7 4 6 BD002075 BD002075 Method of
94      4 66.7 5 6 E12350 E12350 Oligoribonu
95      4 66.7 5 6 AX103515 AX103515 Sequence
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c 100     4 66.7 5 6 AX155668 AX155668 Sequence

ALIGNMENTS

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LOCUS      AX175279          6 bp      DNA      linear      PAT 03-JUL-2001
DEFINITION Sequence 43 from Patent WO0144465.
ACCESSION  AX175279
VERSION     .
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 6)
AUTHORS     Phillips,N.C. and Filion,M.C.
TITLE       Therapeutically useful synthetic oligonucleotides
JOURNAL     Patent: WO 0144465-A 43 21-JUN-2001;
            Bioniche Life Sciences Inc. (CA)
FEATURES    source
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QY      1 GCCCGG 6
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RESULT 2
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LOCUS      AX359007          5 bp      DNA      linear      PAT 13-FEB-2002
DEFINITION Sequence 14 from Patent WO0183737.
ACCESSION  AX359007
VERSION     AX359007.1 GI:18675406
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Nagy,E., Tuboly,T. and Nagy,M.
TITLE       Porcine adenovirus vaccine
JOURNAL     Patent: WO 0183737-A 14 08-NOV-2001;
            UNIVERSITY OF GUELPH (CA)
FEATURES    source
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us-09-735-363a-43.szlm6.rge

Db      1 GCCGG 5

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LOCUS      BD194759          6 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Homogeneous diagnostic assay method utilizing simultaneous target
            and signal amplification.
ACCESSION  BD194759
VERSION     BD194759.1 GI:33004506
KEYWORDS    JP 2002515749-A/24.
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE   1 (bases 1 to 6)
AUTHORS     Hepp,J., Lengyel,Z., Pande,R., Botyanszki,J. and Toth,M.S.
TITLE       Homogeneous diagnostic assay method utilizing simultaneous target
            and signal amplification
JOURNAL     Patent: JP 2002515749-A 24 28-MAY-2002;
            NAVIX INC
COMMENT     OS Unidentified
            PN JP 2002515749-A/24
            PD 28-MAY-2002
            PF 16-JUL-1997 JP 1998508863
            PR 25-JUL-1996 US 08/692825
            PI JOZSEF HEPP,ZSOLT LENGYEL,RAJIV PANDE,JANOS BOTYANSZKI,MIKLOS
            PI SAHIN TOTH
            PC C12Q1/68
            CC Strandedness: Single;
            CC Topology: Linear;
            CC Homogeneous diagnostic assay method utilizing simultaneous CC
            CC signal amplification
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DEFINITION Homogeneous diagnostic assay method utilizing simultaneous target
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ACCESSION  BD194759
VERSION     BD194759.1 GI:33004506
KEYWORDS    JP 2002515749-A/24.
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE   1 (bases 1 to 6)
AUTHORS     Hepp,J., Lengyel,Z., Pande,R., Botyanszki,J. and Toth,M.S.
TITLE       Homogeneous diagnostic assay method utilizing simultaneous target
            and signal amplification
JOURNAL     Patent: JP 2002515749-A 24 28-MAY-2002;
            NAVIX INC
COMMENT     OS Unidentified
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PR	25-JUL-1996	US	08/692825	JOSSEF HEPB,ZSOLT LENGUEL,RAJIV PANDE,JANOS BOTYANSZKI,MIKLOS SAHIN TOTTH
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ACCESSION	BD244954			
VERSION	BD244954.1	GI:33054724		
KEYWORDS	JP 2002528088-A/8.			
SOURCE	Escherichia coli			
ORGANISM	Escherichia coli			
REFERENCE	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.			
AUTHORS	1 (bases 1 to 6)			
TITLE	Russell,D.W. and Hirata,R.K.			
JOURNAL	Targeted gene modification by parvoviral vectors			
COMMENT	Patent: JP 2002528088-A 8 03-SEP-2002; UNIVERSITY OF WASHINGTON			
	OS Escherichia coli			
	PN JP 2002528088-A/8			
	PD 03-SEP-2002			
	PF 27-OCT-1999 JP 2000578469			
	PR 28-OCT-1998 US 60/106191			
	PI DAVID W RUSSELL,ROLI K HIRATA			
	PC C12N15/09,A01K67/027,A61K48/00,C12N5/10,C12Q1/68//A61K35/76,			
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	PC C12N5/00			
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DEFINITION Targeted gene modification by parvoviral vectors.
ACCESSION BD244964
VERSION BD244964.1 GI:33054734
KEYWORDS JP 2002528088-A/18.
SOURCE Escherichia coli
ORGANISM Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
1 (bases 1 to 6)
REFERENCE
  AUTHORS Russell,D.W. and Hirata,R.K.
  TITLE Targeted gene modification by parvoviral vectors
  JOURNAL Patent: JP 2002528088-A 18 03-SEP-2002;
  UNIVERSITY OF WASHINGTON
COMMENT OS Escherichia coli
PN JP 2002528088-A/18
PD 03-SEP-2002
PF 27-OCT-1999 JP 2000578469
PR 28-OCT-1998 US 60/106191
PI DAVID W RUSSELL,ROLI K HIRATA
PC C12N15/09,A01K67/027,A61K48/00,C12N5/10,C12Q1/68//A61K35/76,
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RESULT 9
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DEFINITION Sequence 191 from Patent WO2003106674.
ACCESSION CQ755690
VERSION CQ755690.1 GI:44846495
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
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REFERENCE
  AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
  TITLE Means and methods for regulating gene expression
  JOURNAL Patent: WO 2003106674-A 191 24-DEC-2003;
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DEFINITION Sequence 197 from Patent WO2003106674.
ACCESSION CQ755696
VERSION CQ755696.1 GI:44846501
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
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REFERENCE
  AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
  TITLE Means and methods for regulating gene expression
  JOURNAL Patent: WO 2003106674-A 197 24-DEC-2003;
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VERSION CQ755696.1 GI:44846501
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
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REFERENCE
  AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
  TITLE Means and methods for regulating gene expression
  JOURNAL Patent: WO 2003106674-A 197 24-DEC-2003;
  Chromagenics B.V. (NL)
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DEFINITION Sequence 275 from Patent WO2003106674.
ACCESSION CQ755774
VERSION CQ755774.1 GI:44846579
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
TITLE Means and methods for regulating gene expression
JOURNAL Patent: WO 2003106674-A 275 24-DEC-2003;
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Db 6 GCCGG 2
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ACCESSION CQ755824
VERSION CQ755824.1 GI:44846629
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
TITLE Means and methods for regulating gene expression
JOURNAL Patent: WO 2003106674-A 325 24-DEC-2003;
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ACCESSION CQ755877
VERSION CQ755877.1 GI:44846682

KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
TITLE Means and methods for regulating gene expression
JOURNAL Patent: WO 2003106674-A 378 24-DEC-2003;
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DEFINITION Sequence 378 from Patent WO2003106674.
ACCESSION CQ755877
VERSION CQ755877.1 GI:44846682
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
TITLE Means and methods for regulating gene expression
JOURNAL Patent: WO 2003106674-A 378 24-DEC-2003;
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LOCUS CQ755904 6 bp DNA linear PAT 01-MAR-2004
DEFINITION Sequence 405 from Patent WO2003106674.
ACCESSION CQ755904
VERSION CQ755904.1 GI:44846709
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
TITLE Means and methods for regulating gene expression
JOURNAL Patent: WO 2003106674-A 405 24-DEC-2003;
Chromagenics B.V. (NL)

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Db      5 GCCGG 1
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ACCESSION  CQ756023
VERSION    CQ756023.1 GI:44846828
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Otte,A.P., Kruckeberg,A.L. and Satiijn,D.P.
TITLE      Means and methods for regulating gene expression
JOURNAL    Patent: WO 2003106674-A 524 24-DEC-2003;
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ACCESSION  CQ757928
VERSION    CQ757928.1 GI:44847949
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
TITLE      A method for the simultaneous production of multiple proteins;
           vectors and cells for use therein
JOURNAL    Patent: WO 2003106684-A 232 24-DEC-2003;
           Chromagenics B.V. (NL)
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Db      5 GCCGG 1
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LOCUS      CQ757934
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ACCESSION  CQ757934
VERSION    CQ757934.1 GI:44847955
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
TITLE      A method for the simultaneous production of multiple proteins;
           vectors and cells for use therein
JOURNAL    Patent: WO 2003106684-A 238 24-DEC-2003;
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KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
TITLE      A method for the simultaneous production of multiple proteins;
           vectors and cells for use therein
JOURNAL    Patent: WO 2003106684-A 238 24-DEC-2003;
           Chromagenics B.V. (NL)
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Db      1 GCCGG 5
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DEFINITION Sequence 238 from Patent WO2003106684.
ACCESSION  CQ757934
VERSION    CQ757934.1 GI:44847955
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
TITLE      A method for the simultaneous production of multiple proteins;
           vectors and cells for use therein
JOURNAL    Patent: WO 2003106684-A 238 24-DEC-2003;
           Chromagenics B.V. (NL)
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Sequence 253 from Patent WO2003106684.
ACCESSION
CQ757949
VERSION
CQ757949.1 GI:44847970
KEYWORDS
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SOURCE  synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
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AUTHORS  Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
TITLE    A method for the simultaneous production of multiple proteins;
          vectors and cells for use therein
JOURNAL  Patent: WO 2003106684-A 253 24-DEC-2003;
          Chromagenics B.V. (NL)
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      5 GCCGG 1

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DEFINITION
Sequence 254 from Patent WO2003106684.
ACCESSION
CQ757950
VERSION
CQ757950.1 GI:44847971
KEYWORDS
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SOURCE  synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1
AUTHORS  Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
TITLE    A method for the simultaneous production of multiple proteins;
          vectors and cells for use therein
JOURNAL  Patent: WO 2003106684-A 254 24-DEC-2003;
          Chromagenics B.V. (NL)
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VERSION
CQ757960.1 GI:44847981
KEYWORDS
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SOURCE  synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
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AUTHORS  Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
TITLE    A method for the simultaneous production of multiple proteins;
          vectors and cells for use therein
JOURNAL  Patent: WO 2003106684-A 264 24-DEC-2003;
          Chromagenics B.V. (NL)
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LOCUS   CQ758005/c
DEFINITION
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VERSION
CQ758005.1 GI:44848026
KEYWORDS
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SOURCE  synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
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AUTHORS  Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
TITLE    A method for the simultaneous production of multiple proteins;
          vectors and cells for use therein
JOURNAL  Patent: WO 2003106684-A 309 24-DEC-2003;
          Chromagenics B.V. (NL)
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCCCG 5
Db      6 GCCCG 2

RESULT 29
LOCUS   CQ758012/c
DEFINITION
Sequence 316 from Patent WO2003106684.
ACCESSION
CQ758012

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VERSION CQ758012.1 GI:44848033
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
TITLE A method for the simultaneous production of multiple proteins;
vectors and cells for use therein
JOURNAL Patent: WO 2003106684-A 316 24-DEC-2003;
Chromagenics B.V. (NL)
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/note="oligonucleotide patterns over-represented in STAR
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Best Local Similarity 100.0%; Pred.No. 8e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GCCGG 6
DB 6 GCCGG 2
RESULT 30
CQ758062/c
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DEFINITION Sequence 366 from Patent WO2003106684.
ACCESSION CQ758062
VERSION CQ758062.1 GI:44848083
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
TITLE A method for the simultaneous production of multiple proteins;
vectors and cells for use therein
JOURNAL Patent: WO 2003106684-A 366 24-DEC-2003;
Chromagenics B.V. (NL)
FEATURES
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/db_xref="taxon:32630"
/note="oligonucleotide patterns over-represented in STAR
elements"
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
53.568 Million cell updates/sec

Title: US-09-735-363A-42

Perfect score: 6

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6	4.6	76.7	6	9	US-09-816-763-95
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6	9	US-09-735-363A-47	73.3	4.4	10
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6	15	US-10-267-255-91	73.3	4.4	18
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6	19	US-10-716-029-168	73.3	4.4	28
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ALIGNMENTS

RESULT 1
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; Sequence 42, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillips, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide

Query Match 100.0%; Score 6; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGG 6
Db 1 GGAAGG 6

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; Sequence 14, Application US/09879668
; Patent No. US20020091095A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario C.
; APPLICANT: Phillips, Nigel C.
; TITLE OF INVENTION: Modulation of Fas and FasL Expression
; FILE REFERENCE: 02811-0241 42368-256931
; CURRENT APPLICATION NUMBER: US/09/879,668
; CURRENT FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: PCT/CA00/01467
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/228,925

; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: US 60/266,229
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 09/735,363
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/170,325
; PRIOR FILING DATE: 1999-12-13
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide
US-09-879-668-14

Query Match 100.0%; Score 6; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGG 6
Db 1 GGAAGG 6

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; Sequence 14, Application US/10280274
; Publication No. US2003011976A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Fillion, Mario C.
; TITLE OF INVENTION: Modulation of Fas and FasL Expression
; FILE REFERENCE: 02811-0242 42368-279803
; CURRENT APPLICATION NUMBER: US/10/280,274
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: PCT/CA00/01467
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 09/879,668
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: US 60/228,925
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: US 60/266,229
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 09/735,363
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; PRIOR APPLICATION NUMBER: US 60/170,325
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; FEATURE:
; OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide
US-10-280-274-14

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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGAAGG 6

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; Sequence 86, Application US/10182329
; Publication No. US20040005564A1
; GENERAL INFORMATION:

APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
APPLICANT: MAURO, Vincent P.
APPLICANT: EDELMAN, Gerald M.
APPLICANT: CHAPPELL, Stephen A.
APPLICANT: JONES, Frederick S.
APPLICANT: OWENS, Geoffrey
APPLICANT: MEECH, Robin
TITLE OF INVENTION: METHODS OF IDENTIFYING SYNTHETIC TRANSCRIPTIONAL AND TRANSLATIONAL
FILE REFERENCE: SCRIPI380-1
CURRENT APPLICATION NUMBER: US/10/182,329
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: PCT/US 01/02733
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/261,312
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/230,956
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: US 60/230,852
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: US 60/207,804
PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: US 60/186,496
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 60/178,816
PRIOR FILING DATE: 2000-01-28
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn version 3.0
SEQ ID NO 86
LENGTH: 5
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: core motif
US-10-182-329-86

Query Match 83.3%; Score 5; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAAGG 6
Db 1 GAAGG 5

RESULT 5
US-10-433-258-10
Sequence 10, Application US/10433258
Publication No. US20040132033A1
GENERAL INFORMATION:
APPLICANT: Hong QI
APPLICANT: Alan P. WOLFFE
TITLE OF INVENTION: HUMAN HEPARANASE GENE REGULATORY SEQUENCES
FILE REFERENCE: SABI-016/01US (S22-US1)
CURRENT APPLICATION NUMBER: US/10/433,258
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: PCT/US01/44798
PRIOR FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 6
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: EST1 binding site
US-10-433-258-10

Query Match 83.3%; Score 5; DB 19; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAG 5

Db 2 GGAAG 6
|||||

RESULT 6
US-09-816-763-95
Sequence 95, Application US/09816763
Patent No. US20020110814A1
GENERAL INFORMATION:
APPLICANT: Remacle, Jose
APPLICANT: Renard, Patricia
APPLICANT: Art, Muriel
TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
TITLE OF INVENTION: FACTORS
FILE REFERENCE: VANM212.001AUS
CURRENT APPLICATION NUMBER: US/09/816,763
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: EP 00870057.7
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 150
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 95
LENGTH: 6
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Consensus sequence for transcriptional factor PEA3
US-09-816-763-95

Query Match 76.7%; Score 4.6; DB 9; Length 6;
Best Local Similarity 80.0%; Pred. No. 1e+09;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAG 5
Db 2 GGAAR 6
|||||

RESULT 7
US-10-821-568-95
Sequence 95, Application US/10821568
Publication No. US20040185497A1
GENERAL INFORMATION:
APPLICANT: Remacle, Jose
APPLICANT: Renard, Patricia
APPLICANT: Art, Muriel
TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
TITLE OF INVENTION: FACTORS
FILE REFERENCE: VANM212.001DV1
CURRENT APPLICATION NUMBER: US/10/821,568
CURRENT FILING DATE: 2004-04-08
PRIOR APPLICATION NUMBER: US 09/816,763
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: EP 00870057.7
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 150
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 95
LENGTH: 6
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Consensus sequence for transcriptional factor PEA3
US-10-821-568-95

Query Match 76.7%; Score 4.6; DB 19; Length 6;
Best Local Similarity 80.0%; Pred. No. 1e+09;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAG 5
Db 2 GGAAR 6
|||||

```
Db          2 GGAAR 6

RESULT 8
US-09-735-363A-28/c
; Sequence 28, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Filion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-28

Query Match      73.3%; Score 4.4; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGAAGG 6
        |||||
Db      6 GGACGG 1

RESULT 9
US-09-735-363A-45
; Sequence 45, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Filion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-45

Query Match      73.3%; Score 4.4; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGAAGG 6
        |||||
Db      1 GGAGGG 6

RESULT 10
US-09-735-363A-47
; Sequence 47, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Filion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-47

Query Match      73.3%; Score 4.4; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGAAGG 6
        |||||
Db      6 GGACGG 1

RESULT 11
US-09-879-668-8/c
; Sequence 8, Application US/09879668
; Patent No. US20020091095A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Filion, Mario C.
; TITLE OF INVENTION: Modulation of Fas and FasL Expression
; FILE REFERENCE: 02811-0241 42368-256931
; CURRENT APPLICATION NUMBER: US/09/879,668
; CURRENT FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: PCT/CA00/01467
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/228,925
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: US 60/266,229
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 09/735,363
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/170,325
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide
US-09-879-668-8

Query Match      73.3%; Score 4.4; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGAAGG 6
        |||||
Db      6 GGACGG 1

RESULT 12
US-09-735-363A-47
```

US-09-879-668-17
; Sequence 17, Application US/09879668
; Patent No. US20020091095A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Filion, Mario C.
; TITLE OF INVENTION: Modulation of Fas and FasL Expression
; FILE REFERENCE: 02811-0241 42368-256931
; CURRENT APPLICATION NUMBER: US/09/879,668
; CURRENT FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: PCT/CA00/01467
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/228,925
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: US 60/266,229
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 09/735,363
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/170,325
; PRIOR FILING DATE: 1999-12-13
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide
US-09-879-668-17

Query Match 73.3%; Score 4.4; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
|||
Db 1 GGGAGG 6

RESULT 13
US-09-953-348-91
; Sequence 91, Application US/09953348
; Publication No. US20030134398A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, David. H
; APPLICANT: Mao, Yingqing
; APPLICANT: Varoglu, Mustafa
; APPLICANT: He, Min
; APPLICANT: Sheldon, Paul
; TITLE OF INVENTION: MITOMYCIN BIOSYNTHETIC GENE CLUSTER
; FILE REFERENCE: 600.530US1
; CURRENT APPLICATION NUMBER: US/09/953,348
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: PCT/US00/06394
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/266965
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Streptomyces lavendulae
US-09-953-348-91

Query Match 73.3%; Score 4.4; DB 10; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
|||
Db 1 GAAAGG 6

RESULT 14
US-09-953-348-93
; Sequence 93, Application US/09953348
; Publication No. US20030134398A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, David. H
; APPLICANT: Mao, Yingqing
; APPLICANT: Varoglu, Mustafa
; APPLICANT: He, Min
; APPLICANT: Sheldon, Paul
; TITLE OF INVENTION: MITOMYCIN BIOSYNTHETIC GENE CLUSTER
; FILE REFERENCE: 600.530US1
; CURRENT APPLICATION NUMBER: US/09/953,348
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: PCT/US00/06394
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/266965
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Streptomyces lavendulae
US-09-953-348-93

Query Match 73.3%; Score 4.4; DB 10; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
|||
Db 1 GGAACG 6

RESULT 15
US-10-127-645-3
; Sequence 3, Application US/10127645
; Publication No. US20030045493A1
; GENERAL INFORMATION:
; APPLICANT: Filion, Mario C.
; APPLICANT: Phillips, Nigel C.
; TITLE OF INVENTION: Oligonucleotide Compositions and Their Use to Induce Differentiation
; FILE REFERENCE: 02811-0261 (42368-273010)
; CURRENT APPLICATION NUMBER: US/10/127,645
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US 60/286,158
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-127-645-3

Query Match 73.3%; Score 4.4; DB 14; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
|||
Db 1 GGGAGG 6

RESULT 16
US-10-280-274-8/c
; Sequence 8, Application US/10280274
; Publication No. US20030119776A1
; GENERAL INFORMATION:

/ APPLICANT: Phillips, Nigel C.
/ APPLICANT: Fillion, Mario C.
/ TITLE OF INVENTION: Modulation of Fas and FasL Expression
/ FILE REFERENCE: 02811-0242 42368-279803
/ CURRENT APPLICATION NUMBER: US/10/280,274
/ CURRENT FILING DATE: 2003-02-14
/ PRIOR APPLICATION NUMBER: PCT/CA00/01467
/ PRIOR FILING DATE: 2000-12-12
/ PRIOR APPLICATION NUMBER: US 09/879,668
/ PRIOR FILING DATE: 2001-06-12
/ PRIOR APPLICATION NUMBER: US 60/228,925
/ PRIOR FILING DATE: 2000-08-29
/ PRIOR APPLICATION NUMBER: US 60/266,229
/ PRIOR FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: US 09/735,363
/ PRIOR FILING DATE: 2000-12-12
/ PRIOR APPLICATION NUMBER: US 60/170,325
/ PRIOR FILING DATE: 1999-12-13
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 8
/ LENGTH: 6
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide
US-10-280-274-8

Query Match 73.3%; Score 4.4; DB 15; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
DB 6 GGACGG 1

RESULT 17
US-10-280-274-17
/ Sequence 17, Application US/10280274
/ Publication No. US20030119776A1
/ GENERAL INFORMATION:
/ APPLICANT: Phillips, Nigel C.
/ TITLE OF INVENTION: Modulation of Fas and FasL Expression
/ FILE REFERENCE: 02811-0242 42368-279803
/ CURRENT APPLICATION NUMBER: US/10/280,274
/ CURRENT FILING DATE: 2003-02-14
/ PRIOR APPLICATION NUMBER: PCT/CA00/01467
/ PRIOR FILING DATE: 2000-12-12
/ PRIOR APPLICATION NUMBER: US 09/879,668
/ PRIOR FILING DATE: 2001-06-12
/ PRIOR APPLICATION NUMBER: US 60/228,925
/ PRIOR FILING DATE: 2000-08-29
/ PRIOR APPLICATION NUMBER: US 60/266,229
/ PRIOR FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: US 09/735,363
/ PRIOR FILING DATE: 2000-12-12
/ PRIOR APPLICATION NUMBER: US 60/170,325
/ PRIOR FILING DATE: 1999-12-13
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 17
/ LENGTH: 6
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide
US-10-280-274-17

Query Match 73.3%; Score 4.4; DB 15; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
DB 1 GGACGG 6
RESULT 18
US-10-267-255-91
/ Sequence 91, Application US/10267255
/ Publication No. US20030124689A1
/ GENERAL INFORMATION:
/ APPLICANT: Sherman, D
/ APPLICANT: Mao, Y
/ APPLICANT: Varoglu, M
/ APPLICANT: He, M
/ APPLICANT: Sheldon, P
/ TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
/ FILE REFERENCE: 600.456US1
/ CURRENT APPLICATION NUMBER: US/10/267,255
/ CURRENT FILING DATE: 2002-10-09
/ PRIOR APPLICATION NUMBER: US 09/266,965
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: US 08/624,447
/ PRIOR FILING DATE: 1996-08-19
/ PRIOR APPLICATION NUMBER: PCT/US94/11279
/ PRIOR FILING DATE: 1994-10-06
/ PRIOR APPLICATION NUMBER: US 08/133,963
/ PRIOR FILING DATE: 1993-10-07
/ NUMBER OF SEQ ID NOS: 145
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 91
/ LENGTH: 6
/ TYPE: DNA
/ ORGANISM: Streptomyces lavendulae
US-10-267-255-91

Query Match 73.3%; Score 4.4; DB 15; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
DB 1 GAAAGG 6

RESULT 19
US-10-267-255-93
/ Sequence 93, Application US/10267255
/ Publication No. US20030124689A1
/ GENERAL INFORMATION:
/ APPLICANT: Sherman, D
/ APPLICANT: Mao, Y
/ APPLICANT: Varoglu, M
/ APPLICANT: He, M
/ APPLICANT: Sheldon, P
/ TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
/ FILE REFERENCE: 600.456US1
/ CURRENT APPLICATION NUMBER: US/10/267,255
/ CURRENT FILING DATE: 2002-10-09
/ PRIOR APPLICATION NUMBER: US 09/266,965
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: US 08/624,447
/ PRIOR FILING DATE: 1996-08-19
/ PRIOR APPLICATION NUMBER: PCT/US94/11279
/ PRIOR FILING DATE: 1994-10-06
/ PRIOR APPLICATION NUMBER: US 08/133,963
/ PRIOR FILING DATE: 1993-10-07
/ NUMBER OF SEQ ID NOS: 145
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 93
/ LENGTH: 6
/ TYPE: DNA
/ ORGANISM: Streptomyces lavendulae

US-10-267-255-93

Query Match 73.3%; Score 4.4; DB 15; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAAGG 6
|||
Db 1 GGAACG 6

RESULT 20

US-10-264-280-2
; Sequence 2, Application US/10264280
; Publication No. US20030125290A1
; GENERAL INFORMATION:
; APPLICANT: Fillon, Mario C.
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Herrera-Gayol, Andrea C.
; TITLE OF INVENTION: Therapeutically Useful Triethyleneglycol Cholesteryl Oligonucleotide
; FILE REFERENCE: 02811-0271 42368-277492
; CURRENT APPLICATION NUMBER: US/10/264,280
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 60/326,884
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-264-280-2

Query Match 73.3%; Score 4.4; DB 15; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAAGG 6
|||
Db 1 GGAACG 6

RESULT 21

US-10-264-280-6
; Sequence 6, Application US/10264280
; Publication No. US20030125290A1
; GENERAL INFORMATION:
; APPLICANT: Fillon, Mario C.
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Herrera-Gayol, Andrea C.
; TITLE OF INVENTION: Therapeutically Useful Triethyleneglycol Cholesteryl Oligonucleotide
; FILE REFERENCE: 02811-0271 42368-277492
; CURRENT APPLICATION NUMBER: US/10/264,280
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 60/326,884
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: 3'-Triethyleneglycol (TEG) Cholesteryl Synthetic Oligonucleotide
US-10-264-280-6

Query Match 73.3%; Score 4.4; DB 15; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAAGG 6
|||
Db 1 GGAAGG 6

RESULT 22

US-10-041-860-191/c
; Sequence 191, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R. F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 191
; LENGTH: 6
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-041-860-191

Query Match 73.3%; Score 4.4; DB 16; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAAGG 6
|||
Db 6 GGAAGG 1

RESULT 23

US-10-190-312A-212/c
; Sequence 212, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities;
; FILE REFERENCE: 2183-4993.1
; CURRENT APPLICATION NUMBER: US/10/190,312A
; CURRENT FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/303,199
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 212
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements
US-10-190-312A-212

Query Match 73.3%; Score 4.4; DB 16; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAAGG 6
|||

```
Db          6 GGAGGG 1

RESULT 24
US-10-190-312A-259/c
; Sequence 259, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; TITLE OF INVENTION: methods for detecting and using such DNA sequences
; FILE REFERENCE: 2183-4993.1
; CURRENT APPLICATION NUMBER: US/10/190,312A
; CURRENT FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/303,199
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 259
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements
US-10-190-312A-259

Query Match      73.3%; Score 4.4; DB 16; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGAAGG 6
        |||||
Db      6 GGAAGG 1

RESULT 25
US-10-190-312A-636/c
; Sequence 636, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; TITLE OF INVENTION: methods for detecting and using such DNA sequences
; FILE REFERENCE: 2183-4993.1
; CURRENT APPLICATION NUMBER: US/10/190,312A
; CURRENT FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/303,199
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 636
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Dyad patterns over-represented in STAR elements
US-10-190-312A-636

Query Match      73.3%; Score 4.4; DB 16; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGAAGG 6
        |||||
Db      6 GGAGGG 1

RESULT 26
US-10-420-513A-6
; Sequence 168, Application US/10716029
; Publication No. US20040171038A1
; GENERAL INFORMATION:
; APPLICANT: Philips, Nigel C.
; APPLICANT: Fillon, Mario C.
; TITLE OF INVENTION: Oligonucleotide Compositions and Their Use for the Modulation of
; TITLE OF INVENTION: Immune Response
; FILE REFERENCE: 02811-0301 (42368-283135)
; CURRENT APPLICATION NUMBER: US/10/420,513A
; CURRENT FILING DATE: 2003-04-22
; PRIOR APPLICATION NUMBER: US 60/374,540
; PRIOR FILING DATE: 2002-04-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-420-513A-6

Query Match      73.3%; Score 4.4; DB 18; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGAAGG 6
        |||||
Db      1 GGGAGG 6

RESULT 27
US-10-716-029-165
; Sequence 165, Application US/10716029
; Publication No. US20040171038A1
; GENERAL INFORMATION:
; APPLICANT: Nicklin, Martin
; APPLICANT: Duff, Gordon
; APPLICANT: Kornman, Kenneth
; APPLICANT: Kolpin, Maryam R
; APPLICANT: Hsieh, Chung-Ming
; APPLICANT: Govindaraju, Raju
; APPLICANT: Aziz, Nazneen
; TITLE OF INVENTION: The IL-1 Gene Cluster and Associated Inflammatory Polymorphisms
; TITLE OF INVENTION: and Haplotypes
; FILE REFERENCE: 24299-524 CON
; CURRENT APPLICATION NUMBER: US/10/716,029
; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: 10/351,702
; PRIOR FILING DATE: 2003-01-25
; PRIOR APPLICATION NUMBER: 60/351,951
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 277
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 165
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-716-029-165

Query Match      73.3%; Score 4.4; DB 19; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGAAGG 6
        |||||
Db      1 GGCAGG 6

RESULT 28
US-10-716-029-168
; Sequence 168, Application US/10716029
; Publication No. US20040171038A1
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; GENERAL INFORMATION:
; APPLICANT: Nicklin, Martin
; APPLICANT: Duff, Gordon
; APPLICANT: Kornman, Kenneth
; APPLICANT: Kolpin, Maryam R
; APPLICANT: Hsieh, Chung-Ming
; APPLICANT: Govindaraju, Raju
; APPLICANT: Aziz, Nazneen
; TITLE OF INVENTION: The IL-1 Gene Cluster and Associated Inflammatory Polymorphisms
; FILE REFERENCE: 24299-524 CON
; CURRENT APPLICATION NUMBER: US/10/716,029
; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: 10/351,702
; PRIOR FILING DATE: 2003-01-25
; PRIOR APPLICATION NUMBER: 60/351,951
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 277
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 168
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-716-029-168

Query Match      73.3%; Score 4.4; DB 19; Length 6;
Best Local Similarity 83.3%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGAGG 6
DB      1 GGTAGG 6

RESULT 29
US-10-027-632-177937/c
; Sequence 177937, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 10827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 177937
; LENGTH: 4
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-177937

Query Match      66.7%; Score 4; DB 13; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.5e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGAA 4
DB      1 GGAA 4

us-09-735-363a-42.szlm6.rnpb

Db      4 GGAA 1

RESULT 30
US-10-196-332-8
; Sequence 8, Application US/10196332
; Publication No. US20030087865A1
; GENERAL INFORMATION:
; APPLICANT: Golub, Todd R.
; APPLICANT: Sasaki, Koichi
; APPLICANT: Martinez, Robert V.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: Leukemogenic Transcription Factors
; FILE REFERENCE: 2825.2035-001
; CURRENT APPLICATION NUMBER: US/10/196,332
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: US 60/305,554
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 4
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Repeat sequence
US-10-196-332-8

Query Match      66.7%; Score 4; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.5e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGAA 4
DB      1 GGAA 4

Search completed: July 21, 2005, 07:13:19
Job time : 714.6 secs
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:43:13 ; Search time 57 Seconds
(without alignments)
172.240 Million cell updates/sec

Title: US-09-735-363A-42

Perfect score: 6

Sequence: 1 ggaagg 6

Scoring table: IDENTITY NUC

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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2678

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents NA.*

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4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*

5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	83.3	6	1	US-08-533-912-7
2	4.4	73.3	6	4	US-09-266-965-91
3	4.4	73.3	6	4	US-09-266-965-93
4	4.4	73.3	6	4	US-09-798-542-23
5	4.4	73.3	6	4	US-09-798-542-24
6	4	66.7	5	1	US-08-717-526-76
7	4	66.7	5	3	US-08-873-709-8
8	4	66.7	5	3	US-08-537-765-3
9	4	66.7	5	3	US-08-623-428B-62
10	4	66.7	5	4	US-09-869-875-5
11	4	66.7	5	4	US-09-869-875-11
12	4	66.7	5	5	PCT-US93-03027-8
13	4	66.7	6	1	US-08-211-682-7
14	4	66.7	6	2	US-08-211-682-8
15	4	66.7	6	2	US-08-553-185-5
16	4	66.7	6	2	US-08-442-809A-2
17	4	66.7	6	2	US-08-442-809A-10
18	4	66.7	6	3	US-09-056-868B-14
19	4	66.7	6	3	US-09-632-538C-10
20	4	66.7	6	4	US-09-608-358-50
21	4	66.7	6	4	US-09-608-358-51
22	4	66.7	6	4	US-09-435-327A-1
23	4	66.7	6	4	US-09-585-599A-7
24	4	66.7	6	4	US-09-585-599A-8
25	4	66.7	6	4	US-10-014-973A-16
26	4	66.7	6	4	US-09-851-271A-14
27	4	66.7	6	4	US-10-134-188-13
28	c	29	3.6	4	PCT-US92-08094-63
29	c	30	3.4	5	US-08-488-015B-11
30	c	31	3.4	5	US-07-862-831A-1
31	c	32	3.4	5	US-07-862-831A-2
32	c	33	3.4	5	US-08-126-564A-1
33	c	34	3.4	5	US-08-126-564A-2
34	c	35	3.4	5	US-08-126-564A-3
35	c	36	3.4	5	US-09-153-242-31
36	c	37	3.4	5	US-09-491-795-6
37	c	38	3.4	5	US-10-055-732-14
38	c	39	3.4	5	PCT-US94-09143-1
39	c	40	3.4	5	PCT-US94-09143-2
40	c	41	3.4	6	US-07-791-213D-45
41	c	42	3.4	6	US-08-232-144-6
42	c	43	3.4	6	US-08-242-402-20
43	c	44	3.4	6	US-08-234-613-10
44	c	45	3.4	6	US-08-370-180-19
45	c	46	3.4	6	US-08-488-672-1
46	c	47	3.4	6	US-08-533-912-6
47	c	48	3.4	6	US-08-293-150A-45
48	c	49	3.4	6	US-08-465-590-140
49	c	50	3.4	6	US-08-237-973-10
50	c	51	3.4	6	US-08-237-973-26
51	c	52	3.4	6	US-08-682-423-19
52	c	53	3.4	6	US-08-846-301A-12
53	c	54	3.4	6	US-09-116-032-3
54	c	55	3.4	6	US-08-711-417C-140
55	c	56	3.4	6	US-09-220-794-10
56	c	57	3.4	6	US-09-723-909-140
57	c	58	3.4	6	US-08-708-354-1
58	c	59	3.4	6	US-09-337-619-110
59	c	60	3.4	6	US-09-686-631-12
60	c	61	3.4	6	US-09-657-289A-1
61	c	62	3.4	6	US-08-453-485B-17
62	c	63	3.4	6	US-09-530-663B-16
63	c	64	3.4	6	PCT-US93-05331-1
64	c	65	3.4	6	PCT-US93-08743-140
65	c	66	3.2	53.3	PCT-US95-05141-19
66	c	67	3.2	53.3	PCT-US91-03680-54
67	c	68	3.2	53.3	PCT-US91-03680-56
68	c	69	3.2	53.3	US-08-646-301A-13
69	c	70	3.2	53.3	US-09-632-538C-11
70	c	71	3.2	53.3	US-09-263-692A-8
71	c	72	3	3	PCT-US91-03680-33
72	c	73	3	3	US-08-268-679B-7
73	c	74	3	3	US-08-973-568-55
74	c	75	3	3	US-07-630-288A-7
75	c	76	3	3	US-08-468-049-7
76	c	77	3	3	US-08-807-104-19
77	c	78	3	3	US-08-480-068-19
78	c	79	3	3	US-08-973-568-51
79	c	80	3	3	US-08-973-568-54
80	c	81	3	3	US-08-973-137-19
81	c	82	3	3	US-09-498-608A-8
82	c	83	3	3	US-09-498-608A-9
83	c	84	3	3	CHOLESTEROL-OXIDASE-FROM
84	c	85	3	3	CHOLESTEROL-OXIDASE-FROM
85	c	86	3	3	US-09-248-093-5
86	c	87	3	3	US-09-545-153-2
87	c	88	3	3	PCT-US91-03680-90
88	c	89	3	3	PCT-US92-10024-2
89	c	90	3	3	PCT-US94-06456-9
90	c	91	3	3	PCT-US94-06456-38
91	c	92	3	3	PCT-US94-08023-30
92	c	93	3	3	US-07-630-288A-38
93	c	94	3	3	US-08-247-809A-15
94	c	95	3	3	US-08-116-801C-1
95	c	96	3	3	US-08-116-801C-2
96	c	97	3	3	US-08-435-480-10
97	c	98	3	3	US-08-381-097A-14
98	c	99	3	3	US-08-381-097A-15
99	c	100	3	3	US-08-381-097A-16
100	c	101	3	3	US-08-468-049-38

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Sequence 19, Appl
Sequence 19, Appl
Sequence 51, Appl
Sequence 54, Appl
Sequence 19, Appl
Sequence 9, Appl
Sequence 8, Appl
Sequence 9, Appl
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GENERAL INFORMA
Sequence 5, Appl
Sequence 2, Appl
Sequence 90, Appl
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Sequence 9, Appl
Sequence 38, Appl
Sequence 30, Appl
Sequence 38, Appl
Sequence 15, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 10, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-08-533-912-7
; Sequence 7, Application US/08533912
; Patent No. 5744308
; GENERAL INFORMATION:
; APPLICANT: GUILLOU-BONNICI, Francoise
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: MALLET, Francois
; APPLICANT: LEVASSEUR, Pierre
; APPLICANT: MCALISTER, William
; TITLE OF INVENTION: CHIMERA OLIGONUCLEOTIDE AND ITS
; TITLE OF INVENTION: UTILIZATION FOR OBTAINING TRANSCRIPTS OF A NUCLEIC ACID
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/533,912
; FILING DATE: 26-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94011455
; FILING DATE: 26-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 36613
; TELEPHONE: 703-836-6400
; TELEFAX: 703-836-2787
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-08-533-912-7

Query Match 83.3%; Score 5; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAAGG 6
DB 1 GAAGG 5

RESULT 2
US-09-266-965-91
; Sequence 91, Application US/09266965
; Patent No. 6495348
; GENERAL INFORMATION:
; APPLICANT: Sherman, D
; APPLICANT: Mao, Y
; APPLICANT: Varoglu, M
; APPLICANT: He, M
; APPLICANT: Sheldon, P
; TITLE OF INVENTION: THAT ARE REPLICATION-DEFECTIVE IN MOSQUITOES FOR USE AS

; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
; FILE REFERENCE: 600.456US1
; CURRENT APPLICATION NUMBER: US/09/266,965
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: US 08/624,447
; EARLIER FILING DATE: 1996-08-19
; EARLIER APPLICATION NUMBER: PCT/US94/11279
; EARLIER FILING DATE: 1994-10-06
; EARLIER APPLICATION NUMBER: US 08/133,963
; EARLIER FILING DATE: 1993-10-07
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 91
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Streptomyces lavendulae
US-09-266-965-91

Query Match 73.3%; Score 4.4; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.4e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
DB 1 GGAAGG 6

RESULT 3
US-09-266-965-93
; Sequence 93, Application US/09266965
; Patent No. 6495348
; GENERAL INFORMATION:
; APPLICANT: Sherman, D
; APPLICANT: Mao, Y
; APPLICANT: Varoglu, M
; APPLICANT: He, M
; APPLICANT: Sheldon, P
; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
; FILE REFERENCE: 600.456US1
; CURRENT APPLICATION NUMBER: US/09/266,965
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: US 08/624,447
; EARLIER FILING DATE: 1996-08-19
; EARLIER APPLICATION NUMBER: PCT/US94/11279
; EARLIER FILING DATE: 1994-10-06
; EARLIER APPLICATION NUMBER: US 08/133,963
; EARLIER FILING DATE: 1993-10-07
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 93
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Streptomyces lavendulae
US-09-266-965-93

Query Match 73.3%; Score 4.4; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.4e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
DB 1 GGAAGG 6

RESULT 4
US-09-798-542-23
; Sequence 23, Application US/09798542
; Patent No. 6685948
; GENERAL INFORMATION:
; APPLICANT: Zeng, Lingling
; APPLICANT: Markoff, Lewis
; TITLE OF INVENTION: REPLICATION-DEFECTIVE DENGUE VIRUSES
; TITLE OF INVENTION: THAT ARE REPLICATION-DEFECTIVE IN MOSQUITOES FOR USE AS

; TITLE OF INVENTION: VACCINES
; FILE REFERENCE: NIH145.001C1
; CURRENT APPLICATION NUMBER: US/09/798,542
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: PCT/US 99/02598
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 60/098,981
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 6
; TYPE: RNA
; ORGANISM: Flavivirus, Dengue Type 2
US-09-798-542-23

Query Match 73.3%; Score 4.4; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.4e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 GGAAGG 6
| | | | |
Db 1 GUAAGG 6

RESULT 5
US-09-798-542-24/c
; Sequence 24, Application US/09798542
; Patent No. 6685948
; GENERAL INFORMATION:
; APPLICANT: Zeng, Lingling
; APPLICANT: Markoff, Lewis
; TITLE OF INVENTION: REPLICATION-DEFECTIVE DENGUE VIRUSES
; TITLE OF INVENTION: THAT ARE REPLICATION-DEFECTIVE IN MOSQUITOES FOR USE AS
; FILE OF INVENTION: VACCINES
; FILE REFERENCE: NIH145.001C1
; CURRENT APPLICATION NUMBER: US/09/798,542
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: PCT/US 99/02598
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 60/098,981
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 6
; TYPE: RNA
; ORGANISM: Flavivirus, Dengue Type 2
US-09-798-542-24

Query Match 73.3%; Score 4.4; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 2.4e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 GGAAGG 6
| | | | |
Db 6 GTAAGG 1

RESULT 6
US-08-717-526-76/c
; Sequence 76, Application US/08717526
; Patent No. 5786147
; GENERAL INFORMATION:
; APPLICANT: MABILAT, CLAUDE
; APPLICANT: RAULT, DIDIER
; TITLE OF INVENTION: DETECTION OF ENTEROBACTERIA
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE
; STREET: 700 SOUTH WASHINGTON STREET
; CITY: ALEXANDRIA
; STATE: VA

; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/717,526
; FILING DATE: 17-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BERRIDGE, WILLIAM P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 38732
; TELEPHONE: 703-836-6400
; TELEFAX: 703-836-2787
; INFORMATION FOR SEQ ID NO: 76:
; LENGTH: 5 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-717-526-76

Query Match 66.7%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.9e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAA 4
| | | |
Db 4 GGAA 1

RESULT 7
US-08-873-709-8
; Sequence 8, Application US/08873709
; Patent No. 6037126
; GENERAL INFORMATION:
; APPLICANT: Grossman, Abraham
; TITLE OF INVENTION: COMPOSITIONS, METHODS, KITS AND
; TITLE OF INVENTION: APPARATUS FOR DETERMINING THE PRESENCE OR ABSENCE OF
; TITLE OF INVENTION: PROTEIN COMPONENT OF TELOMERASE ENZYME
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abraham Grossman
; STREET: 666 Washington Avenue
; CITY: Pleasantville
; STATE: NY
; COUNTRY: USA
; ZIP: 10570
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/873,709
; FILING DATE: 12-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Janiuk, Anthony J.
; REGISTRATION NUMBER: 29,809
; REFERENCE/DOCKET NUMBER: Q001/002
; TELEPHONE: 914-747-9108
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: RNA
US-08-873-709-8

Query Match 66.7%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.9e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAA 4
Db 2 GGAA 5

RESULT 8
US-08-537-765-3/c
; Sequence 3, Application US/08537765
; GENERAL INFORMATION:
; APPLICANT: SMITH, Austin Gerard
; APPLICANT: MOUNTFORD, Peter Scott
; APPLICANT: LATHE, Richard Frank
; TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS GENES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farrahaw, Garrett &
; ADDRESSEE: Dunner, L.L.P.
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 02005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/537,765
; FILING DATE: 25-JAN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB94/00849
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9308271.7
; FILING DATE: 21-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9313323.9
; FILING DATE: 28-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9401011.3
; FILING DATE: 20-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, Leslie A
; REGISTRATION NUMBER: 34,872
; REFERENCE/DOCKET NUMBER: 06999.0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-537-765-3

Query Match 66.7%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.9e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAA 4
Db 5 GGAA 2

RESULT 9
US-08-623-428D-62/c
; Sequence 62, Application US/08623428D
; Patent No. 6312890
; GENERAL INFORMATION:
; APPLICANT: W. MARSTON LINEHAN, MICHAEL
; LERMAN, FARIDA LATIF AND BERTON
; ZBAR
; TITLE OF INVENTION: PARTIAL INTRON SEQUENCE
; OF VHL DISEASE GENE AND ITS USE IN DIAGNOSIS
; OF DISEASE CARRIERS
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/623,428D
; FILING DATE: 05-Sep-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/623,428
; FILING DATE: MARCH 28, 1996
; APPLICATION NUMBER: 08/061,889
; FILING DATE: May 14, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kathryn M. Brown
; REGISTRATION NUMBER: 34,556
; REFERENCE/DOCKET NUMBER: 2026-4078US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 62
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 62
US-08-623-428D-62

Query Match 66.7%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.9e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAA 4
Db 5 GGAA 2

RESULT 10
US-09-869-875-5/c
; Sequence 5, Application US/09869875
; Patent No. 6521456
; GENERAL INFORMATION:
; APPLICANT: Siebenkotten, Gregor
; APPLICANT: Christline, Rainer
; TITLE OF INVENTION: USE OF CELLULAR TRANSPORT SYSTEMS FOR THE TRANSFER OF NUCLEIC ACID
; TITLE OF INVENTION: THROUGH THE NUCLEAR ENVELOPE
; FILE REFERENCE: 30430.IUSWO

```
; CURRENT APPLICATION NUMBER: US/09/869,875
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: PCT/DE00/00061
; PRIOR FILING DATE: 2000-01-03
; PRIOR APPLICATION NUMBER: DE 199 00 513.3
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: DE 199 33 939.2
; PRIOR FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA is PNA; mixed peptide/PNA sequence
US-09-869-875-5

Query Match          66.7%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.9e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 AAGG 6
Db      4 AAGG 1

RESULT 11
US-09-869-875-11/c
; Sequence 11, Application US/09869875
; Patent No. 6521456
; GENERAL INFORMATION:
; APPLICANT: Siebenkotten, Gregor
; TITLE OF INVENTION: USE OF CELLULAR TRANSPORT SYSTEMS FOR THE TRANSFER OF NUCLEIC ACID
; FILE REFERENCE: 30430.1USWO
; CURRENT APPLICATION NUMBER: US/09/869,875
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: PCT/DE00/00061
; PRIOR FILING DATE: 2000-01-03
; PRIOR APPLICATION NUMBER: DE 199 00 513.3
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: DE 199 33 939.2
; PRIOR FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 11
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA is PNA; mixed peptide/PNA sequence
US-09-869-875-11

Query Match          66.7%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.9e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGAA 4
Db      5 GGAA 2

RESULT 12
PCT-US93-03027-8
; Sequence 8, Application PC/TUS9303027
; GENERAL INFORMATION:
; APPLICANT: LEONARD, WARREN; TOLEDANO,
; APPLICANT: MICHEL
; TITLE OF INVENTION: CONTROL AND/OR
; TITLE OF INVENTION: PREVENTION OF BINDING OF NF- B/REL/DORSAL
; TITLE OF INVENTION:

; CURRENT APPLICATION NUMBER: US/09/869,875
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: PCT/DE00/00061
; PRIOR FILING DATE: 2000-01-03
; PRIOR APPLICATION NUMBER: DE 199 00 513.3
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: DE 199 33 939.2
; PRIOR FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 11
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA is PNA; mixed peptide/PNA sequence
US-09-869-875-11

Query Match          66.7%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.9e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGAA 4
Db      5 GGAA 2

RESULT 13
US-08-211-682-7
; Sequence 7, Application US/08211682
; Patent No. 5670333
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: EXPRESSION OF POLYPEPTIDES IN E. COLI UNDER
; TITLE OF INVENTION: CONTROL OF THE E. COLI MDH-GENE PROMOTER
; NUMBER OF SEQUENCES: 25
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION NUMBER: US/08/211,682
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
```

```
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/03027
; FILING DATE: 19930401
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/862,987
; FILING DATE: 06-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: P-36,434
; REFERENCE/DOCKET NUMBER: 2026-4010 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: Unknown
; MOLECULE TYPE: oligonucleotide
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: "B" half of Ig- B binding
; NAME/KEY: site
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
PCT-US93-03027-8

Query Match          66.7%; Score 4; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.9e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGAA 4
Db      1 GGAA 4

RESULT 13
US-08-211-682-7
; Sequence 7, Application US/08211682
; Patent No. 5670333
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: EXPRESSION OF POLYPEPTIDES IN E. COLI UNDER
; TITLE OF INVENTION: CONTROL OF THE E. COLI MDH-GENE PROMOTER
; NUMBER OF SEQUENCES: 25
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION NUMBER: US/08/211,682
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
```

```
/
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
US-08-211-682-7

Query Match          66.7%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGG 6
Db 2 AAGG 5

RESULT 14
US-08-211-682-8
/ Sequence 8, Application US/08211682
/ Patent No. 5670333
/ GENERAL INFORMATION:
/ APPLICANT:
/ TITLE OF INVENTION: EXPRESSION OF POLYPEPTIDES IN E. COLI UNDER
/ TITLE OF INVENTION: CONTROL OF THE E. COLI MDH-GENE PROMOTER
/ NUMBER OF SEQUENCES: 25
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/211,682
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
US-08-211-682-8

Query Match          66.7%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAA 4
Db 2 GGAA 5

RESULT 15
US-08-553-185-5
/ Sequence 5, Application US/08553185
/ Patent No. 5922535
/ GENERAL INFORMATION:
/ APPLICANT: Huo Ph.D., Li
/ TITLE OF INVENTION: IDENTIFYING SEQUENCE DIFFERENCES IN
/ TITLE OF INVENTION: NUCLEIC ACID POPULATIONS
/ NUMBER OF SEQUENCES: 11
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Choate, Hall & Stewart
/ STREET: 53 State Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: usa
/ ZIP: 01773
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/553,185
/ FILING DATE: 07-NOV-1995
/ CLASSIFICATION: 435

/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Jarrell Ph.D., Brenda H
/ REGISTRATION NUMBER: 39,223
/ REFERENCE/DOCKET NUMBER: 0379373-0001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 248-5175
/ TELEFAX: (617) 248-4000
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: not relevant
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "DNA"
/ IMMEDIATE SOURCE:
/ CLONE: sequence B
US-08-553-185-5

Query Match          66.7%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAAG 5
Db 1 GAAG 4

RESULT 16
US-08-442-809A-2/c
/ Sequence 2, Application US/08442809A
/ Patent No. 5976873
/ GENERAL INFORMATION:
/ APPLICANT: Bohinski, Robert J.,
/ APPLICANT: Whitsett, Jeffrey A.,
/ TITLE OF INVENTION: Nucleic Acid Sequences
/ TITLE OF INVENTION: Controlling Lung Cell -
/ TITLE OF INVENTION: Specific Gene Expression
/ NUMBER OF SEQUENCES: 76
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
/ ADDRESSEE: Cecchi, Stewart & Olstein
/ STREET: 6 Becker Farm Road
/ CITY: Roseland
/ STATE: New Jersey
/ COUNTRY: USA
/ ZIP: 07068
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch diskette
/ COMPUTER: IBM PS/2
/ OPERATING SYSTEM: MS-DOS
/ SOFTWARE: WordPerfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/442,809A
/ FILING DATE: 17-MAY-1995
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/245,356
/ FILING DATE: 18-MAY-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Olstein, Elliot M.
/ REGISTRATION NUMBER: 24,025
/ REFERENCE/DOCKET NUMBER: 271010-360
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 201-994-1700
/ TELEFAX: 201-994-1744
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6 bases
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: oligonucleotide
```

US-08-442-809A-2

Query Match 66.7%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAAG 5
 ||||
DB 4 GAAG 1

RESULT 17

US-08-442-809A-10
; Sequence 10, Application US/08442809A
; Patent No. 5976873
; GENERAL INFORMATION:
; APPLICANT: Bohinski, Robert J.,
; APPLICANT: Whitsett, Jeffrey A.
; TITLE OF INVENTION: Nucleic Acid Sequences
; TITLE OF INVENTION: Controlling Lung Cell -
; TITLE OF INVENTION: Specific Gene Expression
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,809A
; FILING DATE: 17-MAY-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/245,356
; FILING DATE: 18-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 271010-360
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide

US-08-442-809A-10

Query Match 66.7%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAAG 5
 ||||
DB 3 GAAG 6

RESULT 18

US-09-056-868B-14/c
; Sequence 14, Application US/09056868B
; Patent No. 6316218
; GENERAL INFORMATION:
; APPLICANT: Podolsky, Daniel K.

; TITLE OF INVENTION: INTESTINAL TREFOIL PROTEINS

; FILE REFERENCE: 00786-066005
; CURRENT APPLICATION NUMBER: US/09/056,868B
; CURRENT FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: US 08/476,705
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/191,352
; PRIOR FILING DATE: 1994-02-02
; PRIOR APPLICATION NUMBER: US 08/037,741
; PRIOR FILING DATE: 1993-03-25
; PRIOR APPLICATION NUMBER: US 07/837,192
; PRIOR FILING DATE: 1992-02-13
; PRIOR APPLICATION NUMBER: US 07/655,965
; PRIOR FILING DATE: 1991-02-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated primer
US-09-056-868B-14

Query Match 66.7%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAA 4
 ||||
DB 5 GGAA 2

RESULT 19

US-09-632-538C-10/c
; Sequence 10, Application US/09632538C
; Patent No. 6440674
; GENERAL INFORMATION:
; APPLICANT: Misra, Santosh et al.
; TITLE OF INVENTION: PLANT PROMOTER DERIVED FROM LUMINAL BINDING PROTEIN GENE AND METH
; TITLE OF INVENTION: ITS USE
; FILE REFERENCE: 54359
; CURRENT APPLICATION NUMBER: US/09/632,538C
; CURRENT FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: variation
; LOCATION: (3)
; OTHER INFORMATION: W = a, t, or u
; OTHER INFORMATION: Description of Artificial Sequence: PROMOTER
; OTHER INFORMATION: ELEMENT
US-09-632-538C-10

Query Match 66.7%; Score 4; DB 3; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.4e+08;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
 |||:
DB 6 GGTWGG 1

RESULT 20

US-09-608-958-50
; Sequence 50, Application US/09608958
; Patent No. 6518066
; GENERAL INFORMATION:
; APPLICANT: McBride, K.

; APPLICANT: Oulmassov, T.
; APPLICANT: Miller, P.
; APPLICANT: Anderson, J.C.
; APPLICANT: Crossland, L.
; APPLICANT: Adams, T.
; APPLICANT: Gavrias, V.
; TITLE OF INVENTION: Control of Gene Expression in Eukaryotic Cells
; FILE REFERENCE: 15376/03/US
; CURRENT APPLICATION NUMBER: US/09/608,958
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/148,441
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: 60/177,578
; PRIOR FILING DATE: 2000-01-22
; PRIOR APPLICATION NUMBER: 60/195,690
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-608-958-50

Query Match 66.7%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGG 6
|||
DB 1 AAGG 4

RESULT 21
US-09-608-958-51/c
; Sequence 51, Application US/09608958
; Patent No. 6518066
; GENERAL INFORMATION:
; APPLICANT: McBride, K.
; APPLICANT: Oulmassov, T.
; APPLICANT: Miller, P.
; APPLICANT: Anderson, J.C.
; APPLICANT: Crossland, L.
; APPLICANT: Gavrias, V.
; TITLE OF INVENTION: Control of Gene Expression in Eukaryotic Cells
; FILE REFERENCE: 15376/03/US
; CURRENT APPLICATION NUMBER: US/09/608,958
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/148,441
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: 60/177,578
; PRIOR FILING DATE: 2000-01-22
; PRIOR APPLICATION NUMBER: 60/195,690
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-608-958-51

Query Match 66.7%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAA 4
|||
DB 4 GGAA 1
|||
RESULT 22
US-09-435-327A-1
; Sequence 1, Application US/09435327A
; Patent No. 653766
; GENERAL INFORMATION:
; APPLICANT: Uckun, Fatih M.
; APPLICANT: Crotty, Mya L.
; TITLE OF INVENTION: IKAROS ISOFORMS AND MUTANTS
; FILE REFERENCE: 12152.35USU1
; CURRENT APPLICATION NUMBER: US/09/435,327A
; CURRENT FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: 60/107,229
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-435-327A-1

Query Match 66.7%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAA 4
|||
DB 2 GGAA 5
|||

RESULT 23
US-09-585-599A-7/c
; Sequence 7, Application US/09585599A
; Patent No. 6544780
; GENERAL INFORMATION:
; APPLICANT: Wang, Danher
; TITLE OF INVENTION: GENETIC VACCINE THAT MIMICS NATURAL VIRAL INFECTION AND INDUCES LC
; FILE REFERENCE: 22488-706
; CURRENT APPLICATION NUMBER: US/09/585,599A
; CURRENT FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 6
; TYPE: RNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Modified RNA editing site.
US-09-585-599A-7

Query Match 66.7%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAAG 5
|||
DB 6 GAAG 3
|||

RESULT 24
US-09-585-599A-8/c
; Sequence 8, Application US/09585599A
; Patent No. 6544780
; GENERAL INFORMATION:
; APPLICANT: Wang, Danher
; TITLE OF INVENTION: GENETIC VACCINE THAT MIMICS NATURAL VIRAL INFECTION AND INDUCES LC
; FILE REFERENCE: 22488-706
; CURRENT APPLICATION NUMBER: US/09/585,599A
; CURRENT FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 6
; TYPE: RNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Modified RNA editing site.
US-09-585-599A-7

Query Match 66.7%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FILE REFERENCE: 22488-706
CURRENT APPLICATION NUMBER: US/09/585,599A
CURRENT FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 6
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: DNA of modified RNA editing site.
US-09-585-599A-8

Query Match 66.7%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAAG 5
Db 6 GAAG 3

RESULT 25

US-10-014-973A-16
Sequence 16, Application US/10014973A
Patent No. 6706481
GENERAL INFORMATION:
APPLICANT: Ellington, Andrew
APPLICANT: Jhaveri, Sulay
APPLICANT: Rajendran, Manjula
TITLE OF INVENTION: In Vitro Selection of Signaling Aptamers
FILE REFERENCE: D6297
CURRENT APPLICATION NUMBER: US/10/014,973A
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: US 60/244,010
PRIOR FILING DATE: 2000-10-27
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 16
LENGTH: 6
TYPE: RNA
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: Sequence of the 6 nucleotide motif shared by
Patent No. 6706481
OTHER INFORMATION: Families 1 and 2
US-10-014-973A-16

Query Match 66.7%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAAG 5
Db 3 GAAG 6

RESULT 26

US-09-851-271A-14
Sequence 14, Application US/09851271A
Patent No. 6733970
GENERAL INFORMATION:
APPLICANT: Gendaq Limited
TITLE OF INVENTION: Screening System
FILE REFERENCE: 674538-2003
CURRENT APPLICATION NUMBER: US/09/851,271A
CURRENT FILING DATE: 2001-05-08
PRIOR APPLICATION NUMBER: PCT/GB99/03730
PRIOR FILING DATE: 1999-11-09
PRIOR APPLICATION NUMBER: GB9824544.2
PRIOR FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 14

LENGTH: 6
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: RBS
LOCATION: (1)..(6)
OTHER INFORMATION: bacteriophage T7, gene 10 ribosome binding site
US-09-851-271A-14

Query Match 66.7%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGG 6
Db 1 AAGG 4

RESULT 27

US-10-134-188-13
Sequence 13, Application US/10134188
Patent No. 6803230
GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Wild, Martha
TITLE OF INVENTION: PHAGEMID VECTORS
FILE REFERENCE: 1087-22 (70)
CURRENT APPLICATION NUMBER: US/10/134,188
CURRENT FILING DATE: 2002-04-26
PRIOR APPLICATION NUMBER: US 60/287,355
PRIOR FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 6
TYPE: DNA
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: RBS
US-10-134-188-13

Query Match 66.7%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGG 6
Db 1 AAGG 4

RESULT 28

PCT-US92-08094-63
Sequence 63, Application PC/TUS9208094
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
APPLICANT: Ameto, Edward P.
TITLE OF INVENTION: DIAGNOSING AND TREATING AUTOIMMUNE
DISORDERS
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080-4990
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: PCT/US92/08094
/ FILING DATE: 19920923
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/765222
/ FILING DATE: 23-SEP-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/779445
/ FILING DATE: 18-OCT-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/853362
/ FILING DATE: 18-MAR-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hensley, Max D.
/ REGISTRATION NUMBER: 27,043
/ REFERENCE/DOCKET NUMBER: 734P3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415/225-1994
/ TELEFAX: 415/952-9881
/ TELEX: 910/371-7168
/ INFORMATION FOR SEQ ID NO: 63:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6 bases
/ TYPE: NUCLEIC ACID
/ STRANDEDNESS: single
/ TOPOLOGY: linear
PCT-US92-08094-63

Query Match 66.7%; Score 4; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.4e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGA 4
DB 2 GGA 5

RESULT 29
US-08-488-015B-11/c
/ Sequence 11, Application US/08488015B
/ Patent No. 5780272
/ GENERAL INFORMATION:
/ APPLICANT: Jarrell, Kevin A.
/ TITLE OF INVENTION: INTRON-MEDIATED RECOMBINANT TECHNIQUES
/ TITLE OF INVENTION: AND REAGENTS
/ NUMBER OF SEQUENCES: 29
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Foley, Hoag & Eliot
/ STREET: One Post Office Square
/ CITY: Boston
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: ASCII (text)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/488,015B
/ FILING DATE: 07-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Vincent, Matthew P.
/ REGISTRATION NUMBER: 36,709
/ REFERENCE/DOCKET NUMBER: HUV-008.02
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 832-1000
/ TELEFAX: (617) 832-7000
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single

/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
US-08-488-015B-11

Query Match 60.0%; Score 3.6; DB 1; Length 5;
Best Local Similarity 75.0%; Pred. No. 2.9e+08;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGA 5
DB 5 GGA 2

RESULT 30
US-07-862-831A-1
/ Sequence 1, Application US/07862831A
/ Patent No. 5356802
/ GENERAL INFORMATION:
/ APPLICANT: Chandrasegaran, Srinivasan
/ TITLE OF INVENTION: Functional Domains in FokI Restriction
/ TITLE OF INVENTION: Endonuclease
/ NUMBER OF SEQUENCES: 20
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Cushman, Darby & Cushman
/ STREET: 1615 L St., N.W.
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20036-5601
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/862,831A
/ FILING DATE: 19920403
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kokulis, Paul N.
/ REGISTRATION NUMBER: 16,773
/ REFERENCE/DOCKET NUMBER: PNK/4130/93738/SLO
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-861-3000
/ TELEFAX: 202-822-0944
/ TELEX: 6714627 CUSH
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5 base pairs
/ TYPE: NUCLEIC ACID
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
US-07-862-831A-1

Query Match 56.7%; Score 3.4; DB 1; Length 5;
Best Local Similarity 80.0%; Pred. No. 2.9e+08;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGA 5
DB 1 GGA 5

Search completed: July 21, 2005, 04:29:23
Job time : 61 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:25:43 ; Search time 1348.8 Seconds

(without alignments)
169.325 Million cell updates/sec

Title: US-09-735-363A-42

Perfect score: 6

Sequence: 1 ggaagg 6

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 1216

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gssi: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5	83.3	5	9	CL658581
2	5	83.3	6	9	CL683697
3	4	66.7	4	7	CF307853
4	4	66.7	4	7	CF307853 ABF--01-G
5	4	66.7	4	7	CN755098
6	4	66.7	4	9	CN755098 ID0AAA14D
7	4	66.7	5	9	CL677539
8	4	66.7	5	9	CL673276
9	4	66.7	6	1	AL039947
10	4	66.7	6	1	AL039947 DXPp434J
11	4	66.7	6	1	AL042484
12	3.4	56.7	5	9	AL042484 DXPp434F
13	3.4	56.7	6	9	CF331773
14	3	50.0	3	7	CF300120
15	3	50.0	3	7	CF300120 7LEAF--04
16	3	50.0	3	7	CF309377
17	3	50.0	3	7	CF31041 ABF--03-I
18	3	50.0	3	7	CF315183
19	3	50.0	3	7	CF340104
20	3	50.0	3	7	CO790264
21	3	50.0	3	9	CL654446
22	3	50.0	3	9	CL674562
23	3	50.0	3	9	CL679821
24	3	50.0	3	9	CL694726

AL045617	DKFZp4340	4	1	AL045617
CF300913	7LEAF--05	4	7	CF300913
CF317789	HD--07-J1	4	7	CF317789
CF317847	HD--07-L0	4	7	CF317847
CF318240	HD--08-E1	4	7	CF318240
CF338536	RCL1--01-	4	7	CF338536
CK582549	IST WI5_4	4	7	CK582549
CL651736	PRIO112d_	4	9	CL651736
CL679140	PRIO125b_	4	9	CL679140
CL682759	PRIO134d_	4	9	CL682759
AL042460	DKFZp434E	5	1	AL042460
AL046203	DKFZp434D	5	1	AL046203
CF300878	7LEAF--05	5	7	CF300878
CF327578	NACL--02-	5	7	CF327578
CF332399	NACL--08-	5	7	CF332399
CK584110	IST WI5_1	5	7	CK584110
CO779181	BL005D E0	5	7	CO779181
CL423471	01S0557-0	5	9	CL423471
CL661701	PRIO13C_C	5	9	CL661701
CL685291	PRIO140d_	5	9	CL685291
CL696246	PRIO18c_C	5	9	CL696246
CA850767	D06C11_C1	6	6	CA850767
CA850861	D07D05_G1	6	6	CA850861
CA850904	D07H10_O2	6	6	CA850904
CF302557	7LEAF--08	6	7	CF302557
CF321275	ABF--08-K	6	7	CF321275
CF314367	HD--02-N2	6	7	CF314367
CF338772	RCL1--02-	6	7	CF338772
CL654420	PRIO149C_	6	9	CL654420
CL665420	PRIO149C_	6	9	CL665420
CL672294	PRIO16c_B	6	9	CL672294
CL679615	PRIO126C_	6	9	CL679615
CL687157	PRIO146a_	6	9	CL687157
CL687789	PRIO147d_	6	9	CL687789
CA850974	D08G08_N2	6	6	CA850974
CL655267	PRIO122d_	6	9	CL655267
CL670570	PRIO162C_	6	9	CL670570
CL889653	abf96d10_	6	9	CL889653
CA853329	B07A01.se	6	6	CA853329
CF314074	HD--02-H0	6	7	CF314074
CF323326	HDN--03-I	6	7	CF323326
CO789717	NT007C_G0	6	7	CO789717
CL688637	PRIO14a_B	6	9	CL688637
AL043164	DKFZp434F	6	1	AL043164
CF310635	ABF--05-G	6	7	CF310635
CF338261	RCL1--01-	6	7	CF338261
CL680271	PRIO128C_	6	9	CL680271
CL694328	PRIO163d_	6	9	CL694328
AL039341	DKFZp434F	6	9	AL039341
AL042337	DKFZp434B	6	9	AL042337
AL043859	DKFZp434B	6	9	AL043859
AL047069	DKFZp586P	6	9	AL047069
BX266185	BX266185	6	9	BX266185
BX266563	BX266563	6	9	BX266563
BX267118	BX267118	6	9	BX267118
CA850842	D07B06_C1	6	9	CA850842
CA850952	D08E09_J2	6	9	CA850952
CF280384	14ETL--07	6	9	CF280384
CF280511	14ETL--07	6	9	CF280511
CF281505	14ETL--08	6	9	CF281505
CF282353	14ETL--09	6	9	CF282353
CF291112	14ROOF--00	6	9	CF291112
CF292081	14ROOF--00	6	9	CF292081
CF295832	30DGS--05	6	9	CF295832
CF296698	30DGS--05	6	9	CF296698
CF296910	7LEAF--02	6	9	CF296910
CF299571	7LEAF--03	6	9	CF299571
CF299820	7LEAF--03	6	9	CF299820
CF300639	7LEAF--05	6	9	CF300639
CF301112	7LEAF--05	6	9	CF301112
CF302235	7LEAF--07	6	9	CF302235
CF302259	7LEAF--07	6	9	CF302259
CF307123	HDAl--05-	6	9	CF307123

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98      2 33.3 2 7 CF307878      CF307878 ABF--01-H
99      2 33.3 2 7 CF311389      CF311389 ABF--06-J
100     2 33.3 2 7 CF311851      CF311851 ABF--07-E

ALIGNMENTS

RESULT 1
LOCUS   CL658581
DEFINITION
P. pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION
VERSION   CL658581.1 GI:50141502
SOURCE    GSS.
ORGANISM  Pristionchus pacificus
           Pristionchus pacificus
           Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
           Neodiplogasteridae; Pristionchus.
REFERENCE
AUTHORS   Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE     AppADB: an AcedB database for the nematode satellite organism
JOURNAL   Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT   Contact: Sommer RJ
           Evolutionary Biology
           Max-Planck-Institute for Developmental Biology
           Spemannstr. 37-39, Tuebingen D-72076, Germany
           Tel: 00497071601371
           Fax: 00497071601498
           Email: ralf.sommer@tuebingen.mpg.de
           This library was generated at Caltech, Pasadena, USA and end
           sequenced at Vancouver, Canada.
           Seq primer: T7
           Class: fosmid ends.

FEATURES             source
    source
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    /organism="Pristionchus pacificus"
    /mol_type="genomic DNA"
    /strain="California"
    /db_xref="taxon:54126"
    /clone_lib="Mixed stage fosmid library of P. pacificus
    var. California"
    /note="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Query Match      83.3%; Score 5; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.3e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGAAG 5
        |||||
        5 GGAAG 1

RESULT 3
LOCUS   CF307853/c
DEFINITION
P. pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION
VERSION   CF307853.1 GI:33679614
SOURCE    EST.
ORGANISM  Oryza sativa (japonica cultivar-group)
           Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES             source
    source
    1..4
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="ABF--01-G24"
    /tissue_type="leaf"
    /dev_stage="14 days after germination"
    /lab_host="E.coli DH10B"
    /clone_lib="ABF3-overexpressing transgenic rice plasmid
    cDNA library (ABF)"
    /note="Vector: pCK4-TOPO; Site_1: EcoRI; Leaf was dried
    for 2hrs. Oligo-capped mRNA was reverse transcribed and

Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.

FEATURES             source
    source
    1..5
    /organism="Pristionchus pacificus"
    /mol_type="genomic DNA"
    /strain="California"
    /db_xref="taxon:54126"
    /clone_lib="Mixed stage fosmid library of P. pacificus
    var. California"
    /note="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Query Match      83.3%; Score 5; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.6e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GAAGG 6
        |||||
        1 GAAGG 5

RESULT 2
LOCUS   CL683697/c
DEFINITION
P. pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION
VERSION   CL683697.1 GI:50191457
SOURCE    GSS.
ORGANISM  Pristionchus pacificus
           Pristionchus pacificus
           Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
           Neodiplogasteridae; Pristionchus.
REFERENCE
AUTHORS   Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE     AppADB: an AcedB database for the nematode satellite organism

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then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

ORIGIN

Query Match 66.7%; Score 4; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGG 6

Db |||||

4 AAGG 1

RESULT 4

CN755098/c
LOCUS
DEFINITION CN755098 4 bp mRNA linear EST 19-MAY-2004
ID0AAA14DE08R1 ApMS Acyrthosiphon pisum cDNA clone ID0AAA14DE08
5', mRNA sequence.

ACCESSION CN755098

VERSION 1

KEYWORDS 1 (bases 1 to 4)

SOURCE Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,

ORGANISM Acyrthosiphon pisum (pea aphid)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;

Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

REFERENCE 1 (bases 1 to 4)

AUTHORS Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,

Stern, D., Tagu, D. and Winkler, P.

TITLE An expressed sequence tags database for the pea aphid Acyrthosiphon

pisum

JOURNAL Unpublished (2004)

COMMENT Contact: D. Tagu

INRA Rennes

UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France

Tel: +33.2.23.48.51.65

Fax: +33.2.23.48.51.50

Risk of contamination by bacterial sequences from obligatory

(Buchnera) or facultative endosymbionts. These sequences were

obtained in the frame of the International Consortium of Aphid

Genomics in collaboration with Genoscope

PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 14 row: E column: 8.

Location/Qualifiers

1. .4

/organism="Acyrthosiphon pisum"

/mol_type="mRNA"

/cultivar="developmentstage"

/db_xref="taxon:7029"

/clone="ID0AAA14DE08"

/tissue_type="whole insect"

/dev_stage="nymphs and adults (parthenogenetic females)"

/lab_host="XLI-Blue"

/clone_lib="ApMS"

/notes="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI;

Sample name: ID0AAA ; plant growth place: Department of

Ecology & Evolutionary Biology, Princeton University ;

Soil conditions: Soil, Sowing, date: 01/06/1999 ;

Harvesting date: 01/06/1999 ; Stress date: no stress ;

Description: Aphids inoculated on one-week old Vicia faba

under non-sterile conditions. All parthenogenetic stages

and both winged and wingless adults were collected for

library construction. ; experimental condition: long

photoperiod (16-hr light/8-hr dark at 18 c)"

ORIGIN

Query Match 66.7%; Score 4; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGG 6

Db

|||||

4 AAGG 1

RESULT 5

CN755098/c

LOCUS

DEFINITION CL677539 4 bp DNA linear GSS 09-JUL-2004

PRI0120C.D05_2 - PRI0120C.BR (4) Mixed stage fosmid library of P.

pacificus var. California Pristionchus pacificus genomic, genomic

survey sequence.

ACCESSION CL677539

VERSION 1

KEYWORDS 1 (bases 1 to 4)

SOURCE GSS.

ORGANISM Pristionchus pacificus

Pristionchus pacificus

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;

Neodiplogasteridae; Pristionchus.

REFERENCE 1 (bases 1 to 4)

AUTHORS Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.

TITLE AppaDB: an AcedB database for the nematode satellite organism

Pristionchus pacificus

Nucleic Acids Res. 32 (1), D421-D422 (2004)

JOURNAL Contact: Sommer RJ

COMMENT Max-Planck-Institute for Developmental Biology

Spemannstr. 37-39, Tuebingen D-72076, Germany

Tel: 00497071601371

Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de

This library was generated at Caltech, Pasadena, USA and end

sequenced at Vancouver, Canada.

Seq primer: T7

Class: fosmid ends.

Location/Qualifiers

1. .4

/organism="Pristionchus pacificus"

/mol_type="genomic DNA"

/strain="California"

/db_xref="taxon:54126"

/clone_lib="Mixed stage fosmid library of P. pacificus

var. California"

/note="Vector: pEpifos-5 Fosmid vector"

ORIGIN

Query Match 66.7%; Score 4; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+09;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAAG 5

Db |||||

4 GAAG 1

RESULT 6

CL673276/c

LOCUS

DEFINITION CL673276 5 bp DNA linear GSS 09-JUL-2004

PRI019a.E01 - PRI019a.B21 (5) Mixed stage fosmid library of P.

pacificus var. California Pristionchus pacificus genomic, genomic

survey sequence.

ACCESSION CL673276

VERSION 1

KEYWORDS 1 (bases 1 to 5)

SOURCE GSS.

ORGANISM Pristionchus pacificus

Pristionchus pacificus

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;

Neodiplogasteridae; Pristionchus.

REFERENCE 1 (bases 1 to 5)

AUTHORS Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.

TITLE AppaDB: an AcedB database for the nematode satellite organism

Pristionchus pacificus

Nucleic Acids Res. 32 (1), D421-D422 (2004)

JOURNAL Contact: Sommer RJ

COMMENT Evolutionary Biology

Qy 1 GGAAG 5

```

Db
1 CGAGG 5

RESULT 13
LOCUS
DEFINITION
CL689395
PFI0151a.D04_2 - PFI0151a.BR (6) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
CL689395
CL689395.1 GI:50211303
GSS.
Pristionchus pacificus
Pristionchus pacificus
SOURCE
ORGANISM
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 6)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AppADB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
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/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pPifos-5 Fosmid vector"

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Query Match 56.7%; Score 3.4; DB 9; Length 6;
Best Local Similarity 80.0%; Pred. No. 6.3e+09;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAAGG 6
|||
Db 6 GATGG 2

RESULT 14
CF282217
LOCUS
DEFINITION
CF282217
14ETL--09-K02.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-K02,
mRNA sequence.
CF282217
CF282217.1 GI:33659604
EST.
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
1 (bases 1 to 3)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1..3
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--04-G11"
/tissue_type="leaf"
/dev_stages="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGA 3
|||
Db 1 GGA 3

RESULT 15
CF300120/c
LOCUS
DEFINITION
CF300120
7LEAF--04-G11.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--04-G11, mRNA
sequence.
CF300120
CF300120.1 GI:33671881
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
1 (bases 1 to 3)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1..3
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--04-G11"
/tissue_type="leaf"
/dev_stages="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN

```

```

of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1..3
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--09-K02"
/tissue_type="leaf"
/dev_stages="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGA 3
|||
Db 1 GGA 3

RESULT 15
CF300120/c
LOCUS
DEFINITION
CF300120
7LEAF--04-G11.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--04-G11, mRNA
sequence.
CF300120
CF300120.1 GI:33671881
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
1 (bases 1 to 3)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1..3
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--04-G11"
/tissue_type="leaf"
/dev_stages="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN

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Query Match      50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 AGG 6
      |||
Db      3 AGG 1

RESULT 16
CF309377
LOCUS      3 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--03-119.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--03-119, mRNA sequence.
ACCESSION  CF309377
VERSION     CF309377.1 GI:33681138
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 3)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
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    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="ABF--03-119"
    /tissue_type="leaf"
    /dev_stage="14 days after germination"
    /lab_host="E.coli DH10B"
    /clone_lib="ABF3-overexpressing transgenic rice plasmid
    cDNA library (ABF)"
    /notes="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
    for 2hrs. Oligo-capped mRNA was reverse transcribed and
    then used for PCR. mRNA was prepared from ABA-responsive
    element binding transcription factor 3 overexpression
    line."

FEATURES             source
    source
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    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="ABF--03-119"
    /tissue_type="leaf"
    /dev_stage="14 days after germination"
    /lab_host="E.coli DH10B"
    /clone_lib="ABF3-overexpressing transgenic rice plasmid
    cDNA library (ABF)"
    /notes="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
    for 2hrs. Oligo-capped mRNA was reverse transcribed and
    then used for PCR. mRNA was prepared from ABA-responsive
    element binding transcription factor 3 overexpression
    line."

ORIGIN
Query Match      50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 AAG 5
      |||
Db      1 AAG 3

RESULT 17
CF311041
LOCUS      3 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--06-B17.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--06-B17, mRNA sequence.
ACCESSION  CF311041
VERSION     CF311041.1 GI:33682802
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 3)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
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    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
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    /db_xref="taxon:39947"
    /clone="ABF--03-119"
    /tissue_type="leaf"
    /dev_stage="14 days after germination"
    /lab_host="E.coli DH10B"
    /clone_lib="ABF3-overexpressing transgenic rice plasmid
    cDNA library (ABF)"
    /notes="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
    for 2hrs. Oligo-capped mRNA was reverse transcribed and
    then used for PCR. mRNA was prepared from ABA-responsive
    element binding transcription factor 3 overexpression
    line."

ORIGIN
Query Match      50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 AAG 5
      |||
Db      1 AAG 3

RESULT 17
CF311041
LOCUS      3 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--06-B17.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
            ABF--06-B17, mRNA sequence.
ACCESSION  CF311041
VERSION     CF311041.1 GI:33682802
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 3)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
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    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="ABF--06-B17"
    /tissue_type="leaf"
    /dev_stage="14 days after germination"
    /lab_host="E.coli DH10B"
    /clone_lib="ABF3-overexpressing transgenic rice plasmid
    cDNA library (ABF)"
    /notes="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
    for 2hrs. Oligo-capped mRNA was reverse transcribed and
    then used for PCR. mRNA was prepared from ABA-responsive
    element binding transcription factor 3 overexpression
    line."

```

```

ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 3)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
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    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="ABF--06-B17"
    /tissue_type="leaf"
    /dev_stage="14 days after germination"
    /lab_host="E.coli DH10B"
    /clone_lib="ABF3-overexpressing transgenic rice plasmid
    cDNA library (ABF)"
    /notes="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
    for 2hrs. Oligo-capped mRNA was reverse transcribed and
    then used for PCR. mRNA was prepared from ABA-responsive
    element binding transcription factor 3 overexpression
    line."

ORIGIN
Query Match      50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 AAG 5
      |||
Db      1 AAG 3

RESULT 18
CF315183
LOCUS      3 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--04-A04.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--04-A04, mRNA sequence.
ACCESSION  CF315183
VERSION     CF315183.1 GI:33686944
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 3)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
    source
    1..3
    /organism="Oryza sativa (japonica cultivar-group)"

```

```

/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--04-A04"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: PCRA-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

```

ORIGIN

```

Query Match      50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGA 3

Db |||

Db 1 GGA 3

RESULT 19

CF340104

LOCUS

```

DEFINITION      CF340104      3 bp      mRNA      linear      EST 18-AUG-2003
                  RCL1--06-P10.g1 Regenerated callus lambda phage cDNA library (RCL1)
                  Oryza sativa (japonica cultivar-group) cDNA clone RCL1--06-P10,
                  mRNA sequence.

```

ACCESSION CF340104.1 GI:33828568

VERSION

KEYWORDS

SOURCE

ORGANISM

```

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.

```

REFERENCE 1 (bases 1 to 3)

```

AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)

```

TITLE

JOURNAL

COMMENT

```

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

```

FEATURES

source

1..3

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="RCL1--06-P10"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli SOLR"

/clone_lib="Regenerated callus lambda phage cDNA library

(RCL1)"

```

/notes="Vector: pBluescript SK(+); Site_1: SstI; Site_2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
end with SstI and 3' end with XhoI site. Callus was
induced on 2N6 media for 30 days and cultured for 36hrs on
regenerated media"

```

ORIGIN

```

Query Match      50.0%; Score 3; DB 7; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 3 AAG 5

Db |||

Db 1 AAG 3

RESULT 20

CO790264

LOCUS

```

DEFINITION      CO790264      3 bp      mRNA      linear      EST 05-AUG-2004
                  NT009A_H05 St18-22 Neural tube (NT) Ambystoma mexicanum cDNA 5',
                  similar to hypothetical protein, mRNA sequence.

```

ACCESSION CO790264

VERSION

KEYWORDS

SOURCE

ORGANISM

```

Ambystoma mexicanum (axolotl)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
Ambystoma.

```

REFERENCE 1 (bases 1 to 3)

```

AUTHORS      Habermann,B., Bebin,A.G., Herklotz,S., Volkmer,M., Eckelt,K.,
              Pehlke,K., Epperlein,H.H., Schackert,H.K., Wiebe,G. and Tanaka,E.M.
              An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
              expressed sequence tags from embryonic and regenerating blastema
              cDNA libraries

```

JOURNAL

COMMENT

Genome Biol. (2004) In press

Contact: Elly M. Tanaka

Tanaka lab

```

Max Planck Institute of Molecular Cell Biology and Genetics,
Dresden

```

Pfotenhauerstrasse 108, 01307 Dresden, Germany

Tel: 0049 351 210 2620

Fax: 0049 351 210 1489

Email: tanaka@mpi-cbg.de

Plate: NT009A row: 05 column: H

Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.

Location/Qualifiers

FEATURES source

1..3

/organism="Ambystoma mexicanum"

/mol_type="mRNA"

/db_xref="taxon:8296"

/tissue_type="Neural Tube, Notochord, Somites"

/cell_type="Includes Neural tube, notochord, somites"

/dev_stage="Stage 18-22"

/clone_lib="St18-22 Neural tube (NT)"

/note="Vector: pCMVSPORT6; Site_1: NotI; Site_2: SalI;

Unnormalized cDNA plasmid library prepared by Invitrogen.

Size fractionated mRNA was polyA+ primed and cloned into

NotI-SalI site of pCMVSPORT6. Bacterial host is

EMDH10B-TONA. Average insert size is 1.5 kb.

TAG_LIB=NT"

ORIGIN

Query Match 50.0%; Score 3; DB 7; Length 3;

Best Local Similarity 100.0%; Pred. No. 1.3e+10;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGG 6

Db |||

Db 1 AGG 3

RESULT 21

CL654446

LOCUS

```

DEFINITION      CL654446      3 bp      DNA      linear      GSS 09-JUL-2004
                  PRI0120c_P05 - PRI0120c.B21 (3) Mixed stage foetid library of P.
                  pacificus var. California Pristionchus pacificus genomic, genomic
                  survey sequence.

```

ACCESSION CL654446

VERSION

KEYWORDS

SOURCE

ORGANISM

Pristionchus pacificus

Pristionchus pacificus

```

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 3)
AppDB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1. .3
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/notes="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Query Match 50.0%; Score 3; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAA 4
|||
Db 1 GAA 3

RESULT 22
LOCUS CL674562/c
DEFINITION Pr10112c.A06 2 - PRI0112c.BR (3) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
Accession CL674562.1 GI:50177804
Version CL674562.1
Keywords GSS.
Source Pristionchus pacificus
Organism Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 3)
AppDB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1. .3
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"

FEATURES
source
1. .3
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"

ORIGIN
Query Match 50.0%; Score 3; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAA 4
|||
Db 1 GAA 3

RESULT 22
LOCUS CL674562/c
DEFINITION Pr10112c.A06 2 - PRI0112c.BR (3) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
Accession CL674562.1 GI:50177804
Version CL674562.1
Keywords GSS.
Source Pristionchus pacificus
Organism Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 3)
AppDB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1. .3
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"

FEATURES
source
1. .3
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"

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/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/notes="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Query Match 50.0%; Score 3; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGA 3
|||
Db 3 GGA 1

RESULT 23
LOCUS CL679821/c
DEFINITION CL679821.1 GI:50186536
Accession CL679821.1
Version CL679821.1
Keywords GSS.
Source Pristionchus pacificus
Organism Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 3)
AppDB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1. .3
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/notes="Vector: pEpifos-5 Fosmid vector"

FEATURES
source
1. .3
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"

ORIGIN
Query Match 50.0%; Score 3; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGG 6
|||
Db 3 AGG 1

RESULT 24
LOCUS CL694726
DEFINITION CL694726.1 GI:50216634
Accession CL694726
Version CL694726.1
Keywords GSS.
Source Pristionchus pacificus

```

```

ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 3)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppADB: an AcedB database for the nematode satellite organism
JOURNAL Pristionchus pacificus
COMMENT Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
FEATURES             Location/Qualifiers
     source           1..3
                     /organism="Pristionchus pacificus"
                     /mol_type="genomic DNA"
                     /strain="California"
                     /db_xref="taxon:54126"
                     /clone_lib="Mixed stage fosmid library of P. pacificus
                     var. California"
                     /note="Vector: pEpifos-5 Fosmid vector"
ORIGIN
Query Match      50.0%; Score 3; DB 9; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAA 4
   |||
Db 1 GAA 3

RESULT 25
AL045617/c
LOCUS
DEFINITION
ACCESSION AL045617
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4)
AUTHORS Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
Wienann,S.
TITLE EST (Duesterhoeft, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES             Location/Qualifiers
     source           1..4
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp434O245"
                     /tissue_type="testis"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="434 (synonym: htes3)"
                     /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
ORIGIN
Query Match      50.0%; Score 3; DB 1; Length 4;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAA 4
   |||
Db 1 GAA 3

RESULT 26
CF300913/c
LOCUS
DEFINITION
ACCESSION CF300913
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 4)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@bio.com, bnhnm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source           1..4
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--05-J02"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."
ORIGIN
Query Match      50.0%; Score 3; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGG 6
   |||
Db 4 AGG 2

RESULT 27
CF317789/c
LOCUS
DEFINITION
ACCESSION CF317789
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

```

```

REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1. .4
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--07-J18"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

ORIGIN
Query Match      50.0%; Score 3; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 AAG 5
      |||
Db      4 AAG 2

RESULT 29
LOCUS      CF317847
DEFINITION HD--07-L01.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
              library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
ACCESSION   CF317847
VERSION     CF318240.1 GI:33689608
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 4)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1. .4
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--07-L01"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

ORIGIN
Query Match      50.0%; Score 3; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGA 3
      |||
Db      3 GGA 1

RESULT 28
LOCUS      CF317847/c
DEFINITION HD--07-L01.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
              library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
ACCESSION   CF317847
VERSION     CF317847.1 GI:33689608
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 4)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1. .4
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--07-L01"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

ORIGIN
Query Match      50.0%; Score 3; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 AAG 5
      |||
Db      2 AAG 4

RESULT 29
LOCUS      CF318240
DEFINITION HD--08-E17.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
              library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
ACCESSION   CF318240
VERSION     CF318240.1 GI:33690001
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 4)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1. .4
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--08-E17"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

ORIGIN
Query Match      50.0%; Score 3; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 AAG 5
      |||
Db      2 AAG 4

```

```

RESULT 30
CF338536
LOCUS
DEFINITION
CF338536
4 bp mRNA linear EST 18-AUG-2003
RCL1--01-P22.g1 Regenerated callus lambda phage cDNA library (RCL1)
Oryza sativa (japonica cultivar-group) cDNA clone RCL1--01-P22,
mRNA sequence.
ACCESSION
CF338536
VERSION
CF338536.1 GI:33825460
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 4)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
Location/Qualifiers
1..4
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="RCL1--01-P22"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library
(RCL1)"
/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5',
end with SstI and 3', end with XhoI site. Callus was
induced on 2N6 media for 30 days and cultured for 36hrs on
regenerated media"
ORIGIN
Query Match 50.0%; Score 3; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.5e+09;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGA 3
Db |||
2 GGA 4
Search completed: July 21, 2005, 01:54:36
Job time : 1352.8 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 21:46:09 ; Search time 187.4 Seconds
(without alignments)
189.533 Million cell updates/sec

Title: US-09-735-363A-42

Perfect score: 6

Sequence: 1 ggaagg 6

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 1582

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : N_Geneseq_16Dec04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	83.3	6	13	Adr32744 Human nic
2	5	83.3	6	13	Adr32766 Human nic
3	5	83.3	6	13	Adr32505 Human nic
4	4.4	73.3	6	10	Adel0263 S. lavendu
5	4.4	73.3	6	10	Adel0336 S. lavendu
6	4.4	73.3	6	10	ACA88957 Selection
7	4.4	73.3	6	12	ADJ35621 Stabilisi
8	4	66.7	6	2	Aaq38797 PCR prime
9	4	66.7	6	2	Aaq70690 Triplex f
10	4	66.7	6	4	Aaf91829 Breast-ca
11	4	66.7	6	8	ACC69109 Cucumber
12	4	66.7	6	8	ABZ23991 Nucleotid
13	4	66.7	6	9	ACH50860 Hypotheti
14	4	66.7	6	9	ACH50844 Hypotheti
15	4	66.7	6	10	ADD66333 Ebola GP
16	4	66.7	6	10	ADD66334 Ebola GP
17	4	66.7	6	10	AdE38305 Immune mo
18	4	66.7	6	10	AdE38325 Immune mo
19	4	66.7	6	10	AdE38297 Immune mo
20	4	66.7	6	10	AdE38301 Immune mo

21	4	66.7	6	12	ADK14286	Adk14286 Candida p
22	4	66.7	6	12	ADK14297	Adk14297 Candida p
23	4	66.7	6	12	ADL09220	Adl09220 T3 promot
24	4	66.7	6	13	ADR34774	Adr34774 Human nic
25	4	66.7	6	13	ADR34775	Adr34775 Human nic
26	4	66.7	6	13	ADR34773	Adr34773 Human nic
27	4	66.7	6	13	ADR37260	Adr37260 Human nic
28	4	66.7	6	13	ADR33235	Adr33235 Human nic
29	4	66.7	6	13	ADR32580	Adr32580 Human nic
30	4	66.7	6	13	ADR37262	Adr37262 Human nic
31	4	66.7	6	13	ADR34776	Adr34776 Human nic
32	4	66.7	6	13	ADR37261	Adr37261 Human nic
33	4	66.7	6	13	ADR37263	Adr37263 Human nic
34	3.6	60.0	6	13	ADR35732	Adr35732 Human nic
35	3.6	60.0	6	13	ADR35725	Adr35725 Human nic
36	3.6	60.0	6	13	ADR35729	Adr35729 Human nic
37	3.6	60.0	6	13	ADR35730	Adr35730 Human nic
38	3.6	60.0	6	13	ADR35731	Adr35731 Human nic
39	3.6	60.0	6	13	ADR35728	Adr35728 Human nic
40	3.6	60.0	6	13	ADR35727	Adr35727 Human nic
41	3.6	60.0	6	13	ADR35726	Adr35726 Human nic
42	3.4	56.7	5	3	AAA56981	Aaa56981 Human col
43	3.4	56.7	5	6	ABT12403	Abt12403 Orestes s
44	3.4	56.7	5	8	ACD56683	Acd56683 HBV RT pr
45	3.4	56.7	5	8	ABZ75665	Abz75665 Helicase-
46	3.4	56.7	5	8	ABZ75667	Abz75667 Helicase-
47	3.4	56.7	5	8	ABZ75663	Abz75663 Helicase-
48	3.4	56.7	5	10	ADH60372	Adh60372 Myctophid
49	3.4	56.7	5	10	ACD91697	Acd91697 Human col
50	3.4	56.7	6	2	AAQ61541	Aaq61541 TDT promo
51	3.4	56.7	6	2	AAQ53911	Aaq53911 Portion o
52	3.4	56.7	6	2	AAV45399	Aav45399 TDT promo
53	3.4	56.7	6	3	AAa62709	Aaa62709 FNA clamp
54	3.4	56.7	6	6	ABS78162	Abs78162 Angiogene
55	3.4	56.7	6	8	ACD56688	Acd56688 HBV RT pr
56	3.4	56.7	6	8	ACD56687	Acd56687 HBV RT pr
57	3.4	56.7	6	9	ACD99934	Acd99934 Immunosti
58	3.4	56.7	6	12	ADJ35694	Adj35694 Stabilisi
59	3.4	56.7	6	12	ADJ35808	Adj35808 Stabilisi
60	3.4	56.7	6	12	ADJ35691	Adj35691 Stabilisi
61	3.4	56.7	6	12	ADJ35355	Adj35355 Stabilisi
62	3.4	56.7	6	12	ADO04837	Ado04837 Cpg oligo
63	3.4	56.7	6	13	ADR33236	Adr33236 Human nic
64	3.2	53.3	6	3	AAA28440	Aaa28440 Synthetic
65	3.2	53.3	6	4	AAF91843	Aaf91843 Breast-ca
66	3.3	50.0	3	10	AD58066	Ad58066 Human gen
67	3	50.0	4	4	AAL24357	Aal24357 Human bre
68	3	50.0	4	4	AAF61450	Aaf61450 Cyclin bi
69	3	50.0	4	8	ACD56767	Acd56767 Synthetic
70	3	50.0	4	8	ACD56782	Acd56782 Synthetic
71	3	50.0	4	8	ACD56773	Acd56773 Synthetic
72	3	50.0	4	8	ACD56681	Acd56681 HBV RT pr
73	3	50.0	4	8	ACD56774	Acd56774 Synthetic
74	3	50.0	4	8	ACD56781	Acd56781 Synthetic
75	3	50.0	4	8	ACD56766	Acd56766 Synthetic
76	3	50.0	4	8	ACD56678	Acd56678 HBV RT pr
77	3	50.0	4	8	ACD56758	Acd56758 Synthetic
78	3	50.0	4	8	ACD56759	Acd56759 Synthetic
79	3	50.0	4	12	ADG43024	Adg43024 Human rib
80	3	50.0	4	12	ADO40990	Ado40990 Human cDN
81	3	50.0	5	1	AA93676	Aan93676 Synthetic
82	3	50.0	5	2	AAV72348	Aav72348 US908745
83	3	50.0	5	4	AAI19176	Aai19176 Human bre
84	3	50.0	5	4	AAH56407	Aah56407 Escherich
85	3	50.0	5	6	ABS78153	Abs78153 Angiogene
86	3	50.0	5	6	ABN73147	Abn73147 Bovine em
87	3	50.0	5	6	ABN73154	Abn73154 Bovine em
88	3	50.0	5	8	ACD56685	Acd56685 HBV RT pr
89	3	50.0	5	8	ACD56682	Acd56682 HBV RT pr
90	3	50.0	5	9	ACD99926	Acd99926 Immunosti
91	3	50.0	5	12	ADF90315	Adf90315 NEO ribos
92	3	50.0	5	12	AD161783	Adi61783 NEO ribos
93	3	50.0	5	12	ADM32647	Adm32647 Fragment

94 3 50.0 5 12 ADM88491 Adm88491 Gene expr
 c 95 3 50.0 5 12 ADO05794 ADO05794 Telomere-
 96 3 50.0 6 1 AAN81733 AAN81733 Gcein I r
 c 97 3 50.0 6 1 AAN81733 AAN81733 Gcein I r
 c 98 3 50.0 6 1 AAN93284 AAN93284 Promoter
 99 3 50.0 6 2 AAQ50333 AAQ50333 Ribozyme
 100 3 50.0 6 2 AAQ47786 AAQ47786 Mammalian

ALIGNMENTS

RESULT 1
 ADR32744
 ID ADR32744 standard; DNA; 6 BP.
 XX
 AC ADR32744;
 XX
 DT 04-NOV-2004 (first entry)
 XX
 DE Human nicking agent target DNA #285.
 XX
 DE ss; nicking agent; assay panel; diagnosis; expression pattern;
 KW DNA fingerprinting; nosocomial infection; microbiological assay;
 KW bacterial contamination; genome mapping; bioremediation.
 XX
 OS Homo sapiens.
 XX
 OS WO2004067765-A2.
 FN
 XX
 PD 12-AUG-2004.
 XX
 PD 29-JAN-2004; 2004WO-US002720.
 PF
 XX
 PF 29-JAN-2003; 2003US-0443811P.
 PR
 XX
 PR (KECK-) KECK GRADUATE INST.
 PA
 XX
 PA Van Ness J, Galas DJ, Van Ness LK;
 PI
 XX
 PI WPI; 2004-581010/56.
 DR
 XX
 DR Identifying nucleic acid sample source, useful for identifying bacterial
 PT strains involved in nosocomial infections, comprises treating the nucleic
 PT acid sample with components comprising a nicking agent under nicking
 PT conditions.
 XX
 XX Example 1; Page 76; 238pp; English.

The invention relates to a method of treating a nucleic acid sample with
 components under nicking conditions, where the components comprise a
 nicking agent, and the conditions cause the nicking agent to nick the
 nucleic acid sample to thus produce a family of initiating
 oligonucleotide fragments, and subjecting one or more members of the
 family of initiating oligonucleotide fragments to a characterization
 process to thus provide results. The method is useful for creating an
 assay panel of diagnostic oligonucleotides that can identify any organism
 or individual. The method is useful for characterizing other DNA
 molecules e.g., cDNA, and for characterizing cDNA expression patterns.
 The method, kit or composition is useful for identifying the source
 organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
 non-human animal or human. The method is particularly useful for rapidly
 fingerprinting DNA to identifying prokaryotic and eukaryotic species,
 subspecies, and especially strains or individuals of the subspecies. It
 is especially useful for identifying different bacterial strains involved
 in e.g., nosocomial infections. Furthermore, the method is useful for
 diagnosing bacterial disease in plants and humans, monitoring for
 bacterial content and/or contamination in the environment, monitoring
 food for bacterial contamination, monitoring manufacturing processes for
 bacterial contamination, monitoring quality assurance/quality control of
 laboratory tests involving microbiological assays, tracing bacterial
 contamination and/or outbreaks of bacterial infections, genome mapping,
 monitoring bioremediation sites, and for monitoring agricultural sites

CC for test crops, bacteria and recombinant molecules. This sequence
 CC corresponds to nucleic acid used in the method of the invention.
 XX
 SQ Sequence 6 BP; 2 A; 0 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 83.3%; Score 5; DB 13; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GAAGG 6
 Db 1 GAAGG 5
 RESULT 2
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 ID ADR32766 standard; DNA; 6 BP.
 XX
 AC ADR32766;
 XX
 DT 04-NOV-2004 (first entry)
 XX
 DE Human nicking agent target DNA #307.
 XX
 DE ss; nicking agent; assay panel; diagnosis; expression pattern;
 KW DNA fingerprinting; nosocomial infection; microbiological assay;
 KW bacterial contamination; genome mapping; bioremediation.
 XX
 OS Homo sapiens.
 OS
 XX
 FN WO2004067765-A2.
 PN
 XX
 PD 12-AUG-2004.
 XX
 PD 29-JAN-2004; 2004WO-US002720.
 PF
 XX
 PF 29-JAN-2003; 2003US-0443811P.
 PR
 XX
 PR (KECK-) KECK GRADUATE INST.
 PA
 XX
 PA Van Ness J, Galas DJ, Van Ness LK;
 PI
 XX
 PI WPI; 2004-581010/56.
 DR
 XX
 DR Identifying nucleic acid sample source, useful for identifying bacterial
 PT strains involved in nosocomial infections, comprises treating the nucleic
 PT acid sample with components comprising a nicking agent under nicking
 PT conditions.
 XX
 XX Example 1; Page 76; 238pp; English.
 PS
 CC
 CC The invention relates to a method of treating a nucleic acid sample with
 CC components under nicking conditions, where the components comprise a
 CC nicking agent, and the conditions cause the nicking agent to nick the
 CC nucleic acid sample to thus produce a family of initiating
 CC oligonucleotide fragments, and subjecting one or more members of the
 CC family of initiating oligonucleotide fragments to a characterization
 CC process to thus provide results. The method is useful for creating an
 CC assay panel of diagnostic oligonucleotides that can identify any organism
 CC or individual. The method is useful for characterizing other DNA
 CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
 CC The method, kit or composition is useful for identifying the source
 CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
 CC non-human animal or human. The method is particularly useful for rapidly
 CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
 CC subspecies, and especially strains or individuals of the subspecies. It
 CC is especially useful for identifying different bacterial strains involved
 CC in e.g., nosocomial infections. Furthermore, the method is useful for
 CC diagnosing bacterial disease in plants and humans, monitoring for
 CC bacterial content and/or contamination in the environment, monitoring
 CC food for bacterial contamination, monitoring manufacturing processes for
 CC bacterial contamination, monitoring quality assurance/quality control of
 CC laboratory tests involving microbiological assays, tracing bacterial
 CC contamination and/or outbreaks of bacterial infections, genome mapping,
 CC monitoring bioremediation sites, and for monitoring agricultural sites

CC contamination and/or outbreaks of bacterial infections, genome mapping,
 CC monitoring bioremediation sites, and for monitoring agricultural sites
 CC for test crops, bacteria and recombinant molecules. This sequence
 CC corresponds to nucleic acid used in the method of the invention.

XX
 SQ Sequence 6 BP; 2 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 83.3%; Score 5; DB 13; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAG 5
 |||||
 Db 1 GGAAG 5

RESULT 3
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 ID ADR32505 standard; DNA; 6 BP.
 XX AC ADR32505;
 XX DT 04-NOV-2004 (first entry)
 XX DE Human nicking agent target DNA #46.
 XX ss; nicking agent; assay panel; diagnosis; expression pattern;
 KW DNA fingerprinting; nosocomial infection; microbiological assay;
 KW bacterial contamination; genome mapping; bioremediation.
 XX
 OS Homo sapiens.
 XX WO2004067765-A2.
 PN 12-AUG-2004.
 PD 29-JAN-2004; 2004WO-US002720.
 XX 29-JAN-2003; 2003US-0443811P.
 PF (KECK-) KECK GRADUATE INST.
 PR Van Ness J, Galas DJ, Van Ness LK;
 XX WPI; 2004-581010/56.
 DR Identifying nucleic acid sample source, useful for identifying bacterial
 PT strains involved in nosocomial infections, comprises treating the nucleic
 PT acid sample with components comprising a nicking agent under nicking
 PT conditions.

XX
 PS Example 1; Page 72; 238pp; English.

CC The invention relates to a method of treating a nucleic acid sample with
 CC components under nicking conditions, where the components comprise a
 CC nicking agent, and the conditions cause the nicking agent to nick the
 CC nucleic acid sample to thus produce a family of initiating
 CC oligonucleotide fragments, and subjecting one or more members of the
 CC family of initiating oligonucleotide fragments to a characterization
 CC process to thus provide results. The method is useful for creating an
 CC assay panel of diagnostic oligonucleotides that can identify any organism
 CC or individual. The method is useful for characterizing other DNA
 CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
 CC The method, kit or composition is useful for identifying the source
 CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
 CC non-human animal or human. The method is particularly useful for rapidly
 CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
 CC subspecies, and especially strains or individuals of the subspecies. It
 CC is especially useful for identifying different bacterial strains involved
 CC in e.g., nosocomial infections. Furthermore, the method is useful for
 CC diagnosing bacterial disease in plants and humans, monitoring for
 CC bacterial content and/or contamination in the environment, monitoring
 CC food for bacterial contamination, monitoring manufacturing processes for

CC bacterial contamination, monitoring quality assurance/quality control of
 CC laboratory tests involving microbiological assays, tracing bacterial
 CC contamination and/or outbreaks of bacterial infections, genome mapping,
 CC for test crops, bacteria and recombinant molecules. This sequence
 CC corresponds to nucleic acid used in the method of the invention.

XX
 SQ Sequence 6 BP; 0 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 83.3%; Score 5; DB 13; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAAGG 6
 |||||
 Db 6 GAAGG 2

RESULT 4
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 ID ADEL0263 standard; DNA; 6 BP.
 XX AC ADEL0263;
 XX DT 29-JAN-2004 (first entry)
 XX DE S.lavendulae MitB potential ribosome binding site.
 KW Mitomycin biosynthetic protein; mitomycin C; antibiotic; MC; apoptosis;
 KW tumour hypoxia; cytostatic; anti-tumour agent; cancer; ds;
 KW ribozyme binding site; RBS.
 XX Streptomyces lavendulae.
 XX US2003134398-A1.
 PN 17-JUL-2003.
 PD 12-SEP-2001; 2001US-00953348.
 XX 12-SEP-2001; 2001US-00953348.
 XX (SHER/) SHERMAN D H.
 PA (MAOY/) MAO Y.
 PA (VARO/) VAROGLU M.
 PA (HEMM/) HE M.
 PA (SHEL/) SHELTON P.
 XX Sherman DH, Mao Y, Varoglu M, He M, Sheldon P;
 PI WPI; 2003-863498/80.
 DR New nucleic acid molecule comprising a sequence having mitomycin
 PT biosynthetic gene cluster, useful for enhancing production of
 PT antibiotics.

XX
 PS Disclosure; SEQ ID NO 93; 308pp; English.

XX The invention relates to an isolated and purified nucleic acid molecule
 CC comprising a sequence having mitomycin biosynthetic gene cluster, or its
 CC variant or fragment. Also included are an expression cassette comprising
 CC the novel nucleic acid molecule (operably linked to a promoter functional
 CC in a host cell), a recombinant bacterial host cell in which at least a
 CC portion of a nucleic acid molecule comprising mitomycin biosynthetic gene
 CC cluster is disrupted (resulting in a recombinant host cell that produces
 CC altered levels of mitomycin relative to a corresponding nonrecombinant
 CC bacterial host cell), introducing exogenous DNA into a refractory
 CC Streptomyces strain, identifying a nucleic acid molecule that is related
 CC to at least a portion of a nucleic acid molecule comprising a mitomycin
 CC gene cluster, preparing a compound or its salt from the recombinant host
 CC cell and a product produced by the recombinant host cell. The nucleic
 CC acid encodes a MitT, MitS, MitR, MitQ, MitP, MitO, MitN, MitM, MitL,
 CC MitK, MitJ, MitI, MitH, MitG, MitF, MitE, MitD, MitC, MitB, MitA and/or

CC MmcA-MmcY. The nucleic acid is useful for enhancing production of
CC mitomycin antibiotics, which induce apoptosis and hence are useful as
CC anti-tumour (via tumour hypoxia) agents and are useful in treating
CC cancer. The gene cluster was isolated from Streptomyces lavendulae. The
CC present sequence is a ribosome binding site from a gene encoding a
CC mitomycin biosynthetic protein of the invention.
XX
SQ Sequence 6 BP; 2 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 73.3%; Score 4.4; DB 10; Length 6;
Best Local Similarity 83.3%; Pred. No. 9.7e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
|||
DB 1 GGAACG 6

RESULT 5
ADE10336
ID ADE10336 standard; DNA; 6 BP.
XX
AC ADE10336;
XX

DT 29-JAN-2004 (first entry)
XX

DE S. lavendulae MitA potential ribosome binding site.
XX

XX Mitomycin biosynthetic protein; mitomycin C; antibiotic; MC; apoptosis;
KW tumour hypoxia; cytostatic; anti-tumour agent; cancer; ds;
KW ribosome binding site; RBS.
XX

OS Streptomyces lavendulae.
XX

XX US2003134398-A1.
PN

XX 17-JUL-2003.
PD

PF 12-SEP-2001; 2001US-00953348.
PP

PR 12-SEP-2001; 2001US-00953348.
PX

(SHER/) SHERMAN D H.
XX

PA (MAOY/) MAO Y.
PA

PA (VARO/) VAROGLU M.
PA

PA (HEMM/) HE M.
PA

PA (SHEL/) SHELTON P.
PA

XX Sherman DH, Mao Y, Varoglu M, He M, Sheldon P;
PI WPI; 2003-863498/80.
XX

DR WPI; 2003-863498/80.
XX

XX New nucleic acid molecule comprising a sequence having mitomycin
PT biosynthetic gene cluster, useful for enhancing production of
PT antibiotics.
XX

PS Disclosure; SEQ ID NO 91; 308pp; English.
XX

XX The invention relates to an isolated and purified nucleic acid molecule
CC comprising a sequence having mitomycin biosynthetic gene cluster, or its
CC variant or fragment. Also included are an expression cassette comprising
CC the novel nucleic acid molecule (operably linked to a promoter functional
CC in a host cell), a recombinant bacterial host cell in which at least a
CC portion of a nucleic acid molecule comprising mitomycin biosynthetic gene
CC cluster is disrupted (resulting in a recombinant host cell that produces
CC altered levels of mitomycin relative to a corresponding nonrecombinant
CC bacterial host cell), introducing exogenous DNA into a refractory
CC Streptomycin strain, identifying a nucleic acid molecule that is related
CC to at least a portion of a nucleic acid molecule comprising a mitomycin
CC gene cluster, preparing a compound or its salt from the recombinant host
CC cell and a product produced by the recombinant host cell. The nucleic
CC acid encodes a MitR, MitS, MitR, MitQ, MitP, MitC, MitN, MitM, MitL,
CC MitK, MitJ, MitI, MitH, MitG, MitF, MitE, MitD, MitC, MitB, MitA and/or

CC MmcA-MmcY. The nucleic acid is useful for enhancing production of
CC mitomycin antibiotics, which induce apoptosis and hence are useful as
CC anti-tumour (via tumour hypoxia) agents and are useful in treating
CC cancer. The gene cluster was isolated from Streptomyces lavendulae. The
CC present sequence is a ribosome binding site from a gene encoding a
CC mitomycin biosynthetic protein of the invention.
XX
SQ Sequence 6 BP; 3 A; 0 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 73.3%; Score 4.4; DB 10; Length 6;
Best Local Similarity 83.3%; Pred. No. 9.7e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
|||
DB 1 GGAACG 6

RESULT 6
ACA88957
ID ACA88957 standard; DNA; 6 BP.
XX
AC ACA88957;
XX

DT 08-JUL-2003 (first entry)
XX

DE Selection and amplification of genetic markers PCR related primer #68.
XX

XX Genetic marker selection; multiplex PCR amplification;
KW prenatal diagnostic testing; foetal sex determination;
KW genetic identification; DNA profiling; DNA fingerprinting;
KW forensic analysis; PCR; primer; ss.
XX

OS Homo sapiens.
XX

XX WO2003031646-A1.
PN

XX 17-APR-2003.
PD

PF 14-OCT-2002; 2002WO-AU001388.
PP

PR 12-OCT-2001; 2001AU-00008234.
PR

PR 12-OCT-2001; 2001AU-00008235.
PR

PA (UYQU) UNIV QUEENSLAND.
XX

XX Findlay I, Matthews PL, Mulcahy BK;
PI WPI; 2003-381725/36.
XX

DR WPI; 2003-381725/36.
XX

XX Selecting genetic markers as targets for nucleic acid sequence
PT amplification, useful for improving genetic testing, e.g. fetal sex
PT determination, comprises selecting each of the genetic markers according
PT to a heterozygosity index.
XX

PS Claim 36; Page 40; 64pp; English.
XX

XX The invention describes a method of selecting genetic markers as targets
CC for nucleic acid sequence amplification comprising selecting each of the
CC genetic markers according to a heterozygosity index of 0.5 or greater.
CC Selecting and amplification of genetic markers are useful as targets for
CC nucleic acid sequence amplification, for genetic testing or facilitating
CC multiplex PCR amplification from limiting amounts of target nucleic acid.
CC The methods are also useful for improving genetic diagnostic and
CC screening methods, such as prenatal diagnostic testing, foetal sex
CC determination or genetic identification, e.g. DNA profiling or DNA
CC fingerprinting. The nucleic acid sequence amplification is also useful in
CC forensic analysis of degraded, old, ancient and difficult samples that
CC are difficult to amplify and identify. This sequence represents a PCR
CC primer used in the selection and amplification of genetic markers
XX
SQ Sequence 6 BP; 1 A; 0 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 73.3%; Score 4.4; DB 10; Length 6;
Best Local Similarity 83.3%; Pred. No. 9.7e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
||| ||
Db 1 GGATGG 6

RESULT 7
ADJ35621/c
ID ADJ35621 standard; DNA; 6 BP.
XX
AC ADJ35621;
XX
DT 22-APR-2004 (first entry)
XX
DE Stabilising anti-repression, STAR, element dyad sequence #287.
XX
KW STAR affiliated proteinaceous molecule; post translational modification;
KW stabilising anti-repression; STAR; STAR element; ds; dyad.
XX
OS Unidentified.
XX
PN WO2003106674-A2.
XX
PD 24-DEC-2003.
XX
PF 30-MAY-2003; 2003WO-NL000410.
XX
PR 14-JUN-2002; 2002EP-0007344.
XX
PA (CHRO-) CHROMAGENICS BV.
XX
PI Otte AP, Kruckeberg AL, Satijn DPE;
XX
DR WPI; 2004-082195/08.
XX

Producing proteinaceous molecules in cells by selecting a cell, providing
a nucleic acid encoding a proteinaceous molecule with an Stabilizing Anti
-Repression sequence and expressing proteinaceous molecule.
XX
PS Disclosure; Page 101; 177pp; English.
XX

The invention relates to a method of producing a proteinaceous molecule
(I) in a cell comprising selecting a cell for its suitability for
producing (I), providing a nucleic acid encoding (I) with a nucleic acid
comprising a Stabilising Anti-Repression (STAR) sequence, expressing the
resulting nucleic acid in the cell and collecting (I). The method is
useful for producing (I). A cell line (II) provided with a nucleic acid
comprising a STAR sequence is useful for producing (I). (II) Enables
production of affiliated proteinaceous molecule, as cell carries out
proper post-translational modifications of produced proteins. The present
sequence represents a stabilising anti-repression, STAR, element primer
dyad sequence.
XX
SQ Sequence 6 BP; 0 A; 5 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 73.3%; Score 4.4; DB 12; Length 6;
Best Local Similarity 83.3%; Pred. No. 9.7e+08;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
||| ||
Db 6 GGAGGG 1

RESULT 8
AAQ38797
ID AAQ38797 standard; DNA; 6 BP.
XX
AC AAQ38797;
XX

DT 25-MAR-2003 (revised)
DT 26-JUL-1993 (first entry)
DE PCR primer #11 for analysis of lower TCR Vbeta gene usage in RA SILs.
KW TCR; T cell receptor; autoimmune disease; rheumatoid arthritis; RA;
KW J beta domain; V beta domain; T-cell mediated autoimmune disease;
KW antagonists.
XX
OS Homo sapiens.
XX
PN WO9306135-A1.
XX
PD 01-APR-1993.
XX
PF 23-SEP-1992; 92WO-US008094.
XX
PR 23-SEP-1991; 91US-00765222.
PR 18-OCT-1991; 91US-00779445.
PR 18-MAR-1992; 92US-00853362.
XX
PA (GETH) GENENTECH INC.
XX
PI Amento EP;
XX
XX WPI; 1993-117475/14.
XX
DT T-cell receptor antagonising polypeptide(s) - used in the diagnosis and
PT treatment of auto-immune disorders, partic. rheumatoid arthritis.
XX
PS Example 1; Page 22; 51pp; English.
XX
CC This 5' PCR primer was used with a 3' primer designated a constant region
CC sequence common to all TCR beta transcripts. It was used for the PCR
CC analysis of lower TCR usage in synovial Vbetas. This primer was used for
CC Vbeta family 2, subfamily 4.1, Jbeta 2.7, Cbeta 2 and corresponds to D &
CC J translation AAR34165. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 6 BP; 2 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAA 4
||| |
Db 2 GGAA 5

RESULT 9
AAQ70690/c
ID AAQ70690 standard; DNA; 6 BP.
XX
AC AAQ70690;
XX
DT 25-MAR-2003 (revised)
DT 15-MAR-1995 (first entry)
XX
XX Triplex forming oligonucleotide directed against IL-2 gene.
XX
KW IL-2; upstream region; regulatory element; gene expression; triplex;
KW antisense; inhibition; screening; identification; cancer; breast cancer;
KW carcinoma; autoimmunity; transplantation; HIV;
KW human immunodeficiency virus; ss.
XX
XX Synthetic.
XX
PN WO9417086-A1.
XX
PD 04-AUG-1994.
XX
PF 10-JAN-1994; 94WO-US000348.
XX

PR 25-JAN-1993; 93US-00008897.
XX (APOL-) APOLLON INC.
XX Yoon K, Lu M;
XX WPI; 1994-264018/32.
XX Composition for decreasing gene transcription - comprises
PT oligo:nucleotide or deriv. complementary to target gene region.
XX Claim 18; Page 45; 71pp; English.
XX The IL-2 gene has a purine rich segment with substantial mirror symmetry.
CC The purine rich region is characteristic of a nuclear factor activating T
CC -cell binding site. This triplex forming oligonucleotide directed against
CC the IL-2 region may be used in the treatment of HIV infection, diseases
CC requiring transplantation and, more generally, any disease involving the
CC expression of IL-2. (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 6 BP; 0 A; 2 C; 0 G; 4 T; 0 U; 0 Other;
SQ Query Match 66.7%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGAA 4
DB 5 GGAA 2
RESULT 10
AAF91829/c
ID AAF91829 standard; DNA; 6 BP.
XX AC AAF91829;
XX DT 10-MAY-2001 (first entry)
XX DE Breast-cancer associated protein isoform BPI-56 preferred probe #1.
XX KW Human; breast cancer; breast cancer associated protein isoform; BPI;
XX KW breast cancer associated feature; BF; diagnosis; cytostatic; probe; ss.
XX OS Homo sapiens.
XX PN WO200113117-A2.
XX PD 22-FEB-2001.
XX PF 14-AUG-2000; 2000WO-GB003143.
XX PR 13-AUG-1999; 99GB-00019258.
XX PR 30-MAR-2000; 2000GB-00007754.
XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX PI Herath HMCAC;
XX WPI; 2001-211252/21.
XX Screening, diagnosis or prognosis of breast cancer, by analyzing a sample
PT of serum or plasma by two dimensional electrophoresis to detect the
PT presence or level of a breast cancer-associated feature.
XX Claim 201; Page 45; 146pp; English.
XX The present invention describes a method for the screening, diagnosis or
CC prognosis of breast cancer (BC), determining the stage or severity of BC,
CC and monitoring the effect of therapy administered to a subject having BC,
CC comprising analysing a sample of body fluid by two dimensional
CC electrophoresis to generate a two-dimensional array of features,
CC comprising a chosen feature whose abundance correlates with BC or

CC predicts the onset or course of BC. The method (I) involves: (a)
CC analysing a sample of body fluid from the subject by two-dimensional
CC electrophoresis to generate a two-dimensional array of features,
CC comprising a chosen feature whose relative abundance correlates with BC
CC or predicts the onset of BC; and (b) comparing the abundance of each
CC chosen feature in the sample with the abundance of that chosen feature in
CC the body fluid from one or more persons free from BC, or with a
CC previously determined reference range for that feature in subjects free
CC from BC, or with the abundance of an expression reference feature (ERF)
CC in the test sample. The method is useful for screening, diagnosis or
CC prognosis of breast cancer, determining the stage or severity of BC,
CC monitoring the effect of therapy administered to a subject having BC, and
CC for identifying a subject at risk of developing BC. AAB87186 to AAB87340
CC represents breast cancer associated protein isoform (BPI) peptide
CC sequences, and AAF91643 to AAF91848 represent BPI probes used in the
CC exemplification of the present invention
XX Sequence 6 BP; 0 A; 2 C; 0 G; 4 T; 0 U; 0 Other;
SQ Query Match 66.7%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GAAG 5
DB 6 GAAG 3
RESULT 11
ACC69109
ID ACC69109 standard; DNA; 6 BP.
XX AC ACC69109;
XX DT 10-JUL-2003 (first entry)
XX DE Cucumber BGL related target sequence SEQ ID NO:16.
XX KW Cucumber; expression profiling; DNA sequencing; plant; developmental;
XX KW physiological; horticultural; agricultural; target; ss.
XX OS Cucumis sp.
XX OS Synthetic.
XX PN EP1295950-A1.
XX PD 26-MAR-2003.
XX PF 25-SEP-2001; 2001EP-00203617.
XX PR 25-SEP-2001; 2001EP-00203617.
XX PA (GTDI-) GT DIAGNOSTICS BV.
XX PI Langeveld SA, Van Der Kop DAM, De Boer AD;
XX WPI; 2003-383798/37.
XX Determining developmental/physiological stage of organism (especially in
PT plants), comprises determining expression of first and second genes by
PT hybridizing nucleic acid templates derived from the genes with specific
PT primers.
XX Example; Fig 1A; 27pp; English.
XX The present invention describes a method (M) for determining a
CC developmental or physiological stage of an organism by determining
CC expression of a first and second gene (I)-(II), respectively, or gene
CC fragment. (M) comprises: (a) providing first and second nucleic acid
CC templates (T1)-(T2) derived from (I) and (II), respectively; (b)
CC hybridising first and second primers (P1)-(P2) to (T1) and (T2),
CC respectively; and (c) determining binding of the primers to the templates
CC in one reaction vessel. (M) is useful for determining a developmental or

CC physiological stage of an organism (especially a plant). (M) is
 CC particularly useful for expression profiling for use in testing plant
 CC quality of horticultural and agricultural products. With quality loss,
 CC e.g. stress-induced senescence, oxidative damage or desiccation, the
 CC plant tissues will go through various physiological stages, in which
 CC different genes are switched on or off. The level of expression of these
 CC marker genes reflects the physiological stage and therefore the condition
 CC and quality of the plant and/or product. Quality of fresh products is
 CC generally judged on subjective criteria that usually involves visual
 CC examination. The present invention provides a way of taking objective
 CC quantitative measurements using biotechnology: there is a direct relation
 CC between the pattern of gene expression at the RNA and protein level, and
 CC the physiological status of a cell. The present sequence represents a
 CC cucumber BGL target sequence, which is used in an example from the
 CC present invention.

XX
 XX
 XX Sequence 6 BP; 2 A; 2 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGG 6
 Db 1 AAGG 4

RESULT 12
 ABZ23991/c
 ID ABZ23991 standard; DNA; 6 BP.
 XX AC ABZ23991;
 XX DT 18-MAR-2003 (first entry)
 XX DE Nucleotide sequence of seq Id No. 5.
 XX KW Ligation; topoisomerase; nucleic acid generation; molecular cloning;
 XX KW topoisomerase I; topo65; ds.
 XX OS Synthetic.
 XX PN WO200290522-A2.
 XX PD 14-NOV-2002.
 XX PF 10-MAY-2002; 2002WO-US015072.
 XX PR 10-MAY-2001; 2001US-0290313P.
 XX PR 15-JUN-2001; 2001US-00882274.
 XX PA (UYSA-) UNIV SAN DIEGO STATE FOUND.
 XX PA (EMER-) EMERALD BIOSTRUCTURES INC.
 XX PI Burgin Alex B, Stewart LJ;
 XX WPI; 2003-120543/11.

PT Ligating nucleic acid for generating RNA, by contacting polynucleotide-3'
 PT phosphorothiolate with acceptor polynucleotide, or polynucleotide-
 PT 5'phosphorothiolate with non-sequence specific topoisomerase and
 PT acceptor.

PS Disclosure; Page 101; 105pp; English.

XX The invention relates to ligating a nucleic acid. The method involves:
 CC (a) non-enzymatic ligation by contacting a polynucleotide-3'
 CC phosphorothiolate with an acceptor polynucleotide under conditions that
 CC allow formation of a phosphodiester bond between the polynucleotide-3'
 CC phosphorothiolate and the acceptor polynucleotide; or (b) contacting a
 CC polynucleotide-5'phosphorothiolate with a non-sequence specific
 CC topoisomerase, or its fragment or modification, and an acceptor
 CC polynucleotide under conditions that allow formation of a phosphodiester

CC bond between the polynucleotide-5' phosphorothiolate and the acceptor
 CC polynucleotide, with the proviso that the polynucleotide-5'
 CC phosphorothiolate does not contain the nucleotide sequence shown in
 CC ABZ23991. The method is useful for ligating a nucleic acid, for
 CC generating RNA or DNA molecules, RNA-DNA hybrids, vectors and inserts
 CC useful for molecular cloning and complex polynucleotide structures.
 CC Sequences ABZ23991-993 represent nucleotide sequences that are
 CC particularly excluded from the term polynucleotide-5' phosphorothiolate
 XX
 XX Sequence 6 BP; 0 A; 2 C; 1 G; 2 T; 0 U; 1 Other;

Query Match 66.7%; Score 4; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGG 6
 Db 6 AAGG 3

RESULT 13
 ACH50860
 ID ACH50860 standard; DNA; 6 BP.
 XX AC ACH50860;
 XX DT 13-OCT-2003 (first entry)
 XX DE Hypothetical positively hybridised probe #3 extension probe #4.
 XX KW Probe; ss; sequencing by hybridisation; SBH; genome mapping;
 XX KW biodiversity; genetic disorder.
 XX OS Synthetic.
 XX PN US2003073623-A1.
 XX PD 17-APR-2003.
 XX PF 30-JUL-2001; 2001US-00918995.
 XX PR 30-JUL-2001; 2001US-00918995.
 XX PA (DRMA/) DRMANAC R T.
 XX PA (LABA/) LABAT I.
 XX PA (STAC/) STACHE-CRAIN B.
 XX PA (DICK/) DICKSON M C.
 XX PA (JONE/) JONES L W.
 XX PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
 XX WPI; 2003-615964/58.

PT New polynucleotide sequences obtained from various cDNA libraries, useful
 PT as hybridization probes, as oligomers for PCR, for chromosome and gene
 PT mapping, in the recombinant production of protein, or in generating
 PT antisense DNA or RNA.

XX Example 19; Page 36; 44pp; English.

PS The invention relates to an isolated polynucleotide comprising any one of
 XX 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
 CC determined by the technique of SBH (sequencing by hybridisation). Also
 CC included is a purified polypeptide comprising a sequence corresponding to
 CC a reading frame of the novel polynucleotide. The nucleic acid sequences
 CC are useful in diagnostics as expressed sequence tags (EST) for
 CC identifying expressed genes or for physical mapping of the human genome,
 CC in forensics, in assessing biodiversity, or in identifying mutations
 CC responsible for genetic disorders and other traits. The nucleotide
 CC sequences are also useful as hybridisation probes, as oligomers for PCR,
 CC for chromosome and gene mapping, in the recombinant production of
 CC protein, or in generating antisense DNA or RNA. The purified polypeptide
 CC is useful for generating antibodies specific for it. The present sequence

CC is a hypothetical probe used to illustrate a method of
 CC detecting/determining mutations and polymorphisms
 XX
 SQ Sequence 6 BP; 3 A; 1 C; 2 G; 0 T; 0 U; 0 Other;
 Query Match 66.7%; Score 4; DB 9; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGG 6
 DB 3 AAGG 6

RESULT 14
 ACH50844/c
 ID ACH50844 standard; DNA; 6 BP.
 XX
 AC ACH50844;
 DT 13-OCT-2003 (first entry)
 XX
 DE Hypothetical positively hybridised probe #2.
 XX
 KW Probe; ss; sequencing by hybridisation; SBH; genome mapping;
 KW biodiversity; genetic disorder.
 XX
 OS Synthetic.
 XX
 PN US2003073623-A1.
 XX
 PD 17-APR-2003.
 XX
 PF 30-JUL-2001; 2001US-00918995.
 XX
 PR 30-JUL-2001; 2001US-00918995.
 XX
 PA (DRMA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 XX
 PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
 XX
 DR WPI; 2003-615964/58.
 XX
 XX New polynucleotide sequences obtained from various cDNA libraries, useful
 PT as hybridization probes, as oligomers for PCR, for chromosome and gene
 PT mapping, in the recombinant production of protein, or in generating
 PT antisense DNA or RNA.
 XX
 PS Example 19; Page 36; 44pp; English.
 XX
 CC The invention relates to an isolated polynucleotide comprising any one of
 CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
 CC determined by the technique of SBH (sequencing by hybridisation). Also
 CC included is a purified polypeptide comprising a sequence corresponding to
 CC a reading frame of the novel polynucleotide. The nucleic acid sequences
 CC are useful in diagnostics as expressed sequence tags (EST) for
 CC identifying expressed genes or for physical mapping of the human genome,
 CC in forensics, in assessing biodiversity, or in identifying mutations
 CC responsible for genetic disorders and other traits. The nucleotide
 CC sequences are also useful as hybridisation probes, as oligomers for PCR,
 CC for chromosome and gene mapping, in the recombinant production of
 CC protein, or in generating antisense DNA or RNA. The purified polypeptide
 CC is useful for generating antibodies specific for it. The present sequence
 CC is a hypothetical probe used to illustrate a method of
 CC detecting/determining mutations and polymorphisms
 XX
 SQ Sequence 6 BP; 1 A; 2 C; 0 G; 3 T; 0 U; 0 Other;
 Query Match 66.7%; Score 4; DB 9; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAA 4
 DB 6 GGAA 3

RESULT 15
 ADD66333/c
 ID ADD66333 standard; DNA; 6 BP.
 XX
 AC ADD66333;
 DT 15-JAN-2004 (first entry)
 XX
 DE Ebola GP gene modified DNA.
 XX
 KW viricide; hepatotropic; RNA editing; GP gene; vaccine; immunity enhanced;
 KW infection; influenza; Ebola; Marburg; Arbovirus; hepatitis;
 KW respiratory syncytial virus; herpes simplex virus; human papilloma virus;
 KW HIV infection; ds.
 XX
 OS Ebola virus.
 XX
 PN US2003138459-A1.
 XX
 PD 24-JUL-2003.
 XX
 PF 17-MAR-2003; 2003US-00286332.
 XX
 PR 02-JUN-2000; 2000US-00585599.
 PR 04-JUN-2001; 2001WO-US018238.
 PR 01-NOV-2001; 2001US-00003035.
 XX
 PA (WANG/) WANG D.
 XX
 PI Wang D;
 XX
 DR WPI; 2003-851718/79.
 XX
 PT Enhancing the immunity of a host to infection of a first and second
 PT pathogenic virus, e.g. influenza, hepatitis, respiratory syncytial, or
 PT HIV infections comprises administering to the host a first and a second
 PT recombinant adenovirus.
 XX
 PS Example; SEQ ID NO 7; 185pp; English.
 XX
 CC The invention relates to a method of enhancing the immunity of a host to
 CC infection of a first and second pathogenic virus comprising administering
 CC to the host a first and a second recombinant adenovirus. The method is
 CC useful for enhancing immunity of the host to infections, e.g. influenza,
 CC Ebola, Marburg, Arbovirus, hepatitis, respiratory syncytial, herpes
 CC simplex or human papilloma virus or HIV infections. The present sequence
 CC is used in the exemplification of the invention.
 XX
 SQ Sequence 6 BP; 0 A; 2 C; 0 G; 0 T; 4 U; 0 Other;
 Query Match 66.7%; Score 4; DB 10; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAAG 5
 DB 6 GAAG 3

RESULT 16
 ADD66334/c
 ID ADD66334 standard; mRNA; 6 BP.
 XX
 AC ADD66334;
 XX

DT 15-JAN-2004 (first entry)
XX DE Ebola GP gene mRNA.
XX KW virucide; hepatotropic; RNA editing; GP gene; vaccine; immunity enhanced;
KW infection; influenza; Ebola; Marburg; Arbovirus; hepatitis;
KW respiratory syncytial virus; herpes simplex virus; human papilloma virus;
KW HIV infection; ss.
XX OS Ebola virus.
XX PN US2003138459-A1.
XX PD 24-JUL-2003.
XX PF 17-MAR-2003; 2003US-00286332.
XX PR 02-JUN-2000; 2000US-00585599.
XX PR 04-JUN-2001; 2001WO-US018238.
XX PR 01-NOV-2001; 2001US-00003035.
XX PA (WANG/) WANG D.
XX PI Wang D;
XX XX WPI; 2003-851718/79.
XX XX Enhancing the immunity of a host to infection of a first and second
PT pathogenic virus, e.g. influenza, hepatitis, respiratory syncytial, or
PT HIV infections comprises administering to the host a first and a second
PT recombinant adenovirus.
XX PS Disclosure; SEQ ID NO 8; 185pp; English.
XX XX The invention relates to a method of enhancing the immunity of a host to
CC infection of a first and second pathogenic virus comprising administering
CC to the host a first and a second recombinant adenovirus. The method is
CC useful for enhancing immunity of the host to infections, e.g. influenza,
CC Ebola, Marburg, Arbovirus, hepatitis, respiratory syncytial, herpes
CC simplex or human papilloma virus or HIV infections. The present sequence
CC is used in the exemplification of the invention.
XX XX
SQ Sequence 6 BP; 0 A; 2 C; 0 G; 4 T; 0 U; 0 Other;
Query Match 66.7%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GAAG 5
DB |||||
6 GAAG 3
RESULT 17
ADE38305
ID ADE38305 standard; DNA; 6 BP.
XX AC ADE38305;
XX DT 29-JAN-2004 (first entry)
XX DE Immune modulatory sequence (IMS) hexamer oligonucleotide SEQ ID NO:44.
XX autoimmunity disease; statin; antigen-specific immunomodulatory agent;
KW non-antigen-specific immunomodulatory agent; immunomodulatory;
KW antidiabetic; antiarthritic; vasotropic; gene therapy;
KW multiple sclerosis; insulin dependent diabetes mellitus; IDDM;
KW rheumatoid arthritis; autoimmune uveitis; ss.
XX OS Synthetic.
XX PN WO2003082269-A1.
XX PT Treating an autoimmune disease by co-administering to a patient a statin
XX and an antigen-specific non-antigen-specific immunomodulatory agent.

PD 09-OCT-2003.
XX 31-MAR-2003; 2003WO-US009807.
XX PF 29-MAR-2002; 2002US-0368803P.
XX PR (STRD) UNIV LELAND STANFORD JUNIOR.
XX PA (BAYH-) BAYHILL THERAPEUTICS INC.
XX PI Garren H, Steinman L;
XX PI WPI; 2003-803953/75.
XX DR Treating an autoimmune disease by co-administering to a patient a statin
XX and an antigen-specific non-antigen-specific immunomodulatory agent.
XX PS Disclosure; SEQ ID NO 44; 90pp; English.
XX CC The present invention describes a method for treating an autoimmune
CC disease comprising co-administering to a patient a statin and an antigen-
CC specific/non-antigen-specific immunomodulatory agent. The
CC immunomodulatory agent has antidiabetic, antiarthritic and vasotropic
CC activities, and can be used in gene therapy. The method is useful for
CC treating autoimmune disease e.g., multiple sclerosis, insulin dependent
CC diabetes mellitus (IDDM), rheumatoid arthritis or autoimmune uveitis. The
CC present sequence is used in the exemplification of the present invention.
XX XX
SQ Sequence 6 BP; 2 A; 1 C; 2 G; 1 T; 0 U; 0 Other;
Query Match 66.7%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 AAGG 6
DB |||||
1 AAGG 4
RESULT 18
ADE38325
ID ADE38325 standard; DNA; 6 BP.
XX AC ADE38325;
XX XX 29-JAN-2004 (first entry)
XX DT Immune modulatory sequence (IMS) hexamer oligonucleotide SEQ ID NO:48.
XX DE autoimmunity disease; statin; antigen-specific immunomodulatory agent;
XX KW non-antigen-specific immunomodulatory agent; immunomodulatory;
KW antidiabetic; antiarthritic; vasotropic; gene therapy;
KW multiple sclerosis; insulin dependent diabetes mellitus; IDDM;
KW rheumatoid arthritis; autoimmune uveitis; ss.
XX OS Synthetic.
XX PN WO2003082269-A1.
XX PD 09-OCT-2003.
XX PF 31-MAR-2003; 2003WO-US009807.
XX PR 29-MAR-2002; 2002US-0368803P.
XX XX (STRD) UNIV LELAND STANFORD JUNIOR.
XX PA (BAYH-) BAYHILL THERAPEUTICS INC.
XX PI Garren H, Steinman L;
XX PI WPI; 2003-803953/75.
XX DR Treating an autoimmune disease by co-administering to a patient a statin
XX and an antigen-specific non-antigen-specific immunomodulatory agent.

XX Disclosure; SEQ ID NO 48; 90pp; English.

CC The present invention describes a method for treating an autoimmune

CC disease comprising co-administering to a patient a statin and an antigen-

CC specific/non-antigen-specific immunomodulatory agent. The

CC immunomodulatory agent has antidiabetic, antiarthritic and vasotropic

CC activities, and can be used in gene therapy. The method is useful for

CC treating autoimmune disease e.g., multiple sclerosis, insulin dependent

CC diabetes mellitus (IDDM), rheumatoid arthritis or autoimmune uveitis. The

CC present sequence is used in the exemplification of the present invention.

XX

XX Sequence 6 BP; 2 A; 1 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 10; Length 6;

Best Local Similarity 100.0%; Pred. NO. 9.7e+08;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGG 6

DB 1 AAGG 4

RESULT 19

ADE38297

ID ADE38297 standard; DNA; 6 BP.

AC ADE38297;

XX

XX 29-JAN-2004 (first entry)

DT

DE Immune modulatory sequence (IMS) hexamer oligonucleotide SEQ ID NO:36.

XX autoimmune disease; statin; antigen-specific immunomodulatory agent;

KW non-antigen-specific immunomodulatory agent; immunomodulatory;

KW antidiabetic; antiarthritic; vasotropic; gene therapy;

KW multiple sclerosis; insulin dependent diabetes mellitus; IDDM;

KW rheumatoid arthritis; autoimmune uveitis; ss.

XX

OS Synthetic.

XX

XX WO2003082269-A1.

PN

XX

XX 09-OCT-2003.

PD

XX

XX 31-MAR-2003; 2003WO-US009807.

PF

XX

XX 29-MAR-2002; 2002US-0368803P.

PR

XX (STRD) UNIV LELAND STANFORD JUNIOR.

PA (BAYH-) BAYHILL THERAPEUTICS INC.

XX

XX Garren H, Steinman L;

PI

XX WPI; 2003-803953/75.

DR

XX

XX Treating an autoimmune disease by co-administering to a patient a statin

PT and an antigen-specific non-antigen-specific immunomodulatory agent.

XX

XX Disclosure; SEQ ID NO 36; 90pp; English.

XX

XX The present invention describes a method for treating an autoimmune

CC disease comprising co-administering to a patient a statin and an antigen-

CC specific/non-antigen-specific immunomodulatory agent. The

CC immunomodulatory agent has antidiabetic, antiarthritic and vasotropic

CC activities, and can be used in gene therapy. The method is useful for

CC treating autoimmune disease e.g., multiple sclerosis, insulin dependent

CC diabetes mellitus (IDDM), rheumatoid arthritis or autoimmune uveitis. The

CC present sequence is used in the exemplification of the present invention.

XX

XX Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 10; Length 6;

Best Local Similarity 100.0%; Pred. NO. 9.7e+08;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGG 6

DB 1 AAGG 4

RESULT 21

ADK14286

ID ADK14286 standard; DNA; 6 BP.

XX

XX ADK14286;

XX

XX 20-MAY-2004 (first entry)

DT

Best Local Similarity 100.0%; Pred. NO. 9.7e+08;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGG 6

DB 1 AAGG 4

RESULT 20

ADE38301

ID ADE38301 standard; DNA; 6 BP.

XX

XX ADE38301;

XX

XX 29-JAN-2004 (first entry)

DT

DE Immune modulatory sequence (IMS) hexamer oligonucleotide SEQ ID NO:40.

XX autoimmune disease; statin; antigen-specific immunomodulatory agent;

KW non-antigen-specific immunomodulatory agent; immunomodulatory;

KW antidiabetic; antiarthritic; vasotropic; gene therapy;

KW multiple sclerosis; insulin dependent diabetes mellitus; IDDM;

KW rheumatoid arthritis; autoimmune uveitis; ss.

XX

OS Synthetic.

XX

XX WO2003082269-A1.

PN

XX

XX 09-OCT-2003.

PD

XX

XX 31-MAR-2003; 2003WO-US009807.

PF

XX

XX 29-MAR-2002; 2002US-0368803P.

PR

XX (STRD) UNIV LELAND STANFORD JUNIOR.

PA (BAYH-) BAYHILL THERAPEUTICS INC.

XX

XX Garren H, Steinman L;

PI

XX WPI; 2003-803953/75.

DR

XX

XX Treating an autoimmune disease by co-administering to a patient a statin

PT and an antigen-specific non-antigen-specific immunomodulatory agent.

XX

XX Disclosure; SEQ ID NO 40; 90pp; English.

XX

XX The present invention describes a method for treating an autoimmune

CC disease comprising co-administering to a patient a statin and an antigen-

CC specific/non-antigen-specific immunomodulatory agent. The

CC immunomodulatory agent has antidiabetic, antiarthritic and vasotropic

CC activities, and can be used in gene therapy. The method is useful for

CC treating autoimmune disease e.g., multiple sclerosis, insulin dependent

CC diabetes mellitus (IDDM), rheumatoid arthritis or autoimmune uveitis. The

CC present sequence is used in the exemplification of the present invention.

XX

XX Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 66.7%; Score 4; DB 10; Length 6;

Best Local Similarity 100.0%; Pred. NO. 9.7e+08;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGG 6

DB 1 AAGG 4

RESULT 21

ADK14286

ID ADK14286 standard; DNA; 6 BP.

XX

XX ADK14286;

XX

XX 20-MAY-2004 (first entry)

DT


```

XX WPI; 2004-203788/19.
XX
XX Producing a nucleic acid sequence comprises amplifying double stranded
XX DNA sequence in the presence of first and second primers to produce a
XX first nucleic acid molecule having the double stranded DNA sequence in a
XX head to head orientation.
XX
XX Disclosure; SEQ ID NO 36; 55pp; English.
XX
XX This invention describes a novel method for producing a nucleic acid
XX sequence comprising amplifying the double stranded DNA sequence of
XX interest in the presence of the first primer and the second primer to
XX produce a first nucleic acid molecule comprising the double stranded DNA
XX sequence of interest flanked by at least a portion of the first promoter
XX in a head to head orientation. The method involves providing RNA
XX polymerase that specifically binds to the first promoter and contacting
XX the first nucleic acid molecule with the RNA polymerase to produce double
XX stranded RNA that is complementary to the double stranded DNA sequence of
XX interest. This method further comprises providing a third primer
XX complementary to at least a portion of the first promoter and amplifying
XX the first nucleic acid molecule produced in the presence of the third
XX primer to produce a second nucleic acid molecule comprising the double
XX stranded DNA sequence of interest flanked by the first promoter in a head
XX to head orientation. The method further comprises providing RNA
XX polymerase that specifically binds to the first promoter and contacting
XX the second nucleic acid molecule with the RNA polymerase to produce
XX double stranded RNA that is complementary to the double stranded DNA
XX sequence of interest. The second strand of the double-stranded DNA
XX sequence of interest comprises at least a portion of a second promoter.
XX The second promoter is different from the first promoter. The first
XX promoter comprises T7, T3 or SP6 promoter. The first strand of the double
XX stranded DNA comprises a nucleotide sequence linked to the 3' end of the
XX first promoter, and the first primer further comprises a second sequence
XX complementary to the nucleotide sequence, where the second sequence is
XX linked to the 3' end of the first sequence of the first primer. The first
XX primer comprises a sequence complementary to T7, T3 or SP6 promoter. The
XX first sequence comprises a second primer complementary to at least a
XX portion of a promoter. The methods and kits are useful for producing
XX nucleic acid sequences as powerful alternative tools for functional
XX genomics.
XX
XX Sequence 6 BP; 3 A; 0 C; 3 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 66.7%; Score 4; DB 12; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 9.7e+08;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 AAGG 6
XX ||||
XX 1 AAGG 4
XX
XX Db
XX
XX RESULT 24
XX ADR34774
XX ID ADR34774 standard; DNA; 6 BP.
XX
XX AC ADR34774;
XX
XX DT 04-NOV-2004 (first entry)
XX
XX DE Human nicking agent DNA containing BstNBI restriction site #1194.
XX
XX ss; nicking agent; assay panel; diagnosis; expression pattern;
XX DNA fingerprinting; nosocomial infection; microbiological assay;
XX bacterial contamination; genome mapping; bioremediation.
XX
XX OS Homo sapiens.
XX
XX WO2004067765-A2.
XX
XX PD 12-AUG-2004.
XX
XX
XX 29-JAN-2004; 2004WO-US002720.
XX
XX 29-JAN-2003; 2003US-0443811P.
XX
XX (KECK-) KECK GRADUATE INST.
XX
XX Van Ness J, Galas DJ, Van Ness LK;
XX
XX WPI; 2004-581010/56.
XX
XX Identifying nucleic acid sample source, useful for identifying bacterial
XX strains involved in nosocomial infections, comprises treating the nucleic
XX acid sample with components comprising a nicking agent under nicking
XX conditions.
XX
XX Example 3; Page 105-219; 238pp; English.
XX
XX The invention relates to a method of treating a nucleic acid sample with
XX components under nicking conditions, where the components comprise a
XX nicking agent, and the conditions cause the nicking agent to nick the
XX nucleic acid sample to thus produce a family of initiating
XX oligonucleotide fragments, and subjecting one or more members of the
XX family of initiating oligonucleotide fragments to a characterization
XX process to thus provide results. The method is useful for creating an
XX assay panel of diagnostic oligonucleotides that can identify any organism
XX or individual. The method is useful for characterizing other DNA
XX molecules e.g., cDNA, and for characterizing cDNA expression patterns.
XX The method, kit or composition is useful for identifying the source
XX organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
XX non-human animal or human. The method is particularly useful for rapidly
XX fingerprinting DNA to identifying prokaryotic and eukaryotic species. It
XX is especially useful for identifying different bacterial strains involved
XX in e.g., nosocomial infections. Furthermore, the method is useful for
XX diagnosing bacterial disease in plants and humans, monitoring for
XX bacterial content and/or contamination in the environment, monitoring
XX food for bacterial contamination, monitoring quality assurance/quality control of
XX bacterial contamination, monitoring microbiological assays, tracing bacterial
XX contamination and/or outbreaks of bacterial infections, genome mapping,
XX monitoring bioremediation sites, and for monitoring agricultural sites
XX for test crops, bacteria and recombinant molecules. Sequences ADR33581-
XX ADR37496 correspond to target nucleic acids containing an NBstNBI
XX restriction site and used in the method of the invention.
XX
XX Sequence 6 BP; 2 A; 0 C; 2 G; 1 T; 0 U; 1 Other;
XX
XX Query Match 66.7%; Score 4; DB 13; Length 6;
XX Best Local Similarity 66.7%; Pred. No. 9.7e+08;
XX Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 GGAAGG 6
XX :|||
XX 1 GGAATG 6
XX
XX Db
XX
XX RESULT 25
XX ADR34775
XX ID ADR34775 standard; DNA; 6 BP.
XX
XX AC ADR34775;
XX
XX DT 04-NOV-2004 (first entry)
XX
XX DE Human nicking agent DNA containing BstNBI restriction site #1195.
XX
XX ss; nicking agent; assay panel; diagnosis; expression pattern;
XX DNA fingerprinting; nosocomial infection; microbiological assay;
XX bacterial contamination; genome mapping; bioremediation.
XX
XX OS Homo sapiens.
XX
XX WO2004067765-A2.
XX
XX PN

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XX 12-AUG-2004.
XX 29-JAN-2004; 2004WO-US002720.
XX 29-JAN-2003; 2003US-0443811P.
XX (KECK-) KECK GRADUATE INST.
XX Van Ness J, Galas DJ, Van Ness LX;
XX WPI; 2004-581010/56.
XX Identifying nucleic acid sample source, useful for identifying bacterial
XX strains involved in nosocomial infections, comprises treating the nucleic
XX acid sample with components comprising a nicking agent under nicking
XX conditions.
XX Example 3; Page 105-219; 238pp; English.
XX The invention relates to a method of treating a nucleic acid sample with
XX components under nicking conditions, where the components comprise a
XX nicking agent, and the conditions cause the nicking agent to nick the
XX nucleic acid sample to thus produce a family of initiating
XX oligonucleotide fragments, and subjecting one or more members of the
XX family of initiating oligonucleotide fragments to a characterization
XX process to thus provide results. The method is useful for creating an
XX assay panel of diagnostic oligonucleotides that can identify any organism
XX or individual. The method is useful for characterizing other DNA
XX molecules e.g., cDNA, and for characterizing cDNA expression patterns.
XX The method, kit or composition is useful for identifying the source
XX of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
XX non-human animal or human. The method is particularly useful for rapidly
XX fingerprinting DNA to identifying prokaryotic and eukaryotic species. It
XX is especially useful for identifying different bacterial strains involved
XX in e.g., nosocomial infections. Furthermore, the method is useful for
XX diagnosing bacterial disease in plants and humans, monitoring for
XX bacterial content and/or contamination in the environment, monitoring
XX food for bacterial contamination, monitoring quality assurance/quality control of
XX bacterial contamination, monitoring quality assurance/quality control of
XX laboratory tests involving microbiological assays, tracing bacterial
XX contamination and/or outbreaks of bacterial infections, genome mapping,
XX monitoring bioremediation sites, and for monitoring agricultural sites
XX for test crops, bacteria and recombinant molecules. Sequences ADR33581-
XX ADR37496 correspond to target nucleic acids containing an NBstNBI
XX restriction site and used in the method of the invention.
XX Sequence 6 BP; 2 A; 0 C; 2 G; 1 T; 0 U; 1 Other;
XX
XX Query Match 66.7%; Score 4; DB 13; Length 6;
XX Best Local Similarity 66.7%; Pred. No. 9.7e+08;
XX Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 GGAAGG 6
Db :|||
1 SGAATG 6

RESULT 26
ADR34773
ID ADR34773 standard; DNA; 6 BP.
XX
AC ADR34773;
XX
DT 04-NOV-2004 (first entry)
XX
DE Human nicking agent DNA containing BstNBI restriction site #1193.
XX
XX ss; nicking agent; assay panel; diagnosis; expression pattern;
XX DNA fingerprinting; nosocomial infection; microbiological assay;
XX bacterial contamination; genome mapping; bioremediation.
XX

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OS Homo sapiens.
XX WO2004067765-A2.
XX 12-AUG-2004.
XX 29-JAN-2004; 2004WO-US002720.
XX 29-JAN-2003; 2003US-0443811P.
XX (KECK-) KECK GRADUATE INST.
XX Van Ness J, Galas DJ, Van Ness LX;
XX WPI; 2004-581010/56.
XX Identifying nucleic acid sample source, useful for identifying bacterial
XX strains involved in nosocomial infections, comprises treating the nucleic
XX acid sample with components comprising a nicking agent under nicking
XX conditions.
XX Example 3; Page 105-219; 238pp; English.
XX The invention relates to a method of treating a nucleic acid sample with
XX components under nicking conditions, where the components comprise a
XX nicking agent, and the conditions cause the nicking agent to nick the
XX nucleic acid sample to thus produce a family of initiating
XX oligonucleotide fragments, and subjecting one or more members of the
XX family of initiating oligonucleotide fragments to a characterization
XX process to thus provide results. The method is useful for creating an
XX assay panel of diagnostic oligonucleotides that can identify any organism
XX or individual. The method is useful for characterizing other DNA
XX molecules e.g., cDNA, and for characterizing cDNA expression patterns.
XX The method, kit or composition is useful for identifying the source
XX of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
XX non-human animal or human. The method is particularly useful for rapidly
XX fingerprinting DNA to identifying prokaryotic and eukaryotic species. It
XX is especially useful for identifying different bacterial strains involved
XX in e.g., nosocomial infections. Furthermore, the method is useful for
XX diagnosing bacterial disease in plants and humans, monitoring for
XX bacterial content and/or contamination in the environment, monitoring
XX food for bacterial contamination, monitoring quality assurance/quality control of
XX bacterial contamination, monitoring quality assurance/quality control of
XX laboratory tests involving microbiological assays, tracing bacterial
XX contamination and/or outbreaks of bacterial infections, genome mapping,
XX monitoring bioremediation sites, and for monitoring agricultural sites
XX for test crops, bacteria and recombinant molecules. Sequences ADR33581-
XX ADR37496 correspond to target nucleic acids containing an NBstNBI
XX restriction site and used in the method of the invention.
XX Sequence 6 BP; 2 A; 0 C; 2 G; 1 T; 0 U; 1 Other;
XX
XX Query Match 66.7%; Score 4; DB 13; Length 6;
XX Best Local Similarity 66.7%; Pred. No. 9.7e+08;
XX Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 GGAAGG 6
Db :|||
1 SGAATG 6

RESULT 27
ADR37260
ID ADR37260 standard; DNA; 6 BP.
XX
AC ADR37260;
XX
DT 04-NOV-2004 (first entry)
XX
DE Human nicking agent DNA containing BstNBI restriction site #3680.
XX
XX ss; nicking agent; assay panel; diagnosis; expression pattern;
XX

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KW DNA fingerprinting; nosocomial infection; microbiological assay;
 KW bacterial contamination; genome mapping; bioremediation.
 OS Homo sapiens.
 XX WO2004067765-A2.
 XX 12-AUG-2004.
 XX 29-JAN-2004; 2004WO-US002720.
 XX 29-JAN-2003; 2003US-0443811P.
 XX (KECK-) KECK GRADUATE INST.
 PI Van Ness J, Galas DJ, Van Ness LK;
 XX WPI; 2004-581010/56.
 XX Identifying nucleic acid sample source, useful for identifying bacterial
 PT strains involved in nosocomial infections, comprises treating the nucleic
 PT acid sample with components comprising a nicking agent under nicking
 PT conditions.
 XX Example 3; Page 105-219; 238pp; English.
 XX The invention relates to a method of treating a nucleic acid sample with
 CC components under nicking conditions, where the components comprise a
 CC nicking agent, and the conditions cause the nicking agent to nick the
 CC nucleic acid sample to thus produce a family of initiating
 CC oligonucleotide fragments, and subjecting one or more members of the
 CC family of initiating oligonucleotide fragments to a characterization
 CC process to thus provide results. The method is useful for creating an
 CC assay panel of diagnostic oligonucleotides that can identify any organism
 CC or individual. The method is useful for characterizing other DNA
 CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
 CC The method, kit or composition is useful for identifying the source
 CC of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
 CC non-human animal or human. The method is particularly useful for rapidly
 CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
 CC subspecies, and especially strains or individuals of the subspecies. It
 CC is especially useful for identifying different bacterial strains involved
 CC in e.g., nosocomial infections. Furthermore, the method is useful for
 CC diagnosing bacterial disease in plants and humans, monitoring for
 CC bacterial content and/or contamination in the environment, monitoring
 CC food for bacterial contamination, monitoring quality assurance/quality control of
 CC bacterial contamination, monitoring quality assurance/quality control of
 CC laboratory tests involving microbiological assays, tracing bacterial
 CC contamination and/or outbreaks of bacterial infections, genome mapping,
 CC monitoring bioremediation sites, and for monitoring agricultural sites
 CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-
 CC ADR37496 correspond to target nucleic acids containing an NbscNBI
 CC restriction site and used in the method of the invention.
 XX Sequence 6 BP; 1 A; 0 C; 3 G; 1 T; 0 U; 1 Other;
 SQ Query Match 66.7%; Score 4; DB 13; Length 6;
 Best Local Similarity 66.7%; Pred. No. 9.7e+08;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGAAGG 6
 Db 1 SGATGG 6
 RESULT 28
 ADR33235
 ID ADR33235 standard; DNA; 6 BP.
 XX ADR33235;
 AC ADR33235;
 XX 04-NOV-2004 (first entry)
 DT
 XX

DE Human nicking agent target DNA #776.
 XX ss; nicking agent; assay panel; diagnosis; expression pattern;
 KW DNA fingerprinting; nosocomial infection; microbiological assay;
 KW bacterial contamination; genome mapping; bioremediation.
 OS Homo sapiens.
 XX WO2004067765-A2.
 XX 12-AUG-2004.
 XX 29-JAN-2004; 2004WO-US002720.
 XX 29-JAN-2003; 2003US-0443811P.
 XX (KECK-) KECK GRADUATE INST.
 PI Van Ness J, Galas DJ, Van Ness LK;
 XX WPI; 2004-581010/56.
 XX Identifying nucleic acid sample source, useful for identifying bacterial
 PT strains involved in nosocomial infections, comprises treating the nucleic
 PT acid sample with components comprising a nicking agent under nicking
 PT conditions.
 XX Example 1; Page 84; 238pp; English.
 XX The invention relates to a method of treating a nucleic acid sample with
 CC components under nicking conditions, where the components comprise a
 CC nicking agent, and the conditions cause the nicking agent to nick the
 CC nucleic acid sample to thus produce a family of initiating
 CC oligonucleotide fragments, and subjecting one or more members of the
 CC family of initiating oligonucleotide fragments to a characterization
 CC process to thus provide results. The method is useful for creating an
 CC assay panel of diagnostic oligonucleotides that can identify any organism
 CC or individual. The method is useful for characterizing other DNA
 CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
 CC The method, kit or composition is useful for identifying the source
 CC of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
 CC non-human animal or human. The method is particularly useful for rapidly
 CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
 CC subspecies, and especially strains or individuals of the subspecies. It
 CC is especially useful for identifying different bacterial strains involved
 CC in e.g., nosocomial infections. Furthermore, the method is useful for
 CC diagnosing bacterial disease in plants and humans, monitoring for
 CC bacterial content and/or contamination in the environment, monitoring
 CC food for bacterial contamination, monitoring quality assurance/quality control of
 CC bacterial contamination, monitoring quality assurance/quality control of
 CC laboratory tests involving microbiological assays, tracing bacterial
 CC contamination and/or outbreaks of bacterial infections, genome mapping,
 CC monitoring bioremediation sites, and for monitoring agricultural sites
 CC for test crops, bacteria and recombinant molecules. This sequence
 CC corresponds to nucleic acid used in the method of the invention.
 XX Sequence 6 BP; 4 A; 0 C; 2 G; 0 T; 0 U; 0 Other;
 SQ Query Match 66.7%; Score 4; DB 13; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.7e+08;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GAAG 5
 Db 2 GAAG 5
 RESULT 29
 ADR32580/C
 ID ADR32580 standard; DNA; 6 BP.
 XX ADR32580;
 AC ADR32580;
 XX

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DT 04-NOV-2004 (first entry)
DE Human nicking agent target DNA #121.
KW ss; nicking agent; assay panel; diagnosis; expression pattern;
KW DNA fingerprinting; nosocomial infection; microbiological assay;
KW bacterial contamination; genome mapping; bioremediation.
XX
OS Homo sapiens.
XX
PN WO2004067765-A2.
XX
PD 12-AUG-2004.
XX
PF 29-JAN-2004; 2004WO-US002720.
XX
PR 29-JAN-2003; 2003US-0443811P.
XX
PA (KECK-) KECK GRADUATE INST.
XX
PI Van Ness J, Galas DJ, Van Ness LK;
XX WPI; 2004-581010/56.
XX
PT Identifying nucleic acid sample source, useful for identifying bacterial
PT strains involved in nosocomial infections, comprises treating the nucleic
PT acid sample with components comprising a nicking agent under nicking
PT conditions.
XX
PS Example 1; Page 73; 238pp; English.
XX
CC The invention relates to a method of treating a nucleic acid sample with
CC components under nicking conditions, where the components comprise a
CC nicking agent, and the conditions cause the nicking agent to nick the
CC nucleic acid sample to thus produce a family of initiating
CC oligonucleotide fragments, and subjecting one or more members of the
CC family of initiating oligonucleotide fragments to a characterization
CC process to thus provide results. The method is useful for creating an
CC assay panel of diagnostic oligonucleotides that can identify any organism
CC or individual. The method is useful for characterizing other DNA
CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC The method, kit or composition is useful for identifying the source
CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC non-human animal or human. The method is particularly useful for rapidly
CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
CC subspecies, and especially strains or individuals of the subspecies. It
CC is especially useful for identifying different bacterial strains involved
CC in e.g., nosocomial infections. Furthermore, the method is useful for
CC diagnosing bacterial disease in plants and humans, monitoring for
CC bacterial content and/or contamination in the environment, monitoring
CC food for bacterial contamination, monitoring quality assurance/quality control of
CC bacterial contamination, monitoring quality assurance/quality control of
CC laboratory tests involving microbiological assays, tracing bacterial
CC contamination and/or outbreaks of bacterial infections, genome mapping,
CC monitoring bioremediation sites, and for monitoring agricultural sites
CC for test crops, bacteria and recombinant molecules. This sequence
CC corresponds to nucleic acid used in the method of the invention.
XX
SQ Sequence 6 BP; 1 A; 2 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 66.7%; Score 4; DB 13; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GAAG 5
Db 5 GAAG 2
|||||
RESULT 30
ADR37262
ID ADR37262 standard; DNA; 6 BP.
XX

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AC ADR37262;
XX
DT 04-NOV-2004 (first entry)
XX
DE Human nicking agent DNA containing BstNBI restriction site #3682.
XX
KW ss; nicking agent; assay panel; diagnosis; expression pattern;
KW DNA fingerprinting; nosocomial infection; microbiological assay;
KW bacterial contamination; genome mapping; bioremediation.
XX
OS Homo sapiens.
XX
PN WO2004067765-A2.
XX
PD 12-AUG-2004.
XX
PF 29-JAN-2004; 2004WO-US002720.
XX
PR 29-JAN-2003; 2003US-0443811P.
XX
PA (KECK-) KECK GRADUATE INST.
XX
PI Van Ness J, Galas DJ, Van Ness LK;
XX WPI; 2004-581010/56.
XX
PT Identifying nucleic acid sample source, useful for identifying bacterial
PT strains involved in nosocomial infections, comprises treating the nucleic
PT acid sample with components comprising a nicking agent under nicking
PT conditions.
XX
PS Example 3; Page 105-219; 238pp; English.
XX
CC The invention relates to a method of treating a nucleic acid sample with
CC components under nicking conditions, where the components comprise a
CC nicking agent, and the conditions cause the nicking agent to nick the
CC nucleic acid sample to thus produce a family of initiating
CC oligonucleotide fragments, and subjecting one or more members of the
CC family of initiating oligonucleotide fragments to a characterization
CC process to thus provide results. The method is useful for creating an
CC assay panel of diagnostic oligonucleotides that can identify any organism
CC or individual. The method is useful for characterizing other DNA
CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC The method, kit or composition is useful for identifying the source
CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC non-human animal or human. The method is particularly useful for rapidly
CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
CC subspecies, and especially strains or individuals of the subspecies. It
CC is especially useful for identifying different bacterial strains involved
CC in e.g., nosocomial infections. Furthermore, the method is useful for
CC diagnosing bacterial disease in plants and humans, monitoring for
CC bacterial content and/or contamination in the environment, monitoring
CC food for bacterial contamination, monitoring quality assurance/quality control of
CC bacterial contamination, monitoring quality assurance/quality control of
CC laboratory tests involving microbiological assays, tracing bacterial
CC contamination and/or outbreaks of bacterial infections, genome mapping,
CC monitoring bioremediation sites, and for monitoring agricultural sites
CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-
CC ADR37496 correspond to target nucleic acids containing an NBstNBI
CC restriction site and used in the method of the invention.
XX
SQ Sequence 6 BP; 1 A; 0 C; 3 G; 1 T; 0 U; 1 Other;
Query Match 66.7%; Score 4; DB 13; Length 6;
Best Local Similarity 66.7%; Pred. No. 9.7e+08;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGAAGG 6
Db 1 SGATGG 6
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Search completed: July 20, 2005, 22:59:05

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Job time : 192.4 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 21:47:48 ; Search time 738.2 Seconds
(without alignments)
393.838 Million cell updates/sec

Title: US-09-735-363A-42

Perfect score: 6

Sequence: 1 ggaagg 6

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 4754

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_cm.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	6	100.0	6	AX175278	Sequence
2	5	83.3	5	CQ868961	Sequence
C 3	5	83.3	5	CQ868981	Sequence
4	5	83.3	5	CQ869110	Sequence
C 5	5	83.3	5	CQ869130	Sequence
6	5	83.3	5	AX207361	Sequence
7	5	83.3	6	AX236985	Sequence
8	5	83.3	6	AX557112	Sequence
9	5	83.3	6	AX805872	Sequence
C 10	5	83.3	6	S85691	S85691 p53 [human,
11	4.4	73.3	6	BD269460	BD269460 Mitomycin
12	4.4	73.3	6	BD269461	BD269461 Mitomycin
C 13	4.4	73.3	6	CQ755704	Sequence
C 14	4.4	73.3	6	CQ755751	Sequence
C 15	4.4	73.3	6	CQ756128	Sequence
C 16	4.4	73.3	6	CQ757942	Sequence
C 17	4.4	73.3	6	CQ757989	Sequence
C 18	4.4	73.3	6	CQ758366	Sequence
C 19	4.4	73.3	6	AX175264	Sequence

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AX175283	Sequence	6	6	AX175283	73.3	4.4	21
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AX552608	Sequence	6	6	AX552608	73.3	4.4	C 23
AX743310	Sequence	6	6	AX743310	73.3	4.4	24
AX743314	Sequence	6	6	AX743314	73.3	4.4	25
AX764742	Sequence	6	6	AX764742	73.3	4.4	C 26
AX764789	Sequence	6	6	AX764789	73.3	4.4	C 27
AX765166	Sequence	6	6	AX765166	73.3	4.4	C 28
AX805866	Sequence	6	6	AX805866	73.3	4.4	C 29
AX816715	Sequence	6	6	AX816715	73.3	4.4	30
CQ868975	Sequence	5	6	CQ868975	66.7	4	C 31
CQ868978	Sequence	5	6	CQ868978	66.7	4	C 32
CQ869012	Sequence	5	6	CQ869012	66.7	4	C 33
CQ869124	Sequence	5	6	CQ869124	66.7	4	C 34
CQ869127	Sequence	5	6	CQ869127	66.7	4	C 35
CQ869161	Sequence	5	6	CQ869161	66.7	4	C 36
CQ869240	Sequence	5	6	CQ869240	66.7	4	C 37
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AX103517	Sequence	5	6	AX103517	66.7	4	C 39
AX103518	Sequence	5	6	AX103518	66.7	4	C 40
AX155670	Sequence	5	6	AX155670	66.7	4	C 41
AX155671	Sequence	5	6	AX155671	66.7	4	C 42
S52581	Factor VIII	5	9	S52581	66.7	4	43
BD274470	IKAROS is	6	6	BD274470	66.7	4	44
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CQ755827	Sequence	6	6	CQ755827	66.7	4	C 47
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CQ758059	Sequence	6	6	CQ758059	66.7	4	49
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CQ815479	Sequence	6	6	CQ815479	66.7	4	C 51
AX068968	Sequence	6	6	AX068968	66.7	4	C 52
AX068969	Sequence	6	6	AX068969	66.7	4	C 53
AX103548	Sequence	6	6	AX103548	66.7	4	C 54
AX103549	Sequence	6	6	AX103549	66.7	4	C 55
AX103550	Sequence	6	6	AX103550	66.7	4	C 56
AX155701	Sequence	6	6	AX155701	66.7	4	C 57
AX155702	Sequence	6	6	AX155702	66.7	4	C 58
AX155703	Sequence	6	6	AX155703	66.7	4	C 59
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AX376659	Sequence	6	6	AX376659	66.7	4	C 62
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AX722302	Sequence	6	6	AX722302	66.7	4	66
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AX764859	Sequence	6	6	AX764859	66.7	4	C 68
AX764865	Sequence	6	6	AX764865	66.7	4	69
AX766268	Sequence	6	6	AX766268	66.7	4	70
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AX809607	Sequence	6	6	AX809607	66.7	4	C 72
AX809608	Sequence	6	6	AX809608	66.7	4	C 73
AX456098	Sequence	6	6	AX456098	60.0	3.6	74
AX456099	Sequence	6	6	AX456099	60.0	3.6	75
A70976	Sequence 30	5	6	A70976	56.7	3.4	C 76
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CQ869097	Sequence	5	6	CQ869097	56.7	3.4	C 82
CQ869115	Sequence	5	6	CQ869115	56.7	3.4	C 83
CQ869144	Sequence	5	6	CQ869144	56.7	3.4	C 84
CQ869238	Sequence	5	6	CQ869238	56.7	3.4	C 85
AX059005	Sequence	5	6	AX059005	56.7	3.4	C 86
AX805860	Sequence	5	6	AX805860	56.7	3.4	C 87
AX824553	Sequence	5	6	AX824553	56.7	3.4	C 88
AX824554	Sequence	5	6	AX824554	56.7	3.4	C 89
A93563	Sequence 1	6	6	A93563	56.7	3.4	C 90
CQ755683	Sequence	6	6	CQ755683	56.7	3.4	91
CQ755703	Sequence	6	6	CQ755703	56.7	3.4	C 92

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LOCUS	AX175278	Sequence 42 from Patent WO0144465.						
DEFINITION	AX175278	Sequence 42 from Patent WO0144465.						
ACCESSION	AX175278	Sequence 42 from Patent WO0144465.						
VERSION	AX175278.1	GI:14598646						
KEYWORDS								
SOURCE		synthetic construct						
ORGANISM		other sequences; artificial sequences.						
REFERENCE	1	(bases 1 to 6)						
AUTHORS	Phillips,N.C. and Filion,M.C.							
TITLE	Therapeutically useful synthetic oligonucleotides							
JOURNAL	Patent: WO 0144465-A 42 21-JUN-2001;							
FEATURES	Bioniche Life Sciences Inc. (CA)							
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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
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DB	1	GGAAGG 6						
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CQ868961	CQ868961	Sequence 115 from Patent WO2004074429.	5 bp	DNA	linear	PAT 13-SEP-2004		
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DEFINITION	CQ868961	Sequence 115 from Patent WO2004074429.						
ACCESSION	CQ868961	Sequence 115 from Patent WO2004074429.						
VERSION	CQ868961.1	GI:51998888						
KEYWORDS								
SOURCE		synthetic construct						
ORGANISM		other sequences; artificial sequences.						
REFERENCE	1	(bases 1 to 6)						
AUTHORS	freskg Rd.P.O., Gouliaev,A.H., Thisted,T. and Olsen,E.K.							
TITLE	Method for producing second-generation library							
JOURNAL	Patent: WO 2004074429-A 115 02-SEP-2004;							
FEATURES	Nuevolution A/S (DK)							
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CQ868981/c	CQ868981	Sequence 135 from Patent WO2004074429.	5 bp	DNA	linear	PAT 13-SEP-2004		
LOCUS	CQ868981	Sequence 135 from Patent WO2004074429.						
DEFINITION	CQ868981	Sequence 135 from Patent WO2004074429.						
ACCESSION	CQ868981	Sequence 135 from Patent WO2004074429.						
VERSION	CQ868981.1	GI:51998908						
KEYWORDS								
SOURCE		synthetic construct						
ORGANISM		other sequences; artificial sequences.						
REFERENCE	1	(bases 1 to 6)						
AUTHORS	freskg Rd.P.O., Gouliaev,A.H., Thisted,T. and Olsen,E.K.							
TITLE	Method for producing second-generation library							
JOURNAL	Patent: WO 2004074429-A 135 02-SEP-2004;							
FEATURES	Nuevolution A/S (DK)							
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
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CQ869130/c	CQ869130	Sequence 284 from Patent WO2004074429.	5 bp	DNA	linear	PAT 13-SEP-2004		
LOCUS	CQ869130	Sequence 284 from Patent WO2004074429.						
DEFINITION	CQ869130	Sequence 284 from Patent WO2004074429.						
ACCESSION	CQ869130	Sequence 284 from Patent WO2004074429.						
VERSION	CQ869130.1	GI:51999057						

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
1
AUTHORS freask Rd.P.O., Goulliaev,A.H., Thisted,T. and Olsen,E.K.
TITLE Method for producing second-generation library
JOURNAL Patent: WO 2004074429-A 284 02-SEP-2004;
Nuevolution A/S (DK)

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QY 2 GAAGG 6
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Db 5 GAAGG 1

RESULT 6
LOCUS AX207361 5 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 86 from Patent WO015571.
ACCESSION AX207361
VERSION AX207361.1 GI:15395161
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE
1 (bases 1 to 5)
AUTHORS Mauro,V.P., Edelman,G.M., Chappell,G.M., Jones,P.S., Owens,G. and Meech,R.
TITLE Methods of identifying synthetic transcriptional and translational regulatory elements, and compositions relating to same
JOURNAL Patent: WO 0155371-A 86 02-AUG-2001;
The Scripps Research Institute (US)

FEATURES
source Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="core motif"

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Matches 5; Conservative 0; Mismatches 0;

QY 2 GAAGG 6
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Db 1 GAAGG 5

RESULT 7
LOCUS AX236985 6 bp DNA linear PAT 26-SBP-2001
DEFINITION Sequence 4 from Patent WO0164959.
ACCESSION AX236985
VERSION AX236985.1 GI:15796558
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE
1 (bases 1 to 6)
AUTHORS Goudemir,J., Yates,S.C., Penning,M.T. and weijer van De,L.H.
TITLE Detection of hepatitis b virus rna

JOURNAL Patent: WO 0164959-A 4 07-SEP-2001;
Akzo Nobel N.V. (NL)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotides"

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QY 2 GAAGG 6
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Db 2 GAAGG 6

RESULT 8
LOCUS AX557112 6 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 10 from Patent WO0244353.
ACCESSION AX557112
VERSION AX557112.1 GI:25900165
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE
1
AUTHORS Wolffe,A.P.
TITLE Human Heparanase gene regulatory sequences
JOURNAL Patent: WO 0244353-A 10 06-JUN-2002;
Sangamo Biosciences Inc. (US)

FEATURES
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/db_xref="taxon:32630"
/note="EST1 binding site"

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Matches 5; Conservative 0; Mismatches 0;

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RESULT 9
LOCUS AX805872 6 bp DNA linear PAT 25-NOV-2003
DEFINITION Sequence 18 from Patent WO03060163.
ACCESSION AX805872
VERSION AX805872.1 GI:38522783
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE
1
AUTHORS van Eijk,M.J. and van Schaik,C.
TITLE Discrimination and detection of target nucleotide sequences using mass spectrometry
JOURNAL Patent: WO 03060163-A 18 24-JUL-2003;
Keygene N.V. (NL)

FEATURES
source Location/Qualifiers
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 DEFINITION Sequence 205 from Patent WO2003106674.
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 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
 TITLE Means and methods for regulating gene expression
 JOURNAL Patent: WO 2003106674-A 205 24-DEC-2003;
 Chromagenics B.V. (NL)
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 Db 6 GGAGGG 1
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 LOCUS CQ755751 6 bp DNA linear PAT 01-MAR-2004
 DEFINITION Sequence 252 from Patent WO2003106674.
 ACCESSION CQ755751
 VERSION CQ755751.1 GI:44846556
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
 TITLE Means and methods for regulating gene expression
 JOURNAL Patent: WO 2003106674-A 252 24-DEC-2003;
 Chromagenics B.V. (NL)
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 Db 6 GGAACG 1
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 DEFINITION Sequence 629 from Patent WO2003106674.
 ACCESSION CQ756128
 VERSION CQ756128.1 GI:44846933
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.

other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Otte,A.P., Kruckeberg,A.L. and Satijn,D.P.
 TITLE Means and methods for regulating gene expression
 JOURNAL Patent: WO 2003106674-A 629 24-DEC-2003;
 Chromagenics B.V. (NL)
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 Db 6 GGAGGG 1
 RESULT 16
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 LOCUS CQ757942 6 bp DNA linear PAT 01-MAR-2004
 DEFINITION Sequence 246 from Patent WO2003106684.
 ACCESSION CQ757942
 VERSION CQ757942.1 GI:44847963
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
 TITLE A method for the simultaneous production of multiple proteins;
 JOURNAL vectors and cells for use therein
 Patent: WO 2003106684-A 246 24-DEC-2003;
 Chromagenics B.V. (NL)
 FEATURES
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 Best Local Similarity 83.3%; Pred. No. 8.1e+09;
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 Db 6 GGAGGG 1
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 CQ757989/c
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 DEFINITION Sequence 293 from Patent WO2003106684.
 ACCESSION CQ757989
 VERSION CQ757989.1 GI:44848010
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
 TITLE A method for the simultaneous production of multiple proteins;
 JOURNAL vectors and cells for use therein
 Patent: WO 2003106684-A 293 24-DEC-2003;
 Chromagenics B.V. (NL)

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FEATURES
source
Location/Qualifiers
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/db_xref="taxon:32630"
/note="oligonucleotide patterns over-represented in STAR
elements"

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Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
Db 6 GGACGG 1

RESULT 18
LOCUS
CQ758366/c
DEFINITION
Sequence 670 from Patent WO2003106684.
ACCESSION
CQ758366
VERSION
CQ758366.1 GI:44848387
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
Otte,A.P., Kruckeberg,A.L. and Sewalt,R.G.
TITLE
A method for the simultaneous production of multiple proteins;
vectors and cells for use therein
JOURNAL
Patent: WO 2003106684-A 670 24-DEC-2003;
Chromagenics B.V. (NL)
FEATURES
source
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Dyad patterns over-represented in STAR elements"

ORIGIN

Query Match
Best Local Similarity 73.3%; Score 4.4; DB 6; Length 6;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
Db 6 GGACGG 1

RESULT 19
AX175264/c
LOCUS
AX175264
DEFINITION
Sequence 28 from Patent WO0144465.
ACCESSION
AX175264
VERSION
AX175264.1 GI:14598632
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 6)
AUTHORS
Phillips,N.C. and Fillion,M.C.
TITLE
Therapeutically useful synthetic oligonucleotides
JOURNAL
Patent: WO 0144465-A 28 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
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Query Match
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Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
Db 6 GGACGG 1

RESULT 20
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LOCUS
AX175281
DEFINITION
Sequence 45 from Patent WO0144465.
ACCESSION
AX175281
VERSION
AX175281.1 GI:14598649
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 6)
AUTHORS
Phillips,N.C. and Fillion,M.C.
TITLE
Therapeutically useful synthetic oligonucleotides
JOURNAL
Patent: WO 0144465-A 45 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
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Location/Qualifiers
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Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
Db 1 GGGAGG 6

RESULT 21
AX175283
LOCUS
AX175283
DEFINITION
Sequence 47 from Patent WO0144465.
ACCESSION
AX175283
VERSION
AX175283.1 GI:14598651
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 6)
AUTHORS
Phillips,N.C. and Fillion,M.C.
TITLE
Therapeutically useful synthetic oligonucleotides
JOURNAL
Patent: WO 0144465-A 47 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
source
Location/Qualifiers
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ORIGIN

Query Match
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Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
Db 1 GGGAGG 6

RESULT 22
AX552607
LOCUS
AX552607
DEFINITION
Sequence 47 from Patent WO0144465.
ACCESSION
AX552607
VERSION
AX552607.1 GI:14598651
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 6)
AUTHORS
Phillips,N.C. and Fillion,M.C.
TITLE
Therapeutically useful synthetic oligonucleotides
JOURNAL
Patent: WO 0144465-A 47 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
source
Location/Qualifiers
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LOCUS AX552607 6 bp RNA linear PAT 27-NOV-2002
 DEFINITION Sequence 23 from Patent WO02074963.
 ACCESSION AX552607
 VERSION AX552607.1 GI:25896616
 KEYWORDS Dengue virus type 2
 SOURCE Dengue virus type 2
 ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.

REFERENCE 1
 AUTHORS Markoff, L. and Zeng, L.
 TITLE Dengue viruses that are replication defective in mosquitoes for use as vaccines
 JOURNAL Patent: WO 02074963-A 23 26-SEP-2002;
 THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
 FEATURES source
 1. .6
 /organism="Dengue virus type 2"
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 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
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 Db 1 GTAAGG 6

RESULT 23
 AX552608/c
 LOCUS AX552608 6 bp RNA linear PAT 27-NOV-2002
 DEFINITION Sequence 24 from Patent WO02074963.
 ACCESSION AX552608
 VERSION AX552608.1 GI:25896617
 KEYWORDS Dengue virus type 2
 SOURCE Dengue virus type 2
 ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.

REFERENCE 1
 AUTHORS Markoff, L. and Zeng, L.
 TITLE Dengue viruses that are replication defective in mosquitoes for use as vaccines
 JOURNAL Patent: WO 02074963-A 24 26-SEP-2002;
 THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
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ORIGIN
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 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
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 Db 6 GTAAGG 1

RESULT 24
 AX743310
 LOCUS AX743310 6 bp DNA linear PAT 12-MAY-2003
 DEFINITION Sequence 2 from Patent WO03028764.
 ACCESSION AX743310
 VERSION AX743310.1 GI:30577236
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM

other sequences; artificial sequences.
 1
 REFERENCE
 AUTHORS Phillips, N.C., Filion, M.C. and Herrera-Gayol, A.C.
 TITLE Therapeutically useful triethyleneglycol cholesteryl oligonucleotides
 JOURNAL Patent: WO 03028764-A 2 10-APR-2003;
 Bioniche Life Sciences Inc. (CA) ; Phillips, Nigel C. (CA)
 FEATURES source
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 /note="Synthetic Oligonucleotide"

ORIGIN
 Query Match 73.3%; Score 4.4; DB 6; Length 6;
 Best Local Similarity 83.3%; Pred. No. 8.1e+09;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
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 Db 1 GGGAGG 6

RESULT 25
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 DEFINITION Sequence 6 from Patent WO03028764.
 ACCESSION AX743314
 VERSION AX743314.1 GI:30577240
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 1
 REFERENCE
 AUTHORS Phillips, N.C., Filion, M.C. and Herrera-Gayol, A.C.
 TITLE Therapeutically useful triethyleneglycol cholesteryl oligonucleotides
 JOURNAL Patent: WO 03028764-A 6 10-APR-2003;
 Bioniche Life Sciences Inc. (CA) ; Phillips, Nigel C. (CA)
 FEATURES source
 1. .6
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="Synthetic Oligonucleotide-3'-Triethyleneglycol (TEG) Cholesteryl Synthetic Oligonucleotide"

ORIGIN
 Query Match 73.3%; Score 4.4; DB 6; Length 6;
 Best Local Similarity 83.3%; Pred. No. 8.1e+09;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGG 6
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 Db 1 GGGAGG 6

RESULT 26
 AX764742/c
 LOCUS AX764742 6 bp DNA linear PAT 25-JUN-2003
 DEFINITION Sequence 212 from Patent WO03004704.
 ACCESSION AX764742
 VERSION AX764742.1 GI:32258950
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
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 REFERENCE
 AUTHORS Otte, A.P. and Kruckeberg, A.L.
 TITLE Dna sequences comprising gene transcription regulatory qualities and methods for detecting and using such dna sequences
 JOURNAL Patent: WO 03004704-A 212 16-JAN-2003;

Qy 1 GGAAGG 6
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Db 1 GGAAGG 6

Search completed: July 21, 2005, 00:00:41
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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53.568 Million cell updates/sec

Title: US-09-735-363A-25

Perfect score: 6

Sequence: 1 99999 6

Scoring table: IDENTITY_NUC

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Searched: 7173243 seqs, 3172129809 residues

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Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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2	6	100.0	6	9	US-09-735-363A-74
3	6	100.0	6	9	US-09-735-363A-79
4	6	100.0	6	9	US-09-879-668-5
5	6	100.0	6	14	US-10-127-645-2
6	6	100.0	6	14	US-10-127-645-4
7	6	100.0	6	15	US-10-280-274-5
25	6	100.0	6	9	US-09-735-363A-25
74	6	100.0	6	9	US-09-735-363A-74
79	6	100.0	6	9	US-09-879-668-5
14	6	100.0	6	14	US-10-127-645-2
15	6	100.0	6	15	US-10-280-274-5

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Sequence 20, Appl
Sequence 176692,
Sequence 176713,
Sequence 176718,
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Sequence 3, Appli
Sequence 6, Appli
Sequence 4, Appli
Sequence 44, Appl
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Sequence 39, Appl
Sequence 20, Appl
Sequence 6, Appli
Sequence 109, App
Sequence 110, App
Sequence 31, Appl
Sequence 33, Appl
Sequence 34, Appl

5 8 US-08-463-404-20
4 66.7 5 13 US-10-027-632-176692
4 66.7 5 13 US-10-027-632-176713
4 66.7 5 13 US-10-027-632-176718
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4 66.7 5 14 US-10-028-396A-3
4 66.7 5 14 US-10-172-620-6
4 66.7 5 14 US-10-185-369-4
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4 66.7 5 19 US-10-673-938-39
4 66.7 5 19 US-10-691-633-20
4 66.7 5 20 US-10-604-400-6
4 66.7 6 8 US-08-887-503-109
4 66.7 6 8 US-08-887-505-110
4 66.7 6 9 US-09-735-363A-31
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4 66.7 6 9 US-09-735-363A-34

ALIGNMENTS

RESULT 1
US-09-735-363A-25
; Sequence 25, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-25
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Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTGG 6
DB 1 GGGTGG 6

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US-09-735-363A-74
; Sequence 74, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
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; SOFTWARE: PatentIn version 3.0
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
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QY 1 GGGTGG 6
DB 1 GGGTGG 6

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; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
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; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Synthetic Oligonucleotide
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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTGG 6
DB 6 GGGTGG 1

RESULT 4
US-09-879-668-5
; Sequence 5, Application US/09879668
; Patent No. US20020091095A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Nigel C.
; TITLE OF INVENTION: Modulation of Fas and FasL Expression
; FILE REFERENCE: 02811-0241 42368-256931
; CURRENT APPLICATION NUMBER: US/09/879,668
; CURRENT FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: PCT/CA00/01467
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/228,925
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: US 60/266,229
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 09/735,363
; PRIOR FILING DATE: 2000-12-12
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; PRIOR APPLICATION NUMBER: US 60/170,325
; PRIOR FILING DATE: 1999-12-13
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide
US-09-879-668-5

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Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTGG 6
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Db 1 GGGTGG 6

RESULT 5
US-10-127-645-2
; Sequence 2, Application US/10127645
; Publication No. US20030045493A1
; GENERAL INFORMATION:
; APPLICANT: Filion, Mario C.
; APPLICANT: Phillips, Nigel C.
; TITLE OF INVENTION: Oligonucleotide Compositions and Their Use to Induce Differentiat

; FILE REFERENCE: 02811-0261 (42368-273010)
; CURRENT APPLICATION NUMBER: US/10/127,645
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US 60/286,158
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-127-645-2

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Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTGG 6
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Db 1 GGGTGG 6

RESULT 6
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; Sequence 4, Application US/10127645
; Publication No. US20030045493A1
; GENERAL INFORMATION:
; APPLICANT: Filion, Mario C.
; APPLICANT: Phillips, Nigel C.
; TITLE OF INVENTION: Oligonucleotide Compositions and Their Use to Induce Differentiat

; FILE REFERENCE: 02811-0261 (42368-273010)
; CURRENT APPLICATION NUMBER: US/10/127,645
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US 60/286,158
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-127-645-2

; OTHER INFORMATION: synthetic oligonucleotide
US-10-127-645-4

Query Match 100.0%; Score 6; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTGG 6
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Db 6 GGGTGG 1

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US-10-280-274-5
; Sequence 5, Application US/10280274
; Publication No. US20030119776A1
; GENERAL INFORMATION:
; APPLICANT: Filion, Mario C.
; APPLICANT: Phillips, Nigel C.
; TITLE OF INVENTION: Modulation of Fas and FasL Expression
; FILE REFERENCE: 02811-0242 42368-279803
; CURRENT APPLICATION NUMBER: US/10/280,274
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: PCT/CA00/01467
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 09/879,668
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: US 60/228,925
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: US 60/266,229
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 09/735,363
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/170,325
; PRIOR FILING DATE: 1999-12-13
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide
US-10-280-274-5

Query Match 100.0%; Score 6; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTGG 6
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Db 1 GGGTGG 6

RESULT 8
US-10-264-280-1
; Sequence 1, Application US/10264280
; Publication No. US20030125290A1
; GENERAL INFORMATION:
; APPLICANT: Filion, Mario C.
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Herrera-Gayol, Andrea C.
; TITLE OF INVENTION: Therapeutically Useful Triethyleneglycol Cholesteryl Oligonucleot

; FILE REFERENCE: 02811-0271 42368-277492
; CURRENT APPLICATION NUMBER: US/10/264,280
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 60/326,884
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
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; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-264-280-1

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-264-280-1

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Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTGG 6
|||||
Db 1 GGGTGG 6

RESULT 9

US-10-264-280-3/c
; Sequence 3, Application US/10264280
; Publication No. US20030125290A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario C.
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Herrera-Gayol, Andrea C.
; TITLE OF INVENTION: Therapeutically Useful Triethyleneglycol Cholesteryl Oligonucleotide
; FILE REFERENCE: 02811-0271 42368-277492
; CURRENT APPLICATION NUMBER: US/10/264,280
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 60/326,884
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-264-280-3

Query Match 100.0%; Score 6; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTGG 6
|||||
Db 6 GGGTGG 1

RESULT 10

US-10-264-280-5
; Sequence 5, Application US/10264280
; Publication No. US20030125290A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario C.
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Herrera-Gayol, Andrea C.
; TITLE OF INVENTION: Therapeutically Useful Triethyleneglycol Cholesteryl Oligonucleotide
; FILE REFERENCE: 02811-0271 42368-277492
; CURRENT APPLICATION NUMBER: US/10/264,280
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 60/326,884
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
; NAME/KEY: misc.feature
; OTHER INFORMATION: 3'-Triethyleneglycol (TEG) Cholesteryl Synthetic Oligonucleotide
US-10-264-280-5

Query Match 100.0%; Score 6; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTGG 6
|||||
Db 1 GGGTGG 6

RESULT 11

US-10-264-280-7/c
; Sequence 7, Application US/10264280
; Publication No. US20030125290A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario C.
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Herrera-Gayol, Andrea C.
; TITLE OF INVENTION: Therapeutically Useful Triethyleneglycol Cholesteryl Oligonucleotide
; FILE REFERENCE: 02811-0271 42368-277492
; CURRENT APPLICATION NUMBER: US/10/264,280
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 60/326,884
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
; NAME/KEY: misc.feature
; OTHER INFORMATION: 3'-Triethyleneglycol (TEG) Cholesteryl Synthetic Oligonucleotide
US-10-264-280-7

Query Match 100.0%; Score 6; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTGG 6
|||||
Db 6 GGGTGG 1

RESULT 12

US-10-168-327-1
; Sequence 1, Application US/10168327
; Publication No. US20030176381A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Fillion, Mario C.
; APPLICANT: Herrera-Gayol, Andrea C.
; TITLE OF INVENTION: Hyaluronic Acid in the Treatment of Cancer
; FILE REFERENCE: 02811-0211 (42368-274915)
; CURRENT APPLICATION NUMBER: US/10/168,327
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: PCI/CA00/01562
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-168-327-1

Query Match 100.0%; Score 6; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTGG 6
|||||
Db 1 GGGTGG 6

RESULT 13

US-10-190-312A-252/c

; Sequence 252, Application US/10190312A

; Publication No. US20030199468A1

; GENERAL INFORMATION:

; APPLICANT: Chromagenics B.V.

; APPLICANT: Otte, Arie P.

; APPLICANT: Kruckeberg, Arthur L.

; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities

; FILE REFERENCE: 2183-4993.1

; CURRENT APPLICATION NUMBER: US/10/190,312A

; CURRENT FILING DATE: 2002-07-05

; PRIOR APPLICATION NUMBER: 60/303,199

; PRIOR FILING DATE: 2001-07-05

; NUMBER OF SEQ ID NOS: 1079

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 252

; LENGTH: 6

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements

US-10-190-312A-252

Query Match 100.0%; Score 6; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTGG 6
|||||
Db 6 GGGTGG 1

RESULT 14

US-10-190-312A-1009/c

; Sequence 1009, Application US/10190312A

; Publication No. US20030199468A1

; GENERAL INFORMATION:

; APPLICANT: Chromagenics B.V.

; APPLICANT: Otte, Arie P.

; APPLICANT: Kruckeberg, Arthur L.

; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities

; FILE REFERENCE: 2183-4993.1

; CURRENT APPLICATION NUMBER: US/10/190,312A

; CURRENT FILING DATE: 2002-07-05

; PRIOR APPLICATION NUMBER: 60/303,199

; PRIOR FILING DATE: 2001-07-05

; NUMBER OF SEQ ID NOS: 1079

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1009

; LENGTH: 6

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Dyad patterns over-represented in STAR elements

US-10-190-312A-1009

Query Match 100.0%; Score 6; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTGG 6
|||||
Db 6 GGGTGG 1

RESULT 15

US-10-420-513A-3

; Sequence 3, Application US/10420513A

; Publication No. US20040058883A1

; GENERAL INFORMATION:

; APPLICANT: Phillips, Nigel C.

; APPLICANT: Fillon, Mario C.

; TITLE OF INVENTION: Oligonucleotide Compositions and Their Use for the Modulation of

; FILE REFERENCE: 02811-0301 (42368-283135)

; CURRENT APPLICATION NUMBER: US/10/420,513A

; CURRENT FILING DATE: 2003-04-22

; PRIOR APPLICATION NUMBER: US 60/374,540

; PRIOR FILING DATE: 2002-04-22

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 3

; LENGTH: 6

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic

US-10-420-513A-3

Query Match 100.0%; Score 6; DB 18; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTGG 6
|||||
Db 1 GGGTGG 6

RESULT 16

US-09-735-363A-60

; Sequence 60, Application US/09735363A

; Patent No. US20010041681A1

; GENERAL INFORMATION:

; APPLICANT: Fillon, Mario

; APPLICANT: Phillip, Nigel

; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides

; FILE REFERENCE: 02811-0181

; CURRENT APPLICATION NUMBER: US/09/735,363A

; CURRENT FILING DATE: 2000-12-12

; PRIOR APPLICATION NUMBER: 60/170,325

; PRIOR FILING DATE: 1999-12-13

; PRIOR APPLICATION NUMBER: 60/228,925

; PRIOR FILING DATE: 2000-08-29

; NUMBER OF SEQ ID NOS: 87

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 60

; LENGTH: 5

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Oligonucleotide

US-09-735-363A-60

Query Match 83.3%; Score 5; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGTGG 6
|||||
Db 1 GGGTGG 5

RESULT 17

US-09-735-363A-61

; Sequence 61, Application US/09735363A

; Patent No. US20010041681A1

; GENERAL INFORMATION:

; APPLICANT: Fillon, Mario

```
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 61
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-61

Query Match      83.3%; Score 5; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
Db      1 GGGTG 5

RESULT 18
US-10-185-369-2/c
; Sequence 2, Application US/10185369
; Publication No. US2003008256A1
; GENERAL INFORMATION:
; APPLICANT: Androphy, Elliot
; APPLICANT: Doshi, Nishita
; APPLICANT: Belayew, Alexandra
; TITLE OF INVENTION: Diagnosis and Treatment of Cancer
; FILE REFERENCE: 18475-041
; CURRENT APPLICATION NUMBER: US/10/185,369
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,384
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
US-10-185-369-2

Query Match      83.3%; Score 5; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
Db      5 GGGTG 1

RESULT 19
US-10-628-432-8/c
; Sequence 8, Application US/10628432
; Publication No. US20040142863A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Modified ADAMTS4 molecules
; FILE REFERENCE: AM101378
; CURRENT APPLICATION NUMBER: US/10/628,432
; CURRENT FILING DATE: 2003-07-29
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patentin version 3.1
```

```
; SEQ ID NO 8
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Kozak sequence
US-10-628-432-8

Query Match      83.3%; Score 5; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GGTGG 6
Db      5 GGTGG 1

RESULT 20
US-08-463-404-52
; Sequence 52, Application US/08463404
; Publication No. US20020127634A1
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Jerry W. Shay
; APPLICANT: Woodring E. Wright
; APPLICANT: Elizabeth Blackburn
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
; TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR
; TITLE OF INVENTION: TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,404
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/060,952
; FILING DATE: May 13, 1993
; APPLICATION NUMBER: 07/882,438
; FILING DATE: May 13, 1992
; APPLICATION NUMBER: 08/038,766
; FILING DATE: March 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 202/045
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-463-404-52

Query Match      83.3%; Score 5; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
```

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGG 5
|||||
Db 2 GGTGG 6

RESULT 21

US-09-735-363A-24
; Sequence 24, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-24

Query Match 83.3%; Score 5; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGTGG 6
|||||
Db 1 GGTGG 5

RESULT 22

US-09-735-363A-73
; Sequence 73, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 73
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-73

Query Match 83.3%; Score 5; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGTGG 6
|||||
Db 1 GGTGG 5

RESULT 23

US-09-879-668-4
; Sequence 4, Application US/09879668
; Patent No. US20020091095A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Fillion, Mario C.
; TITLE OF INVENTION: Modulation of Fas and FasL Expression
; FILE REFERENCE: 02811-0241 42368-256931
; CURRENT APPLICATION NUMBER: US/09/879,668
; CURRENT FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: PCT/CA00/01467
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/228,925
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: US 60/266,229
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 09/735,363
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/170,325
; PRIOR FILING DATE: 1999-12-13
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide
US-09-879-668-4

Query Match 83.3%; Score 5; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGTGG 6
|||||
Db 1 GGTGG 5

RESULT 24

US-10-280-274-4
; Sequence 4, Application US/10280274
; Publication No. US20030119776A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Fillion, Mario C.
; TITLE OF INVENTION: Modulation of Fas and FasL Expression
; FILE REFERENCE: 02811-0242 42368-279803
; CURRENT APPLICATION NUMBER: US/10/280,274
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: PCT/CA00/01467
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 09/879,668
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: US 60/228,925
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: US 60/266,229
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 09/735,363
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/170,325
; PRIOR FILING DATE: 1999-12-13
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic phosphodiester oligodeoxynucleotide
US-10-280-274-4

Query Match 83.3%; Score 5; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-10-280-274-4

Query Match 83.3%; Score 5; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09; 0; Indels 0;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

Qy 2 GGTGG 6
Db 1 GGTGG 5

RESULT 25

US-10-232-927A-70
; Sequence 70, Application US/10232927A
; Publication No. US20030190638A1

GENERAL INFORMATION:

APPLICANT: Michael D. West
; Calvin B. Harley
; Scott L. Weinrich
; Catherine M. Strahl
; Michael J. McEachern
; Jerry Shay
; Woodring E. Wright
; Elizabeth H. Blackburn
; Nam Woo Kim
; Homayoun Vaziri

TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
CONDITIONS RELATED TO
TELOMERE LENGTH AND/OR
TELOMERASE ACTIVITY

NUMBER OF SEQUENCES: 80

CORRESPONDENCE ADDRESS:

ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
; Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0

CURRENT APPLICATION DATA: US/10/232,927A

FILING DATE: 29-Aug-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/378,535

FILING DATE: 20-Aug-1999

APPLICATION NUMBER: 08/819,867

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Chambers, Daniel M.

REGISTRATION NUMBER: 34,561

REFERENCE/DOCKET NUMBER: 224/232

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 70:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 70:

US-10-232-927A-70

Query Match

Best Local Similarity 83.3%; Score 5; DB 16; Length 6;

Matches 5; Conservative 0; Mismatches 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
Db 2 GGGTG 6

RESULT 26

US-10-190-312A-214/c

; Sequence 214, Application US/10190312A

; Publication No. US20030199468A1

GENERAL INFORMATION:

APPLICANT: Chromagenics B.V.

APPLICANT: Otte, Arie P.

APPLICANT: Kruckeberg, Arthur L.

TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities

FILE REFERENCE: 2183-4993.1

CURRENT APPLICATION NUMBER: US/10/190,312A

PRIOR FILING DATE: 2002-07-05

PRIOR APPLICATION NUMBER: 60/303,199

PRIOR FILING DATE: 2001-07-05

NUMBER OF SEQ ID NOS: 1079

SOFTWARE: PatentIn version 3.1

SEQ ID NO 214

LENGTH: 6

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements

US-10-190-312A-214

Query Match

Best Local Similarity 83.3%; Score 5; DB 16; Length 6;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
Db 5 GGGTG 1

RESULT 27

US-10-190-312A-234/c

; Sequence 234, Application US/10190312A

; Publication No. US20030199468A1

GENERAL INFORMATION:

APPLICANT: Chromagenics B.V.

APPLICANT: Otte, Arie P.

APPLICANT: Kruckeberg, Arthur L.

TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities

FILE REFERENCE: 2183-4993.1

CURRENT APPLICATION NUMBER: US/10/190,312A

PRIOR FILING DATE: 2002-07-05

PRIOR APPLICATION NUMBER: 60/303,199

PRIOR FILING DATE: 2001-07-05

NUMBER OF SEQ ID NOS: 1079

SOFTWARE: PatentIn version 3.1

SEQ ID NO 234

LENGTH: 6

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements

US-10-190-312A-234

Query Match

Best Local Similarity 83.3%; Score 5; DB 16; Length 6;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
Db 6 GGGTG 2

RESULT 28

US-10-190-312A-242/c
; Sequence 242, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; TITLE OF INVENTION: methods for detecting and using such DNA sequences
; FILE REFERENCE: 2183-4993.1
; CURRENT APPLICATION NUMBER: US/10/190,312A
; CURRENT FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/303,199
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 242
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements
US-10-190-312A-242

Query Match 83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGTGG 6
|||
Db 6 GGTGG 2

RESULT 29

US-10-190-312A-280/c
; Sequence 280, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; TITLE OF INVENTION: methods for detecting and using such DNA sequences
; FILE REFERENCE: 2183-4993.1
; CURRENT APPLICATION NUMBER: US/10/190,312A
; CURRENT FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/303,199
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 280
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements
US-10-190-312A-280

Query Match 83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
|||
Db 5 GGGTG 1

RESULT 30

US-10-190-312A-334/c
; Sequence 334, Application US/10190312A

Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arie P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; TITLE OF INVENTION: methods for detecting and using such DNA sequences
; FILE REFERENCE: 2183-4993.1
; CURRENT APPLICATION NUMBER: US/10/190,312A
; CURRENT FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/303,199
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 334
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide patterns over-represented in STAR elements
US-10-190-312A-334

Query Match 83.3%; Score 5; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGTGG 6
|||
Db 5 GGTGG 1

Search completed: July 21, 2005, 07:13:15
Job time : 712.6 secs

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